



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 117363

To: Phuong Bui
Location: rem 2a15& 2c18
Art Unit: 1638
Tuesday, March 23, 2004

Case Serial Number: 10/059909

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 21:56:37 ; Search time 11831 Seconds
(without alignments)
11481.453 Million cell updates/sec

Title: US-10-059-909-15

Perfect score: 3134

Sequence: 1 ccacgcgtccgcccaggcg.....aaaaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.tod.*

36: em.htg.nam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1780.2	56.8	3167	8	AK072689 Oryza sat
2	1698	54.2	2851	8	AK072869 Oryza sat
3	1582.4	50.5	3003	8	BLYLOXB
4	1523.4	48.6	2516	6	AX660218 Sequence
5	1424.6	45.5	2115	6	AX653247 Sequence
6	1326	42.3	3007	6	AR404677 Sequence
7	1324	42.2	2595	6	AR404678 Sequence
8	1275.2	40.7	2845	8	AF271894 Zea mays
9	1275.2	40.7	2845	8	AF271894 Zea mays
10	1222.2	39.0	2818	6	AR438184 Sequence
11	1222.2	39.0	2818	6	AX469803 Sequence
12	1222.2	39.0	2818	6	AX469867 Sequence
13	1222.2	39.0	2818	8	BLYLOXA
14	1210.2	38.6	2928	8	AK073529 Oryza sat
15	1209	38.6	2613	6	AX653181 Sequence
16	1158.2	36.2	2910	8	BLYLOXC
17	1148.2	36.6	2830	6	E03480
18	1148.2	36.6	2830	8	OSLRNA
19	1130.2	36.1	2830	8	AK103565 Oryza sat
20	1119	35.7	2988	8	AB099850 Oryza sat
21	1119	35.7	3033	6	BD180907 Novel ric
22	1111.6	35.5	1726	8	AK071121 Oryza sat
23	1066.8	34.0	2559	6	AX653886 Sequence
24	1053.4	33.6	2267	8	AF149803 Zea mays
25	1017.8	32.5	1560	8	AK105792 Oryza sat
26	906.4	28.9	155106	8	AC117988 Oryza sat
27	850.6	27.1	3010	8	AK073570 Oryza sat
28	830.6	26.5	124138	8	AC093107 Oryza sat
29	796.6	25.4	2835	8	AF361893 Gossypium
30	777.6	24.8	2582	8	ATH302043 Arabidops
31	774	24.7	2930	8	AK102084 Oryza sat
32	772.6	24.7	2589	8	PD0418043 Prunus du
33	768.8	24.5	2655	8	FRX378035 Fragaria
34	767.6	24.5	2854	8	AD001673 Persea am
35	762.4	24.3	1814	8	TAU32428 Triticum ae
36	760	24.3	5013	8	AF465643 Zea mays
37	751.4	24.0	2574	8	AY182142 Brassica
38	749.6	23.9	200626	8	AC109929 Oryza sat
39	748.2	23.9	2888	8	NTRNLOX1 X84040 N.tabacum m
40	748.2	23.9	3390	6	AX644612 Sequence
41	729.6	23.3	2580	6	AX506809 Sequence
42	729.6	23.3	2580	6	AX651411 Sequence
43	729.6	23.3	2580	8	BT010358 Arabidops
44	729.6	23.3	2797	8	AY093104 Arabidops
45	729.6	23.3	2801	8	ATHLIP0X1 L04637 Arabidops1s

ALIGNMENTS

RESULT 1
AK072689
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J023143H13, full insert sequence.
3167 bp mRNA linear PLN 24-JUL-2003
ACCESSION
AK072689
VERSION
AK072689.1 GI:32982712
KEYWORDS
FLI_CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-Length cDNA Project Team;
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group, Otono, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, E., Ishibiki, J., Kawamata, M., Yoshimura, S., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., MIKANI,
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oato, N., Oca, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice
 Science 301 (5631), 376-379 (2003)
 2752273
 12869764
 2 (bases 1 to 3167)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
 Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
 Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
 Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
 Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
 Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
 Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
 Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K.,
 Nunasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
 Otsu, N., Ota, Y., Otono, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
 Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
 Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
 Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
 Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
 Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.
 Direct Submission
 Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)
 Tel: 81-29-838-7007, Fax: 81-29-838-7007
 This clone is one of the 28K full-length cDNA clones from japonica
 rice.
 URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
 Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
 Miuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 and Genome Exploration Research Group in Riken Genomic Sciences Center
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
 Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oato, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Indels

Gaps

4;

262

320

322

380

382

440

442

500

502

560

562

620

622

680

682

740

742

800

802

860

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1042

1100

1100

1100

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Qy	1043	GC	TTTGGGCATCTCAAGATGTCGGACCTTCCTTTGGGTACTGCTGCGAAGACGAGTCAATCGAGG	11012
Db	1101	GG	TTTGGGCGACCTCAAGATGTCAGACTTCCTTTGGGTACTCTCTTTAAGGCTATTGTTTGAGG	1160
Qy	1103	CT	GTTCCTTCAACACTCGGGGACTTTCTGTCGATGACAGCCCAAGGAGTTCGATTTCGTTTG	1162
Db	1161	GT	GTTCCTCCCAATATTAAGGACCTATGTGATACGACACCAAGGAGTTGATTCCTTTTC	1220
Qy	1163	AG	GATATCTCTCGGGCTCTAAGAGCTGGGCCGAGAGGCACGCCAACACCCACTGATAGCAG	1222
Db	1221	AAG	CATCATGGAACTCTATGAAGGTGGATTGAAGTGGCGCAATGCTCTGCACTAGCAG	1280
Qy	1223	AG	ATCAGGAGAAGATCCCGACGAGTTCTTTCGAGCATTTCTGCCGAAACGGTAGCCATG	1282
Db	1281	AG	ATCAAGAGAGAGATTCCCTTTGAACTTATTAAGATCTTTTGCCAGTTGCTGGC---G	1337
Qy	1283	ACC	ACCGCTAAAGATGCCCTTCCAAATGTCAATCAATCAGATGTGTTGAAAAGGCTC	1342
Db	1338	AT	CAAGCTTTGAAGTTACCCCTACCAATGTTATCAAA-----	1375
Qy	1343	CG	GAGTTTAAGTTTGGCTGGAGACTACGAAGATTTCGCGAGAGAGACACTTGCAGCG	1402
Db	1376	--	GAGGACAAATTTGCTTTGAGGACTGATGAGGAGTTTGACGAGAAATGCTCGCAGGAG	1433
Qy	1403	TGA	ACCCAGTAATCATCAAAACGTCTGACGGAGTTCCCGGTATAAAGCACCCCTGGACCCAA	1462
Db	1434	TTA	ACCCAGTATGATCAAGCGTCTGACGAATTTCCGCGCAAAAGTACTCTGGATCCAA	1493
Qy	1463	GG	CNATGAGAGACCAACGACGACAGATCACTGAACTCACTCCGCGCTAAACATGGGAG	1522
Db	1494	AT	GTGTACGGTGACCATACGAGCAAGATACCGAAGCTCATTTAAGCAACAATGGAGG	1553
Qy	1523	GC	CTGTCGGTGCAGAACGCACTGAGGAACAAGAGGCTTTTCCTCTATAGACCAATGAGCC	1582
Db	1554	GC	CTCAGGTGCAAAATGCACTGAGGGCAACAGGCTTTTCACTCTATAGACCAACGATC	1613
Qy	1583	ATT	TATGTCGGTACTCTCGACGAGATCAACGAGCTGGAGGGGAATTCATCTACGCCAGCA	1642
Db	1614	ACT	TATGTCGGCTTCCTCGAAGAATCAACAAGTTGACGGTAACTTCATATATGCGAGCA	1673
Qy	1643	GG	ACCTTACTTCTCTCAAGAGCATGGACGCTGAGACCCCTGGCCATCGAGCTGAGCC	1702
Db	1674	GG	ACCATTTGCTCTCTGAAGGACATGGACACCTTGAAGCCCTTGGCGATCGAGCTGAGCC	1733
Qy	1703	TG	CCCCACCTTGACGGCAGCAGCGCGCGGCTGACGAAGGTGTACACCCCGGCTCACA	1762
Db	1734	TG	CGCACCCCGATGGCCAGCAGACAGCGCCCGTACGAAGGTGTACACTCCAGCCACA	1793
Qy	1763	CG	CGCTGAGAGGCGACGCTTGGCAGCTCGCAAGGCTTATGCGTGGGTAAACGACTCTG	1822
Db	1794	CG	CGCTGAGAGCGCAATCTGCGAGCTCGCAAGGCTTACGCGCTTCGCTCAACGACTCTG	1853
Qy	1823	CT	TGGCATCAGCTGTATCAGCACTTGGCTGAACACGACGCGGTGATCGAGCCGTTGGTAA	1882
Db	1854	CT	TGSCACACAGCTGTATCAGCCATCTGGCTGAACACTCAGCGCGTGTATCGAGCGTTG	1913
Qy	1883	TC	CGCAAAACCGGACGCTCAGCGTGTGTGATTCCTGTGCAACAGCTGTCTGAGCCCCG	1942
Db	1914	TC	CGACGAACCGGACGCTCAGCGTGTGTGACCGCCGCTGCAAAAGCTGTGAGCCCCG	1973
Qy	1943	AC	CGTGACGCTGAACATCAACGCTGCGACGCGCAGACACTCATCAACGCGCGGGCG	2002
Db	1974	AC	CGGACGATGAACATCAACGCTGTGCAACGCGCAGACACTCATCAACGCGCGATGG	2033
Qy	2003	TC	TCGAGCGCACCGTGTTCCTCTGCAAGTACGCGCTGGGGATGTCTGGCAGACGTTTACA	2062
Db	2034	TC	TCGAGAAGAACGCTCTTCCAGGCAAGTACGCGCTCGAGATGTCTCTCGTGTGTACA	2093
Qy	2063	AG	AGCTGGATTTCAACGACGAGGCTCTCCAGCAGATCTCTGCTCAAGAGAGTGTGGCTG	2122
Db	2094	AG	AATCTGGAAGTTCAACGACGAGGCTCTCCCGTCGATCTCTGTCGAAGAGAGGGTGG	2153
Qy	2123	TG	CGGACCACTCAAGGCCCATATGTGTCTCGACTGTGTTGATCAAGAGACTACCCCTATGCG	2182

Db	2154	TTGCCGACCCGACGAGCCCGGTACAACGTCGCGGTGCTGTGATCAAGAGCATACCCCTGACGCG	2213
Qy	2183	TTGACGGCTCGTTCATCTGCTGGGCGCATCGAGCGGTGGGTCAAGGAGTACTCTGGAACATCT	2242
Db	2214	TGGACGGCTGCTCATCTGCTGGGCGATCGAGCGGTGGGTGGCGAGTACTTGGCCATCT	2273
Qy	2243	ACTACCTTAACGACGGCGAGCTCAGCGTGACGTGAGCTGCAAGGCGTGTGTGAAAGGAGG	2302
Db	2274	ACTACCCCAACGACGGCGTCTCCGGCGACGAGGAGCTGCAAGGCGTGTGTGAAAGGAGG	2333
Qy	2303	TGCGTGAGG-AGGCGCACGGCGACTCAAGGACCGAGACTGTGTGGCCAGGATGGACACC	2361
Db	2334	TGCGGAGGTGGGCCATGCGGACCTCAAGGACGAGACTGTGTGGCCCAAGATGGACACC	2393
Qy	2362	GTCACGAGCTGGCTAGGGCGTGGACGACCATCATCTGGGTGGCATCCGCGCTGCAAGCG	2421
Db	2394	GTCACGAGCTCACCGGGCGTGACCATCATCATCTGGATCGCGTGGCGCTGCAAGCG	2453
Qy	2422	GCTGTCAACTTTGGGCGAGTACCATACGCGGGGTACTCCCGAACCGGCGACGGCCAGC	2481
Db	2454	CGGCTCAACTTTGGCGCAGTACCCTGTCGCGGGTCTCTCCGAAACCGGCGACGGTGAAC	2513
Qy	2482	CGGCGCCGATCCGGAGCCAGGACGACCACTACAAGAGCTGGGAGCGGGGCAAGAAG	2541
Db	2514	CGGCGCGGATCCGGAGCCGGGACCGAGGAGTACGCGAAGCTGGAGCGCGCGGTGAC	2573
Qy	2542	GAGCGGACATGCTGTTCATCCGACCATCACAGCGAGTTCAGACCATCTCTGGGCGATC	2601
Db	2574	GAGCGGACCTGTGTTCATCCACAATCACCAGCGAGTTCAGACCATCTCTCGGCGATC	2633
Qy	2602	TCGCTCATCAGATCTCTCTCCAAAGCACTCCTCCGAGGAGTGTAACCTCGGCCAGCGTGAC	2661
Db	2634	TCGCTCATCAGATCCTGTCCAAAGCACTCCTCCGAGGAGTCTACCTCGGCCAACGCGAC	2693
Qy	2662	GAGCTGATCGCTGGACGTGACAGCGGAGCGCTGATGCTGTTCAAAGATTCGGGAGC	2721
Db	2694	ACGCCGGA---GTGGACGTGGAGCGCCAAAGCGCTGACGCGTTCAGAGGTTTCGGCAGC	2750
Qy	2722	CGGCTGGTCAGATTGAGATCGGATCGGATCAAGACATGAACGACAGTCCGGACTTGAAGAAC	2781
Db	2751	CGGCTGGTGATATCGAGAACCGGATCAAGGACATGAACGGCAACTCGGCGCTCAAGAAC	2810
Qy	2782	CGGAAGGGGCTGTGGAATTCGCGTACATGCTGCTGTATCCCAACAGCTCGGACGTTACC	2841
Db	2811	CGGAACGGGCGGTGAAGATCGCGTACATGCTCTGTATCCCAACACGTCGGATGTCACC	2870
Qy	2842	GGCGAAGGCCGAGGGGCTTACTGCCCATGGGCATTCCCAACAGCATCTCCATATGAGCC	2901
Db	2871	AAGGAGAGGGCCAGGGCTCACCGGCATGGGCATCCCAACAGCATCTCCATCTAGTC	2930
Qy	2902	TGG	2904
Db	2931	TCG	2933

RESULT 2	AK072869	2851 bp	mRNA	linear	PLN 24-JUL-2003
LOCUS	AK072869				
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J023143017, full insert sequence.				
ACCESSION	AK072869	1	GI:32382892		
VERSION	F01_CDNA; CAP trepper.				
KEYWORDS	Oryza sativa (japonica cultivar-group)				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1				
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,				

Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

2 (bases 1 to 2851)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, Y., Ikeda, R., Imamura, K., Imoto, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariawa, R., Niikura, J., Nishi, K., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingayama, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdnaol.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Iida, Y., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,

Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

Location/Qualifiers

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ORIGIN

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RESULT 3

LOCUS	3003 bp	mRNA	linear	PLN 06-JUL-1999
BLYLOXB	Hordeum vulgare	lipoxygenase (LoxB)	mRNA, complete cds.	
BLYLOXB	Hordeum vulgare	lipoxygenase (LoxB)	mRNA, complete cds.	

REIWORDS
SOURCE
ORGANISM

Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triiceae; Hordeum.

REFERENCE
AUTHORS

van Mechelen, J.R., Schuurink, R.C., Smits, M., Graner, A., Douma, A.C., Sedes, N.J., Schmitt, N.F. and Valk, B.E. Molecular characterisation of two lipoxigenases from barley (*Hordeum vulgare* L.). *Plant Mol. Biol.* 39 (6): 1283-1298 (1999).

[illegible]

Sedee, N.J., Schmitt, N.F. and Valk, B.E.
Molecular characterization of two lipoxigenases from barley
Plant Mol. Biol. 39 (6), 1283-1298 (1999)
99308521

JOURNAL
MEDLINE

Plant Mol. Biol. 39 (6), 1283-1298 (1999)
99308521
10380814
2 (bases 1 to 3003)
H. M. W. M. T. P.

PUBMED
REFERENCE
A117506

10380814
2 (bases 1 to 3003)
Van Mechelen, J.R.
Direct Submission
Submitted (08-NOV-1994) pln@biotechnology.com Center for

JOURNAL Submitted (10-JUN-1997) Plantbiotechnology, Center for
Phytotechnology, Wassenaarseweg 64, Leiden 2333AL, Netherlands
REMARK Sequence update by submitter
COMMENT On Jun 10, 1997 this sequence version replaced gi:565215.
Nucleotide sequence analysis revealed that homology with barley
cDNA LoxA (accession number L35931) and the rice L-2 lipoxigenase
(accession number X64396) was significantly higher than that with
dicotyledonous lipoxigenases. mRNAs corresponding to the three
barley lipoxigenase cDNAs are specific for developing and
germinating grain, and do not occur in older vegetative tissues. Up
to now two isoenzymes, lipoxigenase 1 and 2, have been purified
from germinating barley, lipoxigenase 1 and 2, have been purified
encodes lipoxigenase 1, since the amino acid sequence of
proteolytic fragments of isoenzyme 1 were identical to predicted
partial amino acid sequences of the LoxA clone, but not to those of
the LoxB and LoxC clones.
Southern blotting experiments indicate a low copy number of the
three lipoxigenase genes.

FEATURES

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Db 2442 CCAGCCAGTTCCAGACCATCTCTGGGCATCAGCTCATCGAGATCTCTCCAAAGCACTCT 2501
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Qy 2753 CGATGAACGACAGTCCGAGCTTTGAAGAACCGGAAGGGCCTGTGGAATGCGGTACATGC 2812
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Qy 2813 TGCTGTACCCCAACGCTGCGAGCTTACGGCGAGAGCGGCGCTTACTGCGATGG 2872
Db 2679 TGCTGTACCCCAACGCTGCGAGCCCAACCGGAGAGGCGCTGGGGCTCACCGCCATGG 2738
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Db 2739 GCATCCCAACAGCGCTCTCCATCTGAGC 2766

RESULT 4
AX660218 LOCUS 2516 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 575 from Patent WO03000906.
ACCESSION AX660218
VERSION AX660218.1 GI:29162108
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1
AUTHORS Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Katagiri, F., Kreps, J., Provart, N., Riecke, D. and Zhu, T.
TITLE Plant disease resistance genes
JOURNAL Patent: WO 03000906-A 575 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
source 1.2515
/organism="Oryza sativa"
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ORIGIN
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Best Local Similarity 77.5%; Pred No. 4e-213;
Matches 2004; Conservative 0; Mismatches 456; Indels 127; Gaps 8;
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Qy 303 CCGCGGACCGGTGAGGCTGCTCAGAGAGGAGTGTGACGCTCGCGCACTTCAACGCTTC 362
Db 69 CCGTGGAGCGGCGGTCTGGTGAAGAGAGAGTGTCTCGGCTCGCGCACTTCCAGCCTTC 128
Qy 363 GCTCTCGACGCGCTGACAGGATCTCTCGGTGGGACGACGCGCTGCGCTTCCAGCTCGT 422
Db 129 CTTCTCGACGCGCTCCAC----- 147
Qy 423 CAGCGCCACCGCGGCGGACCCCAACAGGGGCGCTGGCAAGGTGGGAGGCGGCGCA 482

QY 2637 CGAGGTGTACCTCGGCGAGCGGTGACGCGCTGTGCTGGACGTCAGACCGCCAGGCGCT 2696
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 QY 2697 GGATGCGTTCAAAAGATTTCGGGAGCGCGCTGGTGCAGATTGAGAAATCGGATCAAGACGAT 2756
 Db 2348 GGACGCGTTCAAGAGGTTTCGGGAGCGCGCTGGTGCAGATTGAGAAATCGGATCAAGACGAT 2407
 QY 2757 GAAACGACAGTCCGACGTTGAAGAACCGGAGGCGCTGTGGAATGCGGTACATGCTGCT 2816
 Db 2408 GAACGCGAATCGGCGCTCAAGAACCGGAGCGCGCTGGAATGCGGTACATGCTGCT 2467
 QY 2817 GTACCCC 2823
 Db 2468 GTACCCC 2474

 RESULT 5
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 LOCUS 2115 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 3117 from Patent WO03000898.
 ACCESSION AX653247
 VERSION AX653247.1 GI:29156061
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1
 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Karagiri, P., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
 Plant genes involved in defense against pathogens
 Patent: WO 03000898-A 3117 03-JAN-2003;
 Syngenta Participations AG (CH)
 Location/Qualifiers
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 Matches 1721; Conservative 0; Mismatches 394; Indels 30; Gaps 3;

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 QY 814 AATCCTGGACCATACAGGAGCATGATCGGCTCTACCGTTACGACTACTACATGACCTT 873
 Db 61 AAAATTGGACCATACAGGAGCATGACCGTATCTACCGTTATGATTACTATACGACCTT 120
 QY 874 GGTGATCCGCAAGGCGAGGACGCTCGGCCGATCTCCGTGGCGAGCCAAAGAACAC 933
 Db 121 GGCCAAACAGAACAAAGCAGTAACTAGTAGACGACGCTCTCGGTGGCAGCCAAAGAACTC 180
 QY 934 CCGTATCCCGCTCGCTCGAGACTGGCGGCACTCCACAAAGAAAGAACCCAAATTCGGAG 993
 Db 181 CCTATCCCGCTCGAGGCAACTGGCGGGGCCCAACAAAGAACTGACCCAAATACAGAA 240
 QY 994 AGCAGGCTTTTCTGTGTGAACCTGAACATCTACGTCGCGGCGTGAACAAAGCTTTGGGCAT 1053
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 QY 1054 CTCAGATGTCGACTTCTTGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCA 1113
 Db 301 CTCAGATGTCGACTTCTTGGTACTCTCTTAAAGGCTATTGTCAGGAGGTTCTCCCA 360
 QY 1114 AACTGGGGACTTTCTGTCGATGACACGCCCAAGGATTCGATTCTGTTTGAAGGATATCTTC 1173

Db 361 ATAAATAGGACCTATGTGATACGACACAAAGGAGTTGATTCTTTTCAAGACATCATG 420
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 Db 421 GAACTCTATTAAGGTGGATTGAAAGTGGCCATGCTCTGCACTAGCAGAGATCAAGAAG 480
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 QY 1294 AAGATGCCCTTCCAAATGTCTCAAAATCAGATGTTGTAAGAAAGGCTCCGAGGATTAAG 1353
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 QY 1354 TTTGGCTGAGGACTGACGAAGATTTCGCGAGAGAGACACTTTCAGAGGCGTGAACCCAGTA 1413
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 Db 1114 CGGCAAGCTCAGGCTGCTGATCCCGTGCAAGCTGCTGAGCCGCTGAGCCGCTACCGTGACG 1173
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 Db 1174 ATGAACATCAACGCTTGGCAGCGCAGCACTCATCAACGCGGATGGCATCTTCGAGAA 1233
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 QY 2074 TTCAACGAGGAGGCTCTCCAGCAGATCTCGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAG 2133
 Db 1294 TTCAACGAGGAGGCTCTCCCGTCGATCTCGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAG 1353
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 Db 1354 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1413
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 Db 1414 GTGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1473

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Db 1474 GACGGCCTGTCTCGCGCGCAGAGAGCTCAGGCGTGTGGAGAGGTGCGGAGGTC 1533
QY 2314 GCGCACGGCAGCTCAAGAGCAGAGAGCTGTGGCCAGAGATGACACCGTCCAGCAGCTG 2373
Db 1534 GGCATCGGACCTCAAGAGCAGAGAGCTGTGGCCAGAGATGACACCGTCCAGAGCTC 1593
QY 2374 GCTAGGGCGTGCAGACCATCATCTGTGGTGGCATCTCGCGCTGACCGCGCTGTCAACTTT 2433
Db 1594 ACCGGGCGTGCACCATCATCTGTGATCGCTCGCGCTGACCGCGCGTCAACTTC 1653
QY 2434 GGGCAGTACCATACCGCGGTACCTCCGAAACCGCGCGACGCGCAGCGCGCGCGATG 2493
Db 1654 GGCAGTACCGGTACCGCGGTTCCTCCGAAACCGCGCGAGCTGAGCGCGCGCGATG 1713
QY 2494 CCGAGCCAGCGCAGCAGCACTCAAGAGCTTGGAGCGGGCAGAGGAGCGGACATG 2553
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Db 1891 TGGAGTTCAGACCGCAGGCGGTGGAGCGGTTCAGAGGTTCGGGAGCGGCTGTGCGAT 1950
QY 2734 ATTGAGATCGGATCAAGAGCATGAACAGCAGTCCGGAATTCGAAGAACCGGAGGGGCT 2793
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QY 2854 GAGGGGTACTGCCATGGGCATTCACAGCATCTCCATATGA 2898
Db 2071 CRAAGGCTCACCAGGCTGGCATCCCAACAGCATCTCCATCTGA 2115

RESULT 6
AR404677
LOCUS 3007 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627797.
ACCESSION AR404677
VERSION AR404677.1 GI:40153344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 3007)
AUTHORS Duvick,J., Maddox,J.R. and Keller,N.P.
TITLE Maize lipoxygenase polynucleotide and methods of use
JOURNAL Patent: US 6627797-A 1 30-SEP-2003;
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 42.3%; Score 1326; DB 6; Length 3007;
Best Local Similarity 71.7%; Pred. No. 2.8e-184;
Matches 1906; Conservative 0; Mismatches 680; Indels 72; Gaps 10;

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QY 366 CTTGACGGCGTCCACAGGATCTCTGGCTGGGACGAGCGGCTGCGCTTCCAGCTCTGTCAG 425
Db 181 CGTTGACAGCATCAGCGAGTTCTCTGGCA-----AGGGGGTCACTTGGCAGCTCATCAG 234
QY 426 CGCCACCGCGCGACCCAGCAACCGGGGGCGGTGGCAAGGTGGGGAGGCGGCGCACCT 485
Db 235 CTCCACCTCTCTGACGCGCAACACCGCGGGCGGTGGGGCGGAGCGCAACCT 294
QY 486 GGAGAGGCGGTGTGTCTGCTCAAGTCCAGGGGACGGGAGACCTGTGTACCGGTGAG 545
Db 295 GGAGAGGTGGTGAAGCTTGGCTGCGCTGACACCGGCGAGTCCAAAGTTCGGCGCTCAC 354
QY 546 CTTGAGTGGGA---CGAGTCCAGAGGCATCCCGGGGCGCTCTGCTCAGGAACTTGCA 602
Db 355 GTTCGACTGGAGGTGGAGAGCTGGAGTCCCGGGGCGCTGTCTCAAGAACACCA 414
QY 603 GCACGCGAGTTCTTCTCAAGAGCTCACCTCGAGGGGTGCCAGGAGGAGGACCGT 662
Db 415 CGCGCGCGAGTTCTTCTCAAGACATCACCTCGACGAGTGGCGCGCGCGCGCGCT 474
QY 663 CGTCTTCTGTCGCCAACTCTGTGGGTCTACCCGCAACAAGCTCTACTCCAGGAACGCACTT 722
Db 475 CACCTTCTGTCGCCAACTCTGTGGGTCTACCCCGGGGCGAGTACCGCTTCAACCGGTCTT 534
QY 723 CTTGCCAAAGCAACCTATCTGCGAGCAAAATCCCGGGGCGGTGTGTGCTTATCGGCA 782
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QY 843 CGTCTACGTTACGACTACTACAAATGACTTGTGTATCCCGCAAGAGGCGGAGAGCAGC 902
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QY 903 TCGGCGGATCTCGGTGGCGAGCAAGAACACCGGTATCCCGCTGCTGCGAGAACTGGCGG 962
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Db 826 CTACGTCCCGGGAGCGAGCGCTTGGCCACCTCAAGATGTCGACTTCTTGGGTACTC 885
QY 1083 GCTGAAGACGATCATCGAGCTGTCTTCCAAACACTGGGAGCTTTCTGTGATGACAGCC 1142
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Db 1121 -----GAGGACAAAGCGGTGGAGGACCGAGGAGTTTCG 1158
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Db	2239	GAACAGGCCCA	CGGTGAGCCGGGCGCGGATGCTCCGGAGCCCGGAGCAAGAGTACGAGGA	2298
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Db	2299	GCTGG-----	AGCGGACCCGGAGCGCGCTTCATCCACACCATCACGAGCCAGAT	2349
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Db	2350	CCAGACATCATCGGCATCTCGCTCATCGAGATCTCTTCCAAAGCATCTCTCCGACAGGT	2409	
Qy	2643	GTACTCTGGGCCAGCGTGACGAGCTGATCGCTGGAGCTCAGAGCCAGCCAAAGCGCTGGATGC	2702	
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Qy	2703	GTTCAAAGAATTCGGGACCGGCTGTGTGCAGATGTGAAATPGGAATPGGATCAAGACGATGAACGA	2762	
Db	2467	GTTCAAGAGGTTTCAGCGACCGCTGTGTCAAGATCGAGGGCAAGGTGTTGGCGCGAGAACC	2526	
Qy	2763	CAGTCCGGACTTGAAGAACC	CGGAAGCGGCTGTGGAAATGCCCCTACATGCTGCTGTACCC	2822
Db	2527	CGACCCGCACTGAGGAACAGGAACGCCGCCCGGAGTTCCTCTATGCTGCTCTATCC	2586	
Qy	2823	CAACACGTCCGACGTTTACCGGCGAGAGGCGGAGGGGCTTACTGCCATGGGCATTCCCAA	2882	
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Qy	2883	CAGCATCTCCATATGAC	2900	
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DEFINITION	Sequence 2 from patent US 6627797.			
ACCESSION	AR404678			
VERSION	AR404678.1	GI:40153345		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 2595)			
AUTHORS	Duvick,J., Maddox,J.R. and Keller,N.P.			
TITLE	Maize lipoxygenase polynucleotide and methods of use			
JOURNAL	Patent: US 6627797-A 2 30-SEP-2003;			
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Qy	246	CGGGTTCGGGACCGGCTGACCGGAAAGAACAGGAGGCGTGGAGCGAGGGCAAGATCCG	305	
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Qy	306	CGCACGGTGAGGCTGGTCAAGAAGGAGGTGCTGGAGCTCGCGACTTCAAGCCCTCGCT	365	
Db	58	-GGACGGTGTGCTCATGCGGAAAGAACGTGCTGGACCTCAAGCATTCGGGCCACCGT	116	
Qy	366	CTTCGACGGGCTCCACAGGATCCTCGGCTGGGACGACGCGGTGCTTCAGCTGTCAG	425	
Db	117	CGTTGACAGCATCAGCGAGTTCCTCGGCA-----AGGGGGTCACCTGCGAGTCAATCAG	170	
Qy	426	CGCACCGGGCGGACCCAGCAACGGGGGCGTGCAGAGGTGGGAAGCGGCGCACCT	485	
Db	171	CTCAACCTCTGTCGACGCGCAACACGGCAACCGCGGGCGGGTCTGGGGCGGAGCGCACT	230	
Qy	486	GGAGGAGGGGCTGCTGCTCGCTCAAGTTCACGGCGGACGGGGAGACCGCTGTACCGGTGAG	545	

[illegible]

Db	1275	CATCCTGGACCAACACAGACCGCTTTCATGCGGTTCTCTATCGAGCTCAACAACCTGGAGGG	1334
Qy	1523	GAACTTTCATCTTAGCCAGCAGGACCCCTACTGTCTTCTGAAGAGCATGGCACGCTGAAGCC	1682
Db	1335	CAACTTCATCTACGCCACACGAGACGCTCTTCTTCTCGCGGCGACGGCAGGCTCGCGCC	1394
Qy	1583	CCTGGCCATCGAGCTGAGCCTGCCCCACCCTGTAGCGGCACAGCGCGCGGTTCAGCAA	1742
Db	1395	CCTCGCCATCGAGCTTAGCGAGCGGTATCTGACGCGGGACCTCACCGTGGCCCAAGAGCAA	1454
Qy	1743	GGTGTACACCCCGGCTCACACCGCGGTCGAGGCGCACGCTGTGCAGCTGCCCAAGGCTTA	1802
Db	1455	GGTCTACACGCCGGCGTCCAGCGCGGTCTGAGGCGCTGGGTGTGGAGCTCGCAAGGCTTA	1514
Qy	1803	TGCTCGGTAAACGACTCTCGCTGGCATCAGCTGTATCAGCCATCTGGCTGAACACGACGCG	1862
Db	1515	TGTGCGCGTCAACCGACTCTGGCTGGACCAACTCTGTACGACACTGTGGCTGAACACCCACGC	1574
Qy	1863	GGTGATCGAGCGGTTCTGTAATCCGCAAAACCGGACGCTCAGCGTGTGTGCATCCCGTGCA	1922
Db	1575	GGTGATGAGCGGTTCTGTGATTCGGACGAACCGCGAGCTGAGGTGACGCAACCGGTGCA	1634
Qy	1923	CAAGCTCTGAGCGCCGCACTACCGTGACACGCTGGAACATCAACGCCCTTGSCACGCCAGAC	1982
Db	1635	CAAGCTCTTAGCTCGCACTTCGCGACACCATATGACCATCAACCGCTGGCGGGGAGAC	1694
Qy	1983	ACTCATCAACGCGGGCGGCTCTTCGAGCGCACCGGTCTCCCTGCAAGGTACGCGCTGGG	2042
Db	1695	GCTCATCAACGGCGCGGCACTTTCGAGATGACCGCTTCTCCGCGCAAGTACGCGCTGGG	1754
Qy	2043	GATGTCGGCAGACGCTGTACAAAGAGCTGGAAATTTCAACGACGAGGCTCTCCACGACATCT	2102
Db	1755	CATGTCCTCGGTGTACAAAGAGCTGGAATCTTCCGAGCAGGGCTCTCCGCGGACCT	1814
Qy	2103	GTCTAAGAGAGGTGTGGCTGTGCGGACACGAGTCAAGCCCATATGGTGTCCGATGCTGAT	2162
Db	1815	GTCTAAGAGGGGCGTGGCGGTGCGGACCGCTCCAGCCCGTACAAGGTGCGGCTGTGAT	1874
Qy	2163	CAAGGACTACCCCTATATGCCGTTACGCGGCTCTGTCACTGTGTGGCGCATCAAGCGGTGGT	2222
Db	1875	CGAGGACTACCGTATCGCGAGCGACGGGCTGGCCATCTGGACGCCATCGAGCAGTGGT	1934
Qy	2223	CAAGGAGTACTTGGAATCTACTACTCTTAACGACGGGAGCTCCAGCGTACGTGAGCT	2282
Db	1935	GGGCGAGTACTTGCCACTTACTTACCCGACGACGGCGGCTCTCGGGGCGACAGAGGCT	1994
Qy	2283	GCAGGCGTGTGAAAGGAGGTGCTGAGGAGGCGCACGGGACCTCAAGGACCGAGACTG	2342
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Db	2055	GTGGCCCAAGATGACGAGCGGCTGTGGAGCTTCGCGAGCGGCTGCAACCATCATCTTGGAT	2114
Qy	2403	GGCATCCGCGCTGACGCGGCTGTCAACTTGGGCAGTACCCATATGCGGGTACCTCCC	2462
Db	2115	CGGCTGGCGGCTTCAACGCGCGCTGTCACTTCGGCCAGTACCGGTACGCGGGTACCTCCC	2174
Qy	2463	GAACCGGCCGACGCGCGCCCGATGCGCGGAGCCAGGACGCAAGCACTACAAGAA	2522
Db	2175	GAACAGGCCCAACGCTGAGCGCGCGCGGATGCGCGAGCCCGGAGCAAGAGTACGAGGA	2234
Qy	2523	GCTGGGAGCGGGGAGAAAGGAGCGGACATGTGTGTTTATCCGCAACCATCAACGAGCAGTT	2582
Db	2235	GCTGG-----ACGGGACCCGAGCGCGGCTTATCCACCATCATCAAGGACGAGT	2285
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Qy	2643	GTACTTCGGCAGCGGTGACGAGCCTGATCGCTGGAGCTGTAGACGCCAAGCGCTGATGC	2702
Db	2346	GTACTTCGGCAGCGGACACCCCGA---GTGGACTTCGACGCGCGGGCGTGGCGC	2402

QY	2703	GTTCAAAAGATTGGGAGCCGGCTGGTGCAGATTGAGATCGGATCAAGACGATGAACGA	2762	Db	9	CGGGATCATCGACGGGCTGACCGGGCGGAAACGACATGCGCGCTCAAG-----	57
Db	2403	GTTCAAAGAGGTTACGACGACGGCTGGTCAAGATCGAGGCAAGTGGTGGCGGAGAACCG	2462	QY	306	CGSCACGGTGAAGGCTGGTCAAGAGAGGCTGCTGAGCGTGGGAGCTTCAACGCGCTCGCT	365
QY	2763	CAGTCGGGACATTGAGACCGGAGGCGCTTGGAAATGCGTACATGCTGCTGTACCC	2822	Db	58	GGACCGTGGTGGTCTCATCGCAAGAACGCTGTGACCTCAACGACTTCGGGCGCACCGT	116
Db	2463	CGACCGGAGCTGAGAAACAGAACGCGCCCGCGAGTTCCTCCATGCTGCTCTATCC	2522	QY	366	CTTCGACCGCGCTCCACAGGATCTCGGCTGGGACGACGCGCTGCTGCTTCCAGCTGCTCAG	425
QY	2823	CAACACGTCGGACGTTTACCGCGAGAGCGCGAGGCGCTTACTGCCATGGGCAATCCCAA	2882	Db	117	CGTTGACAGCATCAGCGAGTTCTCGGCA-----AGGGGGTCACTGCGACATCATCAG	170
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QY	2883	CAGCATCTCCCATGCA	2898	Db	171	CTCCACCTCTGTCGACGCGCAACACGCGGCGGGTGGGGGCGGAGCGCACT	230
Db	2580	CAGCATCTCCCATGCA	2595	QY	486	GGAGGAGCGCTGGTGTGCTCAAGTCCACGCGCGAGCGGGGAGACCGTGTATCCGGGTGAG	545
RESULT 8				Db	231	GGAGCAGTGGCTGACGAGCCTGCGTGTGACGACGCGCGGAGTCCAAGTTCGGGCTCAC	290
LOCUS	AF329371	2595 bp	mRNA	linear	546	CTTCGAGTGGGA---CGAGTGCAGAGGATCCCGGGCGGCGCTCTGCTCAGGAACCTGCA	602
DEFINITION	Zea mays lipoxigenase mRNA, complete cds.			Db	291	GTTCGACTGGGAGTGGAGAGCTGGGAGTGGCGGGCGGCTGCTGCTCAAGAAACAACA	350
ACCESSION	AF329371			QY	603	GCACGCGGAGTTCCTTCCTCAAGACGCTCACCTTCGAGGCGCTCCAGGCAAGGGCACCGT	662
VERSION	AF329371.1	GI:12620876		Db	351	CGCGCGGAGTTCCTTCCTCAAGCAATCACCTTCGACGACGCTGCCGCGCGCGCGCT	410
KEYWORDS				QY	663	CGTCTTCGTCGCAACTGCTGGGCTTACCGGCAAGCTCTTACTCCAGGAACGATCTT	722
SOURCE				Db	411	CACCTTCGTCGCAACTCTCTGGGTCTACCCCGCGGCGAAGTACCGCTCAACCGCGTCTT	470
ORGANISM				QY	723	CTTCGCCAACGACACTATCTGCCAGCAAAATGCGCGCGGCTTGGTGGCTTATCGGCA	782
				Db	471	CTTCTCCACGATACGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	530
				QY	783	AGATGAGCTCAAGATTCTCCGTCGCGAGCAATATCTCTGCAACATACAGGAGCATGATCG	842
REFERENCE	Wilson, R.A., Maddox, J., Duwick, J. and Keller, N.P.			Db	531	CGACGAGCTCCCAACCTCCGCGCGGAGACAGCAGGCGGCGCTTACAGGAGCAGACCG	590
AUTHORS	Direct Submission			QY	843	CGTCTACGCTTACGACTACTACAATGACTTGGTGTATCCCGACAGGCGGAAGACACGC	902
TITLE	Submitted (14-DEC-2000) Plant Pathology and Microbiology, Texas A&M			Db	591	CGTGTACGCTACGAGCTTACACGACTCGGCGAGCGCGCGCGCGCGCGCGCGCGCG	644
JOURNAL	University, TAMUS 2132, College Station, TX 77843, USA			QY	903	TCGCGCGATCTCTGCTGGGAGCCAAAGAACCGCGTATCCCGTCTGCTGCTGCTGCTGCTGCT	962
REFERENCE	Location/Qualifiers			Db	645	GCGCGCATCTCTCGCGGCTCGCGGACACCGCTTACCGCGCGCTCGCGCGCGCGCGCG	704
AUTHORS	1..2595			QY	963	GCACCCCAACAAGAAAGACCCAAATTCGAGAGCAGGCTTTCTCTGCTGCTGCTGCTGCTGCT	1022
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FEATURES	/mol_type="mRNA"			Db	762	CTACCTGCGCGGAGCAGCGCTTCGCGCACCTCAAGATGCTCGGACTTCTCTGCTGCTGCTGCT	821
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	/translation="MLSGIIDGLTGANKHRLKGVVLMKKNVLDLNDPGATVVDVSI			Db	942	CAAGTCCAGGCGCTCGAGGACATGCGCAAGCTTCTCCGCTCGAGCTGCTGCTGCTGCTGCTGCT	1001
	EFLGKVTCLISSTLVDAANGNRVGAANLEQWLTLSPSTTGESKFGVTFDEV			QY	1263	TCGCGCAACCGTAGCCATGACCAACCGCTAAAGATGCCCTTCCAAATGTCTCAAAATC	1322
	EKLGVGAVVKNHAAEFPLKTTLDVPGAVTFVANSWYYPAGKYRNVFVFN			Db	1002	CCTCCC---CGCGCGGGGAGTACCTGCTCAGCTCCCATCCACAGATCATCCAA--	1056
	DTYLPSPAPALFPRGRKPTDPSNDRSLVQIYVPRDRFGLHKLMSDFLGYIK			QY	1323	AGATGTTGTAAGGCGTCCGAGTTTAAAGTTTGGCTGGAGGACTGACGAGAGTTCG	1382
	ALTCGIIIPAVRTVDTTPGDFSDODIINLYEGGKLPKIQALEDMKLPFLQVLDL						
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	IEDYVASDGLATWHAIEQWVGLYATYIPDDGALRGDELOAWKEVEVGHGDKD						
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	KEYELEDRPERGFIHITSOIOTIGISLIEILSKHSDENVYLGORDPEWTSARA						
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	GIPNSI51"						
ORIGIN							
Query Match	42.2%;	Score 1324;	DB 8;	Length 2595;			
Best Local Similarity	71.7%;	Pred. No. 5.6e-184;					
Matches 1904;	Conservative 0;	Mismatches 680;	Indels 72;	Gaps 10;			
QY	246	CGGGTTCGGACCGGCTGACGGGAAAGAACAGAGGCGGTGGAGCGGCGCAAGATCCG	305				

1057	Db	-----GAGGACAAGAACCGCTGGAGGACCGAAGAGAGTTCCG	1094
1383	QY	GAGAGAGACATTGTCAGGCGTGAAACCGAGTAATCATCAAAACGTCGTGACGAGTTGCCCGC	1442
1095	Db	GCGGAGGTGCTCGCGGCGCTCAACCGATGSGTATCACCGCGCTCACGGAGTTCGCGC	1154
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1155	Db	CAAGAGCAGCTGGACCCCGACAGTACGGCGACCAACGACGATCACGGGGAGCA	1214
1503	QY	CATCCGGCATAAACATGSGAGGCTGTGCGGTGCAGAACGCACTGAGGAACAAGAGGCTCTT	1562
1215	Db	CATCGAAGAAACCTCGAGGCGCTCACGGTGCAGCAGCGCTGACGGCAACAGGCTCTA	1274
1563	QY	CATCCTAGACCAACCATGACCAATTTCATGCCGTACTCGACGAGATCAACGAGCTGGAGG	1622
1275	Db	CATCCTGGACCAACACGACCGCTTCATGCCGTTCCTCATCGACGTCAACAACTGGAGG	1334
1623	QY	GAATTCATCTACGCCAGAGAGACCTTACTGTTCCTGAAGGACGATGGCAGCGTGAAGCC	1682
1335	Db	CAACTTCATCTACGCCACCGAGACGCTCTTCTTCCTCGCGGCGGACGGCAGGCTCGCGC	1394
1683	QY	CCTGGCCATCGAGCTGAGCTGCCACCTCGACGGCCAGCAGCGCGCGCGTCAAGCAA	1742
1395	Db	CCTCGCATCGAGCTCAGCGAGCGGTACATCGACGGGACCTCACGTGSCCAAGACAA	1454
1743	QY	GGTGTAACCCCGGCTCACACGGCGTGCAGGGCCACGCTTGGCAGCTGCCCAAGGTTTA	1802
1455	Db	GGTCTACACCCCGCGTCCAGCGCGCTGCAGGGCTTGGGTGGCAGCTGCCCAAGGCTTA	1514
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2163	QY	CAAGGACTACCCCTATCCGTTGACGGGCTCGTCACTGTGGGCGATCGAGCGGTGGGT	2222
1875	Db	CGAGGACTACCCGTACCGAGCGACGGGCTGGCCATCTGGCACGCCATCGAGCAGTGGGT	1934
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1935	Db	GGGCGAGTACTTGCCCATCTACTACCCGACGACGGCGCGCTGCGGGGCGACGAGGAGCT	1994
2283	QY	GCAGGCGTGTGAAGAGGTGCGTGAAGGCGGCACGGGCACTCAAGACCCGAGACTG	2342
1995	Db	GCAGGCGTGTGAAGAGGTGCGCAGAGTTCGGGCAACGGGCAACCAAGACCGCGCCTG	2054
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Qy	2643	GTACCTCGGCACGGCTGACGAGCCTCATCGCTGGAGCTGACAGCCCAAGSGCGTGGATGC	2702
Db	2346	GTACCTCGGCACGGCGACACCCCGCA---GTGACCTCGAGCCCGCGCGCTGCGCGC	2402
Qy	2703	GTTCAAAGAATTCCGGAGCCGCGTGTGTGCAGATTGAGAAATCGGATCAAGACGATGAACGA	2762
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Qy	2883	CAGCATCTCCATATGA	2898
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RESULT 9
AF271894

AF21634	LOCUS	AF271894	2845 bp	mRNA	linear	PLN 14-JUN-2000
				lipoxxygenase (LOX)	complete cds.	
				DEFINITION		
				Zea mays		

DEFINITION
ACCESSION
VERSION

VERSION
KEYWORDS
SOURCE

SOURCE
ORGANI

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFRENC
AUTHOR

AUTHORS Han, O., Choi, E., Kim, Y. and Kim, E.-S.
TITLE Methyl Jasmonate Induces Biphasic Accumulation of Lipoxxygenase mRNA in Maize Seedlings

JOURNAL
REFERENCE

REFERENCE
AUTHOR
TITLE

TITLE
JOURNA

FEATURES

1009

gen

SLLDGIGEFLLGRGVTCLISSTVVDVPPNNGRKLGAESLQWLLNPPPLLSBNFR
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ORIGIN

Query Match 40.7%; Score 1275.2; DB 8; Length 2845;
Best Local Similarity 68.9%; Pred. No. 7.6e-177;
Matches 1921; Conservative 0; Mismatches 808; Indels 61; Gaps 10;
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QY 398 ACGAGCGGCTCGCTTCCAGCTCGTCAGCGCCACCGCGCGACCCAGCAACGGGGCC 457
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DB 1871 CGTCGAGCCGCTACAGGATACGCTGCTGGTGGAGGACTACCCGCTACGCGTGGAGCGGC 1930
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DEFINITION Sequence 10 from patent US 6660915.
ACCESSION AR438184
VERSION AR438184.1 GI:40204686
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
1 (bases 1 to 2818)
Duma,A.C., Doderer,A., Cameron-Mills,V., Skadhauge,B., Bech,L.M.,
Schmitt,N., Heister,J.C. and van Mechelen,J.R.
Low lipoxigenase 1 barley
Patent: US 6660915-A 10 09-DEC-2003;
Location/Qualifiers
source 1..2818
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ORIGIN

Query Match 39.0%; Score 1222.2; DB 6; Length 2818;
Best Local Similarity 69.0%; Pred. No. 4.3e-169;
Matches 1868; Conservative 0; Mismatches 758; Indels 81; Gaps 11;

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RESULT 11

AX469803
LOCUS 2818 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 10 from Patent WO02053720.
ACCESSION AX469803
VERSION AX469803.1 GI:22205059
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1
REFERENCE
AUTHORS Bech, L.M., Douma, A.C., van Mechelen, J.R., Doderer, A., Schmitt, N.,
Cameron-Mills, V., Heister, J.C. and Skadhauge, B.
TITLE Low-lipoxygenase 1 barley
JOURNAL Patent: WO 02053720-A 10 11-JUL-2002;
CARLSBERG RES LAB (DK); KRONENBOURG BRASSERIES (FR); HEINEKEN TECH

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RESULT 13
BLYLOXA
LOCUS
DEFINITION
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ACCESSION
L35931
VERSION
L35931.1 GI:532571
KEYWORDS
carotene oxidase; linoleate:oxygen oxidoreductase; lipoxidase;
lipoxigenase 1.
SOURCE
Hordeum vulgare
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE
AUTHORS
van Mechelen,J.R., Smits,M., Douma,A.C., Rouster,J.,
Cameron-Williams,V., Heidekamp,F. and Valk,B.E.
TITLE
Primary structure of a lipoxigenase from barley grain as deduced
from its cDNA sequence
JOURNAL
Biochim. Biophys. Acta 1254 (2), 221-225 (1995)
MEDLINE
95127754
PUBMED
7827128
COMMENT
Original source text: Hordeum vulgare DNA.
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Query Match	39.0%; Score 1222.2; DB 8; Length 2818;	
Best Local Similarity	69.0%; Pred. No. 4,3e-159;	
Matches 1868; Conservative	0; Mismatches 758; Indels 81; Gaps 11;	
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NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kubumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Brakawa, T., Canincini, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Ito, M., Ito, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saiboh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

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SUMMARIES

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ALIGNMENTS

RESULT 1
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XX
DT 06-NOV-2003 (first entry)
XX
DE Corn (Zea mays) lipoxxygenase isozyme 4 cDNA.
KW Lipoxxygenase; hydroperoxidation; polyunsaturated fatty acid; plant;
KW fatty acid metabolite synthesis; signal molecule; growth regulation;
KW development regulation; plant development; wound response;
KW genetic mapping; hyperoxidation catalysis; Corn; gene; ss.
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XX (PEAR//) PEARLSTEIN R W.
XX (RAFA//) RAFALSKI J A.
XX (SHEN//) SHEN J B.
XX (THOR//) THORPE C J.
XX (TING//) TINGEY S V.
XX (WENG//) WENG Z.

CAHOON EB, Kinney AJ, Klein TW, Lee J, Pearlstein RW;
Rafalski JA, Shen JB, Thorpe CJ, Tingeey SV, Weng Z;
WPI; 2003-567325/53.

P-PSDB; AAO27494.

New isolated polynucleotides encoding plant lipoxygenases, useful in genetic mapping, particularly in catalyzing hyperoxidation of polyunsaturated fatty acids.

Claim 6; Page 27-29; 36pp; English.

This invention relates to novel nucleotide sequences which encode proteins which have lipoxygenase activity. Lipoxygenases are membrane bound ubiquitous enzymes which catalyse the hydroperoxidation of polyunsaturated fatty acids in the first step of signal molecule synthesis. Products of this pathway are found as fatty acid molecules involved in growth and development regulation. A knowledge of the amino acid sequence of lipoxygenases may allow the understanding of plant development and wound response. The polynucleotides, polypeptides and lipoxygenases of the invention may therefore be useful in genetic mapping and particularly for catalyzing hydroperoxidation of polyunsaturated fatty acids. The present sequence is the cDNA sequence of the Corn (Zea mays) lipoxygenase protein 4 of the invention

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QY 601 CAGCAGCGGAGTTCCTTCAGAGCGTCACTTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CAGCAGCGGAGTTCCTTCAGAGCGTCACTTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

QY 661 GTCTGCTTCGTCGCCAACTCGTGGGTCTACCCGCGCAAGCTCTACTCCAGAGGAGGAG 720
DB 661 GTCTGCTTCGTCGCCAACTCGTGGGTCTACCCGCGCGTCTGAGGAGGAGGAGGAGGAGG 720

661 GTCTGCTTCGTCGCCAACTCGTGGGTCTACCCGCGCAAGCTCTACTCCAGAGGAGGAG 720
721 TTCTTGGCCAAACGACACTATCTCCGAGCAAAATGCGGGCGGTGGTGGCTTATTCGG 780
721 TTCTTGGCCAAACGACACTATCTCCGAGCAAAATGCGGGCGGTGGTGGCTTATTCGG 780
781 CAAGATGAGCTCAAGATTCTCCGTTGGCGAGATATCTCTGGACCATACAGGAGCATGAT 840
781 CAAGATGAGCTCAAGATTCTCCGTTGGCGAGATATCTCTGGACCATACAGGAGCATGAT 840
841 CGCTCTACCGTTACGACTACTACAATGACTCTGGTATCCGACAGAGGCGAGAGACAC 900
841 CGCTCTACCGTTACGACTACTACAATGACTCTGGTATCCGACAGAGGCGAGAGACAC 900
901 GCTCGGCGATCTTCGTTGGCGAGCAACACCGGTATCCCGTCTCGCTCGAGACTGGC 960
901 GCTCGGCGATCTTCGTTGGCGAGCAACACCGGTATCCCGTCTCGCTCGAGACTGGC 960
961 CGGCAACCAACAAAGAAAGACCAAAATTCGAGAGGAGGCTTTTCTGCTGAACCTGAAC 1020
961 CGGCAACCAACAAAGAAAGACCAAAATTCGAGAGGAGGCTTTTCTGCTGAACCTGAAC 1020
1021 ATCTACGCTCCGCTGACGAAACGCTTTGGGATCTCAAGATGCGGACTTCTTGGGTAC 1080
1021 ATCTACGCTCCGCTGACGAAACGCTTTGGGATCTCAAGATGCGGACTTCTTGGGTAC 1080
1081 TCGCTGAAGACGATCATCGAGGCTGTCTTCCAAACCTGGGACTTTCGTCGATGACAG 1140
1081 TCGCTGAAGACGATCATCGAGGCTGTCTTCCAAACCTGGGACTTTCGTCGATGACAG 1140
1141 CCAAGGAGTTCGATTCTGTTGAGGATATCTCTGGGCTTACGAGTGGGCCCGAGAGGCA 1200
1141 CCAAGGAGTTCGATTCTGTTGAGGATATCTCTGGGCTTACGAGTGGGCCCGAGAGGCA 1200
1201 CCAACAAACCACTGATGAGAGATCAGGAGAGATCCCGAGGAGTTCCTTCCGAAGC 1260
1201 CCAACAAACCACTGATGAGAGATCAGGAGAGATCCCGAGGAGTTCCTTCCGAAGC 1260
1261 ATTCTGCGAAACCGGTAGCCATGACCCCGCTAAAGATGCGCTTCCAAATGTCTCAAA 1320
1261 ATTCTGCGAAACCGGTAGCCATGACCCCGCTAAAGATGCGCTTCCAAATGTCTCAAA 1320
1321 TCAGATGTTGTTGAAAAGGCTCCGAGTTCGAGTTCGTTGGTGGAGGACTGACGAGAGTTC 1380
1321 TCAGATGTTGTTGAAAAGGCTCCGAGTTCGAGTTCGTTGGTGGAGGACTGACGAGAGTTC 1380
1381 GCGAGAGAGACACTTCGAGGCGTGAACCCAGTAAATCATCAAACTCTGACGAGTTCCTCC 1440
1381 GCGAGAGAGACACTTCGAGGCGTGAACCCAGTAAATCATCAAACTCTGACGAGTTCCTCC 1440
1441 GCTAAAGACACCTTGGACCCAGGAGTACGGAGACCAACAGGAGATCACTGAGCT 1500
1441 GCTAAAGACACCTTGGACCCAGGAGTACGGAGACCAACAGGAGATCACTGAGCT 1500
1501 CACATCCGGCATTAACATGGAGGCTGTCTGGTGCAGAACGCACTGAGGAGAACAGAGGCTC 1560
1501 CACATCCGGCATTAACATGGAGGCTGTCTGGTGCAGAACGCACTGAGGAGAACAGAGGCTC 1560
1561 TTCTCTCTAGACCACTGACCATTTCTGCGGTACTCGAGAGATCAACGAGCTGGAG 1620
1561 TTCTCTCTAGACCACTGACCATTTCTGCGGTACTCGAGAGATCAACGAGCTGGAG 1620
1621 GGGAACTTCTATCTACGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
1621 GGGAACTTCTATCTACGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
1681 CCCTTGGCGATTCGAGTTCGCTTCCCACTCTGTTCTCTGAGGAGGAGGAGGAGGAGGAG 1740
1681 CCCTTGGCGATTCGAGTTCGCTTCCCACTCTGTTCTCTGAGGAGGAGGAGGAGGAGGAG 1740
1741 AAGGTGTACACCCCGGCTCACACCGGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
1741 AAGGTGTACACCCCGGCTCACACCGGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
1741 AAGGTGTACACCCCGGCTCACACCGGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800

QY 1801 TATGCTCGTAAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGACACGCAC 1860
Db 1801 TATGCTCGTAAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGACACGCAC 1860
QY 1861 GCGGTGATCGAGCGGTTGTAATCCGACAAACCGGAGCTCAGCGTGGTGCATCCCGTG 1920
Db 1861 GCGGTGATCGAGCGGTTGTAATCCGACAAACCGGAGCTCAGCGTGGTGCATCCCGTG 1920
QY 1921 CACAAGCTGTCAGCCGACCTACCGTGACAGCTGAACATCAACGCCCTTGGACGCCAG 1980
Db 1921 CACAAGCTGTCAGCCGACCTACCGTGACAGCTGAACATCAACGCCCTTGGACGCCAG 1980
QY 1981 AACTCATCAACGCCGCGGCTCTTCCAGCGCACCGTGTTCCTGCAAAAGTACGCGCTG 2040
Db 1981 AACTCATCAACGCCGCGGCTCTTCCAGCGCACCGTGTTCCTGCAAAAGTACGCGCTG 2040
QY 2041 GGGATGTCGGCAGACGTGTACAAGAGCTGGAATTTCAACGACGAGCTCTCCAGCAGAT 2100
Db 2041 GGGATGTCGGCAGACGTGTACAAGAGCTGGAATTTCAACGAGCGGCTCTCCAGCAGAT 2100
QY 2101 CTCGTCAAGAGAGTGTGGCTGTGCCGACCAAGTCAAGCCCATATGTTGCCGACTGCTG 2160
Db 2101 CTCGTCAAGAGAGTGTGGCTGTGCCGACCAAGTCAAGCCCATATGTTGCCGACTGCTG 2160
QY 2161 ATCAAGNACTACCTTATCCGCTTGAACGCGCTGCTGATCTGTTGGGCGATCGAGCGGTG 2220
Db 2161 ATCAAGNACTACCTTATCCGCTTGAACGCGCTGCTGATCTGTTGGGCGATCGAGCGGTG 2220
QY 2221 GTCAAGAGTACCTTGGACATCTACTACCTAACGACGCGAGCTCCAGCGTGAAGTGGAG 2280
Db 2221 GTCAAGAGTACCTTGGACATCTACTACCTAACGACGCGAGCTCCAGCGTGAAGTGGAG 2280
QY 2281 CTGACGCGTGTGGAGAGAGTGTGGTGAAGAGCGGCAACGCGGCTCAAGGACCGAGAC 2340
Db 2281 CTGACGCGTGTGGAGAGAGTGTGGTGAAGAGCGGCAACGCGGCTCAAGGACCGAGAC 2340
QY 2341 TGGTGGCCAGATGGACACCGTCCAGAGCTGCTAGGCGTGCAGACCATCATCTGG 2400
Db 2341 TGGTGGCCAGATGGACACCGTCCAGAGCTGCTAGGCGTGCAGACCATCATCTGG 2400
QY 2401 GTGCACTCCGCTGCAACGCGCTGTCACTTTGGGAGTACCCNTACGCGGCTACCTC 2460
Db 2401 GTGCACTCCGCTGCAACGCGCTGTCACTTTGGGAGTACCCNTACGCGGCTACCTC 2460
QY 2461 CCGAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2520
Db 2461 CCGAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2520
QY 2521 AAGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2580
Db 2521 AAGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2580
QY 2581 TTCCAGACCATCTGGGCGCTGCTGATCAGATCTCTCCAGGACCTCTCCGAGGAG 2640
Db 2581 TTCCAGACCATCTGGGCGCTGCTGATCAGATCTCTCCAGGACCTCTCCGAGGAG 2640
QY 2641 GTGTACCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700
Db 2641 GTGTACCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700
QY 2701 GCGTTCAAAAGATTTCGGGAGCGGCTGGTGCAGATTGAGATCGGATCAAGACGATGAC 2760
Db 2701 GCGTTCAAAAGATTTCGGGAGCGGCTGGTGCAGATTGAGATCGGATCAAGACGATGAC 2760
QY 2761 GACAGTCCGACATTGAAGAACCGGAGGCGGCTGTGGAATGCGTACATGCTGCTGAC 2820
Db 2761 GACAGTCCGACATTGAAGAACCGGAGGCGGCTGTGGAATGCGTACATGCTGCTGAC 2820
QY 2821 CCAACACGTCGACGTTACCGGCGAAGCGCGGCGGCTTACTGCCATGGCAATTC 2880
Db 2821 CCAACACGTCGACGTTACCGGCGAAGCGCGGCGGCTTACTGCCATGGCAATTC 2880

QY 2881 AACAGATCTCATATGAGCCCTGGGAGATGCTGCTAGTAATTTGTTGCTGCTGCGC 2940
Db 2881 AACAGATCTCATATGAGCCCTGGGAGATGCTGCTAGTAATTTGTTGCTGCTGCGC 2940
QY 2941 CGTGCGATGTTGTTCTTTCATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 CGTGCGATGTTGTTCTTTCATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
QY 3001 ATGATCTTTGTTAGGTTGAGGAGGAGTCCAGCTTGAATTTGTTGCTGCTGCTGCT 3060
Db 3001 ATGATCTTTGTTAGGTTGAGGAGGAGTCCAGCTTGAATTTGTTGCTGCTGCTGCT 3060
QY 3061 TCTTGTGTTAATAAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
Db 3061 TCTTGTGTTAATAAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
QY 3121 AAAAAAAG 3134
Db 3121 AAAAAAAG 3134
RESULT 2
ID ADA48505 standard; DNA; 2516 BP.
XX ADA48505;
XX 20-NOV-2003 (first entry)
DT 20-NOV-2003 (first entry)
XX Rice gene conferring disease resistance in plants.
DE disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.
XX Oryza sativa.
XX WO2003000906-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002WO-IB002453.
XX 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0352277P.
PR 22-MAR-2002; 2002US-0366535P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Krebs J, Provart N, Rieke D, Zhu T;
XX WPI; 2003-184052/18.
DR P-PSDB; ADA48506.
XX New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX Claim 1; SEQ ID NO 575; 299pp; English.
XX The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a gene
CC conferring disease resistance used in the invention.
SQ Sequence 2516 BP; 578 A; 745 C; 739 G; 454 T; 0 U; 0 Other;
Query Match 48.6%; Score 1523.4; DB 8; Length 2516;
Best Local Similarity 77.5%; Pred. No. 5e-261;
Matches 2004; Conservative 0; Mismatches 456; Indels 127; Gaps 8;

QY 243 GCACGGGCTCGCGACCGGTGCTGCGGAAAGAAACAGAGGCGGTGAGAGGCGGCAAGAT 302
Db |||||
QY 9 GCAGGGGCTCTTTGACAGGTGTGACGGGGAGGACAGAGGGCGTGGAGGAGGAGAT 68
Db |||||
QY 303 CCGGGGACCGGTGAGGGTGTCTGAGAGAGGTGCTGGACGTGCGGCACTTCAAACGCTTC 362
Db |||||
QY 69 CCGTGGACCGCGGTGCTGTGTGAGAGAGGACGTGCTCGGCTCGGCGACTTCACGCTTC 128
QY 363 GCTCTCTCGACGGGGTCCACAGGATCCTCGGTGGGACGCGGGTCCGCTTCAGACTCGT 422
Db |||||
QY 129 CTTCTCTCGACGGGGTCCAC 147
QY 423 CAGCGCACCGCGGCGGACCGCCAGACACGGGGGCGGTGGCAAGTGGGGAAGCGGCGCA 482
Db |||||
QY 148 -----CAATGGAGGGAGGGGAGCTGGGGAAGCGGCGCA 183
QY 483 CTTGGAGGCGGTGGTGTGCTCAAGTCCACGGGGGACCGGGAGACCGTGTACCGGT 542
Db |||||
QY 184 CTTGGAGGAGCTGGTGTGACGATGAGTTCGACGGGGCGGGGAGTCCGTTGTTCCGGGT 243
QY 543 GAGCTTCGAGTGGGACGAGTTCGAGGGGATCCCGGGCGCGTCTCGGTCAAGAACTGCA 602
Db |||||
QY 244 GCGGTTTCGAGTGGGACGAGTTCGAGGGGATCCCGGGCGCGTCCGTGCTCAACAACTCCAA 303
QY 603 GCACGCGAGTCTCTCTCAAGACGCTCACCTTCGAGGGGCTCCAGGCAAGGGCACCGT 662
Db |||||
QY 304 CCGGTCCGAGTTCTTCTCAAGACGCTCACCTTCGAGGGGCTCCCGGCAAGGGCACCGT 363
QY 663 CGTCTTCGTCGCAACTCGTGGGTCTACCGGCAACAGCTCTACTCCAGAAACGCACTTT 722
Db |||||
QY 364 CGTCTTCGTCGCAACTCGTGGATCTACCGGCGGCAACTACCACTAGAGCGGTCTT 423
QY 723 CTTTCGCAACGACACTATCTCGGAGCAAAATGCGGGGCGGTGGTCCCTTATCGGCA 782
Db |||||
QY 424 CTTTCGCAACG-----ATTTCGCTAGCAAAATGCTGACCTTTGATCCCTTACCGGCA 477
QY 783 AGATGAGCTCAAGATTCTCGTGGCGACGATAATCTCTGGACCAATACAGGAGCATGATCG 842
Db |||||
QY 478 AGAAGAACTCAACATTTACAGGGGACGGTAAATTTGGACCAATACAGGAGCATGACCG 537
QY 843 CGTCTACGTTAGACTTACTACTGATGACCTTGTGATCCGACAAAGGGCGAGACACCG 902
Db |||||
QY 538 TATCTACGTTATGATTAATTAACGACCTTGCCCAACAGAACAGAAAGGAGTAACTAGT 597
QY 903 TCGCGCGATCCTCGGTGGGACCAAGAACACCGGTATCCCGTGGTGGGAGTGGCGG 962
Db |||||
QY 598 ACGACAGTCTCGGTGGGACCAAGAACTCCCTATCCCGTTCGAGGACGAACTGGCGG 657
QY 963 GCACCCCAAGAA-----AGACCCAAATTCGAGAGGAGGCTTTCTGCTGAACCTGA 1018
Db |||||
QY 658 GGGCCCAACAAAGACTGTGAGCCCAATACAGAAAGCAGGCTTCTCTGCTGGACTTGA 717
QY 1019 ACATCTACGTCCTCGGTGGGACCAAGCGCTTTGGGCACTCTCAAGATGTCGAGCTTCTTGGGT 1078
Db |||||
QY 718 ACATTTATGTCCTCACGCGACGACGTTCCGGCACTCCAGATGTCAGACTTCTTGGT 777
QY 1079 ACTCGTGAAGACATCATCGAGGCTGTCTTCCAAACACTGGGGACTTTTCGTCGATGACA 1138
Db |||||
QY 778 ACTCTCTTAAGGCTATGTTGAGGGTGTCTCCCAATAAAGGACCTATGTCGATACGA 837
QY 1139 CGGCCAAGGAGTTCGATTCGTTTGAAGATATCTCGGGTCTACGAGCTGGGCCAGAGG 1198
Db |||||
QY 838 CACCAAGGAGTTGATCTTTTCAAGACNATCATGGAATCTATGAAGTGAATTGAAG 897
QY 1199 CACCCAAACCACTGATAGCAGATCAGGAAGAGATCCCGACGAGTTCCTTCGAA 1258
Db |||||
QY 898 TGGCCCAATGCTCTGCACTAGCAGATCAAGAAGAGAGTTCCTTTTGAACCTTATTAAGA 957
QY 1259 GCATTCGCGAAGCGTAGCATGACCCCGCTTAAGATGCCCTTCCAAATGTCATCA 1318
Db |||||
QY 958 GTCTTTGCCAGTTGCTGGC---GATCAAGTCTTGAAGTTACCCCTACCAATGTTATCA 1014

QY 1319 AATCAGATGTGTTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGAGGACTGACGAAAGT 1378
Db |||||
QY 1015 AA-----GAAATTTGCTTGGAGGACTGATGAGAGT 1045
QY 1379 TCGCGAGAGACACTTTCGAGGCGTGAAACCCAGTAATCATCAACAGTCTGTCAGGAGTTC 1438
Db |||||
QY 1046 TTGCACGAGAAATCTCCGAGGAGTTAAACCCAGTATGATCAAGCGTCTGACG----- 1098
QY 1439 CCGCTAAAGACACCTCGACCCAAAGGAGTACGAGAGACCAACACGACAAAGATCACTGAAG 1498
Db |||||
QY 1099 -----AGTACTCTGGATCCAAATGTGTACGGTGACCATCCAGCAAGATCAACGAAG 1150
QY 1499 CTCACTCCGCAATAATGGGAGGCTGTGCGTGGAGAAAGCACTGAGGAAACGAGGCG 1558
Db |||||
QY 1151 CTCACTTAAGCAACAATGGAGGGCTCAACGGTGAATAATGCACTGAAGGGCAACAGGC 1210
QY 1559 TCTTCATCTAGACCAACCATGACCATTTTCATGCGGTACTCGACGAGATCAACGAGCTGG 1618
Db |||||
QY 1211 TTTTCATCTTAGACCAACCATGATCATCTTCATGCGTTCCTGGCAAGATCAACGAGTTGG 1270
QY 1619 AGGGAACTTCATCTACGCGAGAGGACCTCTATCTGTTCTGAAAGGACGATGGGACGCTGA 1678
Db |||||
QY 1271 ACGGTAACTTCATATATGCGAGCAGGACCATTTCTGCTCTTGAAGGACGATGGCACCTGA 1330
QY 1679 AGCCCTGGCATCGAGCTGAGCCTGCCACCTGACGCGCCAGCAGCGGCGGCGGTCA 1738
Db |||||
QY 1331 AGCCCTGGCGATCGAGCTGAGCCTGCCACCCGATGCCAGCAGCAGCGGCGGCTCA 1390
QY 1739 GCAAGGTGTACACCCCGGCTCACACCGGCTGAGGGGCCACGCTCTGGCAGCTCGCCMAAG 1798
Db |||||
QY 1391 GCAAGGTGTACACCTCCAGCCAAACACCGGCGCTCGAGAGCCAAATCTGGCAGCTCGCCAAAG 1450
QY 1799 CTTATGCTCGTAAACGACTTCTGCTGGCATCAGCTGATCAGCAGCTGCTGCTGAACACGC 1858
Db |||||
QY 1451 CTTAGCCTCGTCAACGACTCTGCTTGGCAACAGCTGATGACCACTGCTGACACTC 1510
QY 1859 ACGCGGTGATGAGCCGCTTCTTAATCGCAAAACCGGACGCTCAGCGTGGTGCATCCCG 1918
Db |||||
QY 1511 ACGCGGTGATCGAGCGCTTCTGATCGGACGAAACCGGACGCTCAGCGTGGTGCACCCCG 1570
QY 1919 TGCAACAGCTGCTGAGCCCGCATCTACCGTGCAGCGCTGAACATCAACGCGCTGCACGCG 1978
Db |||||
QY 1571 TGCAACAGCTGCTGAGCCCGCATCTACCGGACAGATGAACATCAACGCTCTGGCAGCG 1630
QY 1979 AGACACTCATCAACCGCGCGGCTTCTTCGAGCGCACCGTGTTCCTTCGAAAGTACGCG 2038
Db |||||
QY 1631 AGACACTCATCAACCGCGATGGCATCTTCGAGAAGACCGTCTTCCAGGCAAGTACGCG 1690
QY 2039 TGGGATGTCGGCAGACGTGTCAAGAGCTGGATTTCAACGAGCAGGCTCTCCAGCAG 2098
Db |||||
QY 1691 TCGAGATGTCCTCGTGTACAAAGAACTGGAAGTTTCAACGAGCAGGCTCTCCCGCTCG 1750
QY 2099 ATCTCGTCA--AGAGAGGTGTGGCTGTGCGCGACCAAGTCAAGCCCATATGTTGTCGACT 2156
Db |||||
QY 1751 ATCTCGTCAAGAGAGAGGGGTGGCGGTGCCGACCCGACGAGCCGTTACAACGTCGGCT 1810
QY 2157 GCTGATCAGGACTTACCCCTATGCCGTTGACGGGCTGTCATCTGTTGGGCGATCGAGCG 2216
Db |||||
QY 1811 GCTGATCAGGACTTACCCGTAACCGCTGAGCGGGCTGTTGATCTGTTGGGCGATTCGAGCG 1870
QY 2217 GTGGGTCAAGGAGTACCTGGACATCTACTACCTTAACGACGGGAGCTCCAGGGTGAAGT 2276
Db |||||
QY 1871 GTGGGTGGCGAGTACCTGGCCATCTACTACCCCAACGACGCGGTGCTCCGCGCGACGA 1930
QY 2277 GGACTCGAGGCTGTGGAGGAGGTGCTGAGGAGGCGCACGCGACCTCAAGGACCG 2336
Db |||||
QY 1931 GGAGCTCAGCGGTGGTGGAGGAGGTGCGCGAGGTTCGCGCATTTGGCCACTTCAGGACCA 1990
QY 2337 AGACTGTGGCCCGAGGATGACACCGTCCAGCAGCTGGCTAGGCGGTGACGACCATCAT 2396
Db |||||
QY 1991 GGAATGTGGCCCGAGATGACACCGTCCAGGAGCTCACCCGGGCGTGCACCATCATCAT 2050
QY 2397 CTGGGTGGCATTCGCGGCTGCACGCGGCTGTCAAATTTTGGGCGATACCCATACGCGCGGTA 2456

QY 1654 TTCCTGAAGGAGCGATGGCAGCGCTGAAGCCCTCGCCATCGAGCTGAGCTGCCCCACCCCT 1713
Db CTCCTGAAGGAGCGATGGCAGCGCTGAAGCCCTCGCCATCGAGCTGAGCTGCCCCACCCCT 933
QY 1714 GACGGCAGCAGCGCGCGGCTCAGCAAGGTGTACACCCCGGCTCACACCGGCGTCGAG 1773
Db GATGGCAGCAGCAGCGCGGCTCAGCAAGGTGTACACCCCGGCTCACACCGGCGTCGAG 993
QY 1774 GGCACGCTGCGCAGCTCGCAGAGCTTATGCTTGGGTAAACGACCTGTGCTGGCATACG 1833
Db AGCCAAATCTGGCAGCTCGCAGAGCTTATGCTTGGGTAAACGACCTGTGCTGGCATACG 1053
QY 1834 CTGATCAGCCACTGCGTGAACACGACGCGGTGTATCGAGCGGTTCGTATCGCGGCAAC 1893
Db CTGATCAGCCACTGCGTGAACACGACGCGGTGTATCGAGCGGTTCGTATCGCGGCAAC 1113
QY 1894 CGGAGCTGACGCGTGGTGCATCCCGTGCACAAGCTGTGAGCCCGCACTACCGTGACAG 1953
Db CGGAGCTGACGCGTGGTGCATCCCGTGCACAAGCTGTGAGCCCGCACTACCGTGACAG 1173
QY 1954 CTGACATCAGCCCTGGCAGCCGACACTCATCAACGCGCGCGCTTCGAGCGC 2013
Db ATGACATCAGCCCTGGCAGCCGACACTCATCAACGCGCGCTTCGAGCGC 1233
QY 2014 ACCGTGTCCCTGCAAAAGTACGCGCTGGGATGTGCGCAGACGTGTACAAGAGCTGGAAT 2073
Db ACCGTGTCCCTGCAAAAGTACGCGCTGGGATGTGCGCAGACGTGTACAAGAGCTGGAAT 1293
QY 2074 TTCAACAGCAGGCTCTCCAGCAGATCTCTGTCAGAGAGGTGTGCTGCGGACAG 2133
Db TTCAACAGCAGGCTCTCCAGCAGATCTCTGTCAGAGAGGTGTGCTGCGGACAG 1353
QY 2134 TCAGCCCATATGTGTCCGACTGCTGATCAAGGACTTACCCCTATGCGTTGACGGGCTC 2193
Db ACAGCCCGTACACGTCGCGTCTGTATCAAGGACTTACCCCTATGCGTTGACGGGCTC 1413
QY 2194 GTCATCTGTGGCGATCGAGCGGTGGTCAAGGAGTACTTGACATCTACTACCCATAAC 2253
Db GTCATCTGTGGCGATCGAGCGGTGGTCAAGGAGTACTTGACATCTACTACTACCCATAAC 1473
QY 2254 GACGGCAGCTCCAGCGTGCAGTGCAGCTGCAGCGCTGGTGAAGAGGTGGTGAAGGAG 2313
Db GACGGCAGCTCCAGCGTGCAGTGCAGCTGCAGCGCTGGTGAAGAGGTGGTGAAGGAG 1533
QY 2314 GCGCAGCGCAGCTCAAGGACCGAGACTGTGTGCGCCAGGATGACACCGTCCAGCAGCTG 2373
Db GGCCATGGCAGCTCAAGGACCGAGACTGTGTGCGCCAGGATGACACCGTCCAGCAGCTG 1593
QY 2374 GCTAGGCGGTGCGAGCATCATCTGGTGGCATCCGCGTGCACGCGGTGTCACTTT 2433
Db ACCGGCGTGCACCATCATCTGGTGGCATCCGCGTGCACGCGGTGTCACTTT 1653
QY 2434 GGGCAGTACCCATACGCGGCTACCTCCGAAACCGGCGCAGCGCGCGCGCGCGATG 2493
Db GGGCAGTACCCATACGCGGCTACCTCCGAAACCGGCGCAGCGCGCGCGCGCGATG 1713
QY 2494 CCGGAGCGCAGCGCAGCTACAGAGCTGGAGCGGGCAGAGGAGGCGGAGCATG 2553
Db CCGGAGCGCAGCGCAGCTACAGAGCTGGAGCGGGCAGAGGAGGCGGAGCATG 1773
QY 2554 GTGTTCATCCGACCATACAGCCAGTTCAGACCATCTTGGGCACTCTCGTCTCATCGAG 2613
Db GTGTTCATCCGACCATACAGCCAGTTCAGACCATCTTGGGCACTCTCGTCTCATCGAG 1833
QY 2614 ATCTCTCAGACACTCTCGACGAGGTACTTGGCGCAGGTGACAGCGCTGATCGC 2673
Db ATCTCTCAGACACTCTCGACGAGGTACTTGGCGCAGGTGACAGCGCTGATCGC --G 1890
QY 2674 TGGACGTCAAGCGCAGGCGCTGGATGCTTCAAAGATTCGGGAGCGCGCTGGTGCAG 2733
Db TGGACGTCAAGCGCAGGCGCTGGATGCTTCAAAGATTCGGGAGCGCGCTGGTGCAG 1950
QY 2734 ATTGAGATCGGATCAAGACGATGAACGACGTCCGGAATTGAAGAACCGGAGGCGCT 2793

Db 1951 ATCGAGAACCGGATCAAGGACATGAACGGCAACTCGGCGCTCAAGAACCGGACGGCGC 2010
QY 2794 GTGGAAATGCGGTACATCTGTGTACCCCAACACGTGCGGACGTTACCGGCGGAGAGGCC 2853
Db 2011 GTGAGATGCGGTACATCTGTGTACCCCAACACGTGCGGATGTACCAAGGAGAGGGC 2070
QY 2854 GAGGGGCTTACTGCGATGGGCAATTCGCCAACAGCATCTCCATATGA 2898
Db 2071 CAAGGGCTCAAGCGCCATGGCATCCCAACAGCATCTCCATCTGA 2115

RESULT 4

ABK88441

ID ABK88441 standard; cDNA; 2818 BP.

XX AC ABK88441;

XX DT 07-OCT-2002 (first entry)

XX DE Barley lipoxigenase 1, LOX-1, cDNA.

XX KW Barley; plant; ss; gene; lipoxigenase-1; LOX-1; transgenic; beer;

XX KW beverage; malt; organoleptic property; brewing; trans-2-nonenal; 72N;

XX OS elevated storage temperature; flavour stability; shelf-life.

XX OS Hordeum vulgare.

FH Key

FT CDS

FT 69..2657

FT /*tag= a

FT /product= "LOX-1"

XX WO200253720-A1.

XX PD 11-JUL-2002.

XX PF 29-DEC-2000; 2000WO-IB002045.

XX PR 29-DEC-2000; 2000WO-IB002045.

XX PA (CARL-) CARLSBERG RES LAB.

XX PA (HETB) HEINIKEN TECH SERVICES BV.

XX PA (BRAS-) BRASSERIES KRONENBOURG SA.

XX PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;

XX PI Schmitt N, Heistek JC, Van Mechelen JR;

XX XX WPI; 2002-557741/59.

XX DR F-PSDB; AAU99691.

XX PT Novel barley cultivar having reduced lipoxigenase 1 activity and which

XX PT expresses mutant lipoxigenase protein, useful in brewing processes to

XX PT reduce formation of off-flavors in brewed products e.g. beer during

XX PT storage.

XX PS Example 3; Page 89-91; 112pp; English.

XX CC The invention relates to a barley plant or portion comprising a mutant

XX CC lipoxigenase-1 (LOX-1) protein, characterised by a reduction or absence

XX CC of LOX activity as compared to a non-mutated control, or comprising a

XX CC heterologous nucleic acid sequence expressing an antisense sequence to a

XX CC portion of a transcribed region of barley lox-1 gene, operably linked to

XX CC a promoter and a transcription terminator sequence. Also included are

XX CC grain or plant progeny produced from the barley plant or its portion, a

XX CC plant product produced from the barley plant or its portion or progeny,

XX CC and a beverage e.g. beer, manufactured using the plant product, plant or

XX CC its portion or progeny. The mutated barley plant, portions, progeny and

XX CC products are useful in the manufacture of a beverage, preferably malt or

XX CC beer, for stabilising organoleptic properties of a brewed product over a

XX CC measured period of time for the manufacture of a brewed product having

XX CC reduced levels of free trans-2-nonenal (72N) over a measured period of

XX CC time or under conditions of elevated storage temperature and for the

QY	510	GTCCACGGCGGACGGGGAGACGGTGTACCGGGTGAGCTTCGAGTGGGA---CGAGTCCGA566
DB	326	GTGCTGACGACGGGGGAGTCCAAGTTCGGGCTCACCTTCGACTGGGAGTGGGAAGACT385
QY	567	GGGCATCCCGGCGCGCTTCCTGGTCAAGAACTGTGAGCACGCCGAGTTCCTTCCTCAAGAC626
DB	386	CGGGTGC CGGCGGCATCGTTCGTAACAACTACACAGCTCCGAGTTCCTGCTTAAAC445
QY	627	GCTCACCTCTGAGGCGTCCAG---GCAAGGACCGTGTCTTCGTGGCAACTGTGTC683
DB	446	CATCACCTTCACGACGTCCTCCGCGCGCAGCGGCAACCTCACTTCGTTCGCAACTCATG505
QY	684	GGTCTTACCCGCACAAAGCTCTACTCCAGGAACGGATCTTCTTCGCAACAGCACTCTACT743
DB	506	GATCTACCCGCGCCCACTACCGATACAGCGCGTCTTCTTCGCAACAGCACTACCT565
QY	744	CCGAGCAAAATGCGGGCGGCTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCCTCG803
DB	566	GCCGAGCCAGATGCGCGCGGCTGAAGCCGTATCCGACACAGAGCTCCGAAACCTGCG625
QY	804	TGGCGACGATTAATCTGTGACCATACCAAGAGCATGATCGCGTCTACCGTTACGACTACTA863
DB	626	TGGCGACGACCAAGCGGCCGTACCAAGGAGCAAGACCGCATCTACGCTACGACGCTA685
QY	864	CAATGACCTTGGTGATCCGACAAAGGGGAAGAGACGCTCGGCGGATCTTCGTGTGGAG923
DB	686	CAACGACCTCGGCGAG-----GGCGGCCCTCTCTCGCGGCAA724
QY	924	CCAAGAACCCCGTATCCCGCTCGTGCAGAACTGGCGGCAACCCCAACAAGAAAGACCC983
DB	725	CTCCGACCACTTACCGCGCGCGGCGCGCACGAGGGCAAGCCCAAGCCACGCAACC784
QY	984	AAATTGGAGAGCAGGCTTTCTGTGAACCTGAACTACGTCCCGGTGACGAACG1043
DB	785	GAGCCTGGAGAGCGGGTGTCTGCTGTGGA---GCAGATCTACGTGCGCGGACGAGAA841
QY	1044	CTTTGGGACTCTAAGATGTCGGACTTCTTGGGTACTCGCTGAAGACGATCATCGAGGC1103
DB	842	GTTCGGCACTCAAGAGCTCCGACTCTCTGGGCTATCTCATGAAGGCGATCAGCGAGG901
QY	1104	TGTTCTTCCAACTGCGGACTTTCTGTGATGACACGCCCAAGAGTTCGATTCGTTGA1163
DB	902	CATCTGCGGCGCGTGCGCACTACGTGGACCAACCCCGCGGAGTTGACTCCTTCCA961
QY	1164	GGATATCTCGGGCTCTACGAGCTGGGCCAGAGGCCACCAACCACTGATAGCAGA1223
DB	962	GGACATCATCAACTCTATGAGCGCGCATCAAGCTGCCAAGGTGCGCCCTTGGAGGA1021
QY	1224	GATCAGGAAGAAGATCCCCACGAGTTCCTTCGAAGCATTTCTGCCAAACGGTAGCCATGA1283
DB	1022	GCTCCGTAAGCAGTTCCTCGGTCCAGCTCATCAAGGACCTCTCTCCCGTGGCGCG---GA1078
QY	1284	CCACCCGCTAAGATGCCCTTCCAAATGTCTCAATTCAGATGTGTTGAAAAGGGCTCC1343
DB	1079	CTCCCTGCTTAAGTCTCCCGTGCCTCCCACTATC-----CA1114
QY	1344	GGAGTTTAAAGTTTGGCTGGAGGACTGACGAAGAGTTCGCGAGAGAGACATTGCGAGCGT1403
DB	1115	GGAGAACAAAGCAGCGTGGAGGACCGACGAGGAGTTTCGACGGAGGTGCTTCGCGCGCT1174
QY	1404	GAACCCAGTATCATCAAAAGTGTGACGGAGTTCCTCCGCTTAAAGCACTTCGACCCCAAG1463
DB	1175	CAACCCGGTCAATGATACGGGTCTCAAGGAGTTCCTCCCAAAAGTAGTCTGACCCCTAG1234
QY	1464	GCAGTAGCGGAGACCAACCAAGAGATCATCTGAAGCTCACATCCGCATTAACATGGGAGG1523
DB	1235	CAAGTTTGTGTGACCAACCAAGCACCATCAAGCGGAGSCATAGAGAAGAACTCTGAGGG1294
QY	1524	CCTGTCCGTGAGAACCGCATGAGGAACAGAGGCTCTTTCATCTCTAGACCAACCATGACCA1583
DB	1295	CCTCACGGTGCAGCAGCGCTGGAAGACACAGGCTGTACATCTCTGATCACCATGACCG1354

1584	QY	TTTTATGCCGCTACCTCGACGAGATCAACAGCTGTGGAGGGAACTTTCATCTACGCCACGAG	1643
1585	DB	GTTTCATGCCGTTCTGTATCGACGTCFAACAACCTGCTCCCGCAACTTCATCTACGCCACGAG	1703
1644	QY	GACCCCTACTGTTCTCTGAAGGACGATGCAGCTGAAGCCCTGTGCCATCGAGGTGAGCCT	1703
1704	DB	GACCCCTCTTCTCTCTGCGCGGACGCGAGGCTCACGCCGCTCGCCATCGAGCTGAGCGA	1744
1704	QY	GCCCGCACCTGACGGCGCAGCAGCGCGCGCGGTTCAGCAAGGTGTACACCCCGGTTCACAC	1763
1745	DB	GCCCATCATCCAGGCGCGCTTACACGGGCAAGAGCAAGGTTTACACGCGCGGTGCCCGAG	1834
1764	QY	CGG--CGTCGAGGGCCACGTCCTGGCAGCTCGCCAAAGGCTTATGCCCTGCGTAAACGACTC	1820
1835	DB	CGGCTCGTCTGAGGCTGGGTGTGGAGCTCGCCAAAGGCTTACGTGCCGTCTAATGACTC	1894
1821	QY	TGCCCTGGCATCAGCTGATCAGCCACTGGCTGAACACACGACGCGGTGATCGAGCGGTTCGT	1880
1895	DB	CGGGTGGCACCGAGCTCGTCAACCTGGCTGAACACTCACGCGGTGATGAGCGGTTCGT	1654
1881	QY	AATCGCACAAACGGCGAGCTCAGCGTGGTGCATCCCGTGCAACAGCTGCTGAGCCGCA	1940
1955	DB	GATCTCGACGAACCGGCACTTACGTGTCGACCGCGGTGCAAAAGCTGCTGAGCCGCGCA	1714
1941	QY	CTACCGTGCACGCTGAACACTCAACGCCCTGGGACGCGCAGACACTCATCAACGCCCGCGG	2000
1715	DB	CTACCGCGACACCATGACCATCAACCGCTGCGCGGCGACAGCTCATCAACGCCCGCGCG	1774
2001	QY	CGTCTTCGAGGGCACCGTGTTCCTGCAAAAGTACGCGCTGGGATGTGCGGCACAGTGTA	2060
1775	DB	CATCTTCGAGATGACGCTGTTCGCGGCAAGTTTCGCTGGGATGTGCGCGCGTGTGTGA	1834
2061	QY	CAAGAGCTGGAAATTTCAACGAGCAGGCTCTCCACGACAGATCTCGTCAAGAGAGGTCTGGC	2120
1835	DB	CAAGACTGGAAATTTCAACGAGCAGGACTGCGGACGATCTCATCAAGAGGGGCGATGGC	1894
2121	QY	TGTGCCGGAACGAGTCAAGCCCATATGTTGTTCGACTGCTGATCAAGACTTACCCCTATGC	2180
1895	DB	GGTGGAGGACCGCTCGAGCCGTCGAAGGTGCGGTTGCTGGTTCGGACTTACCCGTACGC	1954
2181	QY	CGTTGACGGGCTCGTTCATCTGTTGGCGATCGAGCGGTGGTCAAGGAGTACCTGAGCAT	2240
1955	DB	GGCGGACGGCTGCGGATCTGGCAGCCATTGACGCACTGAGCAGTACGTGAGCGATCTCTG	2014
2241	QY	CTACTACCTTAACGACGGCGAGCTCCAGCGTGTGAGCTGCGAGCTGCGAGCGGTGGGAGGA	2300
2015	DB	CTACTACCCGAAACGACGGCGTGTGACAGGCGCATACGAGGTGCGAGCGGTGGTGAAGGA	2074
2301	QY	GGTTCGTGAGGACGGCACGGCCACCTCAAGGACCGAGACTGGTGGCCCAAGTATGACAC	2360
2075	DB	GACGCGGAGGTCTGGGACCGGCCACTCAAGGACGCCCCATGGTGGCCCCAAGATGCAAG	2134
2361	QY	CGTCCAGCACTGGCTAGGGCGTGCACGACCATCATCTGGGTGGCATTCGCGCTGCACGC	2420
2135	DB	TGTCGGGAGCTGGCCAAAGCGTGTGACCCACCATCATCTGGATCGGGTTCGGCGTGTATGC	2194
2421	QY	GGCTGTCAAATTTGGGAGTACCCATACGCGGGTACCTCCGAAACGGCGCGACGCGCAG	2480
2195	DB	GGCAGTCAACTTTCGGGCACTACCCCTACGCGGGTTCCTCCCGAAACGGCGCGACGCTGAG	2254
2481	QY	CCGCGCCCGATCCCGGAGCGGACGACGACACTACAAGAGCTGGGAGCGGGGCGAGAA	2540
2255	DB	CCGGCGCGCATTCGCGGAGCCCGGACGAGGAGTACGCGAGCTGG-----AGCG	2305
2541	QY	GGAGGGGACATGGTGTTCATCCGCAACCATCACAGCCAGTTCCAGACCATCTCGGCAT	2600
2306	DB	CGACCGGAGCGGCGCTTTCATCCACACCATCACAGCCAGATCCACAGCCATCATCGGCGT	2365
2601	QY	CTCGCTCATCGAGTCTCTTCAAGCACTCTCTCCGACGAGGTGTACTCTGGCCAGCGTGA	2660
2366	DB	GTCTGCTGTGAGGTGCTGTGGAAGCACTCTCTCCGACGAGCTGTACTCTGGGACGCGGA	2425
2661	QY	CGAGCTGTATCGCTGGACGCTCAGACGCCCAAGCGCTGGATTCGCTTCAAAAGATTCCGGAG	2720

Db 2426 CAGCCCGA---GTGACCTCGACCAAGGCCCTGGAGGTGTTCAAGCGTTGAGCA 2482
 QY 2721 CCGGCTGGTGCAGATTGAGATCGATCAAGACGATGAAGACGACGATTCGGAATTCGAAGA 2780
 Db 2483 CCGGCTGGTGGATCGAGACGAGCAAGGTGGTGGGCATGAACCATGACCCCGAGCTCAAGA 2542
 QY 2781 CCGGAAGGCGCTGTGGAATGCGTACATGCTGTGTACCCCAACACGATCGGACGTTAC 2840
 Db 2543 CCGCAAGCGCCCGCTAAGTTTCCCTACATGTGCTCTACCCCAACACCTCCGACCA 2602
 QY 2841 CCGCGAAGAGCGGAGGCGTTACTGCCATGGGCATTCCTCAACAGCATTCATATGAC 2900
 Db 2603 GGGCG---CGGTGCGCGGGTTACCGCCCAAGGCGATCCCAACAGCATTCATCTAATC 2659
 QY 2901 CTGGGCA 2907
 Db 2660 TAAGCCA 2666

RESULT 6

ADA69728

ID ADA69728 standard; DNA; 2613 BP.

AC ADA69728;

XX 20-NOV-2003 (first entry)

DT Rice gene, SEQ ID 3051.

XX Plant; bacterial infection; fungal infection; viral infection; rice;

XX gene; ds.

XX Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to

XX pathogenic infection for conferring resistance or tolerance to a plant to

XX bacterial, fungal or viral infection by determining or detecting plant

XX gene expression.

XX Claim 6; SEQ ID NO 3051; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes

XX involved in plant resistance or response to pathogenic infection. M1

XX comprises identifying a gene whose expression is significantly altered in

XX the incompatible interaction of plant gene expression relative to

XX expression of the gene in an uninfected plant, in a mutant plant that

XX does not express a gene associated with response to pathogenic infection,

XX or in a corresponding incompatible or compatible interaction. (M1) is

XX useful for conferring resistance to resistance or tolerance to a plant to

XX bacterial, fungal or viral infection. The present sequence was used to

XX illustrate the invention.

XX Sequence 2613 BP; 488 A; 947 C; 797 G; 380 T; 0 U; 1 Other;

XX Query Match 38.6%; Score 1209; DB 7; Length 2613;

XX Best Local Similarity 69.7%; Pred. No. 3.2e-205;

XX Matches 1827; Conservative 1; Mismatches 712; Indels 81; Gaps 11;

QY 302 TCCGCGGCAAGTTCAGGCTGTTCAAGAGAGAGTGTGTGACGTCGGGAGCTTCAAGCGCT 361
 Db 50 TCAAGGGCTCTCCCTGCTCTCATGCGCAAGAACCCCTCGACATCAACGACTTCGGGCGCCA 109
 QY 362 CGTCTCTCGAGCGGCTCCACAGGATCTCTCGGCTGGGACGACGCGGCTCGCTTCCAGCTCG 421
 Db 110 CCGTCATCGAGCGCATCTCGAGTTCCTCGGCGG-----CGGCGTCACTGCGAGCTCG 163
 QY 422 TCAGCGCACCGGCGGCGACCCAGCAACGCGGCGGCTGTGCAAGTGTGGGAGGCGGCGC 481
 Db 164 TCAGCTCTCTCCCTGCTCGACCCCAACAAATGGGAACAGGGGGAGGDTGGGACCGGACGCA 223
 QY 482 ACCTTGAGAGGAGGGGTGCTGCTCAAGTTCACGCGGACGCGGGGAGACCGTGTACCGGG 541
 Db 224 GCCTGAGACGAGTGGCTGACGAGCTGCGGTGCTGACGACGCGGAGAGTCCAACTTCGGGG 283
 QY 542 TGAGCTTCGAGTGGGA---CGAGTCGAGAGGAGATCCGGGCGGCTGCTGCTCAGGAAC 598
 Db 284 TGAGTTTCGAGTGGGAGGTGGGAAGATGGGCATACCCGCGCCATCATCGTCAAGAACA 343
 QY 599 TGCAGCACGCGGAGTTCCTTCTCAAGACGCTCACCTCGAGGGCGTCCCAAGGCAAGGGCA 658
 Db 344 ACCAGCGCGGAGTTCCTTCTCAAGACCATCACCTCGACACGTCCTCCGCGCACGGCG 403
 QY 659 CGTCTGCTTCTGTCGCGCAACTCGTGGGTCTACCCGCAACAGCTCTACTCCAGGAAGCA 718
 Db 404 CCGTCTGCTTCTGTCGCGCAACTCTGATCTACCCGCTTCCAAAGTATCGCTACAACCGCG 463
 QY 719 TCTTCTTTCGCAACGACACCTATCTGCGGAGCAAAATGCGCGGGGTTCGTCCTTATC 778
 Db 464 TCTTCTTCTCAACGACACTTCACTCCGAGCAAGATGCGCGGGGCTGAGCGCTACC 523
 QY 779 GGCAAGATGAGCTCAAGATTCTCCGTGGGACCAATATCTGACCATACACAGAGCATG 838
 Db 524 GCGACGACGAGCTCCGCAACTGCGGGCGCACACACGAGGGCCCGCTACACGAGCACG 583
 QY 839 ATGCGCTACCGTTACGACTACTACATGACCTTGTGATCCGACACAGGGGGAAGAGC 898
 Db 584 ACCGCTTACCGCTACGACTCTCAACGACTTGGCGAGCCGACTCCGCG-----A 637
 QY 899 ACCTCGCGCGATCTCTCGTGGGACCAAGAACCCCGTATCCCGCTGCTGAGAACTG 958
 Db 638 ACCCTCGCTCTCTCGGCGGCTCCCGACCGCCCTACCTCGCGCGGCGCACCG 697
 QY 959 GCGGCAACCAACAAAGAAAGACCCAAATTCGAGAGGAGCGCTTTCCTGCTCAACTGA 1018
 Db 698 GCGCAAAACCCACCAAACTGACCCACCGCGAGAGAGGCTGTCTTCTGCTGA---GA 754
 QY 1019 ACATCTACGTCGCGCTGACGAACGCTTTGGGCACTCTCAAGATGTCGGACTTCTTGGGT 1078
 Db 755 ACATCTAGTGCCACGCGGACGAGCGGTTGCGGCACCTGAAGATGGCGGACTTCTGGGT 814
 QY 1079 ACTGCTGAAGACGATCATCGAGGCTGTTCTTCCAACTGGGGACTTTCGTGATGACA 1138
 Db 815 ACTCCATCAAGGCGCTGTCGACGCGCATCGTGGCGGATCCGCACTACGTCGACCTCA 874
 QY 1139 CGCCCAAGGAGTTCGATTCTGTTGAGGATATCTCTCGGCTCTACGAGCTGGGCGGCAAGG 1198
 Db 875 CACCGCGGAGTTCGACTCTTCAAGGACATCTCAAGCTTACGAGGCGGCTCAAGC 934
 QY 1199 CACCAACCAACCACTGATAGAGATGAGGAAGATCCCGAGGAGTTCCTTCGAA 1258
 Db 935 TGCCAGCATCCCGCGCTGGAGAGCTCGCAAGCGCTTCCCTCTCCAGCTCGTCAAGG 994
 QY 1259 GCATTTCGCGAAGCGGTAGGCATGACCAACCGCTAAAGATGCCCTTCCAAATGTATCA 1318
 Db 995 ACCTCATCCCGCGGCGGCG---GACTACTCTCAAGCTCCCATGCGGACGTCATC- 1050
 QY 1319 AATCAGATGTTGAAAGAGCTCCGGAGTTTAAAGTTTGGCTGGAGAGCTGACGAAGAT 1378
 Db 1051 -----CGGAGGACAAAGAGCGGTGGATGATCGGACGAGT 1087

QY 1379 TCGGAGAGACACTTGCAGCGGTGAACCCAGTAATCATCAACAGCTCTGACGAGTTCC 1438
Db 1088 TCGCCCGGAGATCTTCCGCGGCTCAACCCATGTTATCGCCGCTCACCGAGTTCC 1147
QY 1439 CCGTAAAGCACCTGTGACCCAAAGGAGTACGAGACCAACACAGCAAGATCACTGAAG 1498
Db 1148 CGCGCGAGCGGCTCGACCCGCGAGTACGCGACCAAGACGAGCACCATCACGCGG 1207
QY 1499 CTACATCCGSCATAACATAGGAGGCTGTGCGGTGCAAGACGCACTGAGGAACAAGAGGC 1558
Db 1208 CGCAGTGCAGCGGCTGAGGGGTCAACGTCGACAGGCGATCGAGGCAACCTTC 1267
QY 1559 TCTTATCTTAGACCAATGACCATTTTCAATGCGGTACCTGACGAGATCAACAGAGCTGG 1618
Db 1268 TCTAGTGTGAGACCAACACGATCATTTTCAATGCGGTACTTGTGGATATCAATAGCCTCG 1327
QY 1619 AGGGGAATCTTATCTAGCAGCAGGACCTTCTTCTGAGGAGATGACAGCTGA 1678
Db 1328 ACAGCACTTATCTAAGCAGCGAGCTGTCTTCTGCGCGGAGCGGACGCTGG 1387
QY 1679 AGCCCTGGCCATCGAGTGAAGCTGCCCCAC----CCTGACGGCCAGCAGCGGCGCGG 1735
Db 1388 CGCGCTCGCCATCGAGTGTGCGGACCTGACAGGACGAGCGGCTGATCACCGCCA 1447
QY 1736 TCAGCAGGTGTACACCCCGC-----TCAACCGGCTGAGGGCC 1777
Db 1448 GGAGCACGTGTACACCGCGCGCGCGCGGCGGACCGCGCGCGGCTGAGGTGT 1507
QY 1778 ACGTCTGGCAGCTCGCCAGGCTTATGCTGCGGTAAACGACTCTGCTGCGCATCAGCTGA 1837
Db 1508 GGGTGTGGAGCTCGCCAAAGGCTGACGTCAACGTGAAGACTACTGCTGGACACGCTGA 1567
QY 1838 TCAGCAGTGGCTGAACACGACGCGGTGATCGAGCGGTTCGTAATCGGACAAACCGGC 1897
Db 1568 TCAGCCACTGCTCAACACGACGCGGTGATGAGCGCTTCTGTCATGCGCCACCAACCGGC 1627
QY 1898 AGCTCAGCGTGTGCATCCCGTGCACAAAGCTGTGAGCCGCACTACCGTGACACGCTGA 1957
Db 1628 AGCTCAGCGTGGCGACCCCGGTGCACAAAGCTGTGCTGCGCACTACCGGACACCATGA 1687
QY 1958 ACATCAAGCGCTGGCAGCGGACGACATCATCAAGCGCGCGGCTTTCGAGCGGACCG 2017
Db 1688 CCATCAACGCGCTGGCGCGGACGCTCATCAACGCGCGGCTTTCGAGATGACCG 1747
QY 2018 TGTTCCTGCAAGTACGCTGGGATGTGCGGACGCTGACAGAGCTGAATTTCA 2077
Db 1748 TGTTCGCGGAGACGCGCTGCGATGTGCGGCTTCTAAGGACTGAGCTTCG 1807
QY 2078 ACAGCAGGCTTCTCCAGCAGATCTCTCAAGAGAGGTGTGCTGTCCCGACCACTCAA 2137
Db 1808 CCGACCAAGCGCTCCCGACGACCTTGTCAAGCGCGGCTGCGGCTGCGGACCCGCGCA 1867
QY 2138 GCCCATATGCTCCGACTGCTGATCAAGACTACCCCTATGCGGTGACGGCTCGTCA 2197
Db 1868 GCCGTACAGGTGCGGCTGCTATCAGGACTACCCGTACGCAACAGCGGCTGGCG 1927
QY 2198 TCTGTTGGCGATCGAGCGGTGGTCAAGGAGTACCTGACATCTACTACCTTAACGAG 2257
Db 1928 TCTGGCAGCATCGAGCAGTGGSCCAACGAGTACCTCGCCATCTACTACCCCAACGAG 1987
QY 2258 GCGAGCTTCCAGCTGAGCTGAGCTGAGCGGTGTGGAAGAGGTGCTGAGAGCGGC 2317
Db 1988 GCGTGTCTCCAGGCGACCGCGAGCTGACGCGTGGTGAAGAGGTCCGCGAGGTCCGCG 2047
QY 2318 ACGGCAGCTCAAGGACCGGAGCTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGTA 2377
Db 2048 ATGSCGACATCAAGACGCGAGCTGTGTGCGCGGAGTGAAGAGGTGGGAGCTGCTCA 2107
QY 2378 GGGGTGACGACCATCATCTGGTGGCATCCGCGTGCACGCGGTGTCACTTTGGGC 2437
Db 2108 AGCGTGGCGCACCATCATCTGATGGGTCCGCGTGCACGCGCGCTCACTTCGGGC 2167
QY 2438 AGTACCCATACGCGGCTACTCTCCGAACCGGCGGACCGCGCGCGGCGGCGGCGG 2497

Db 2168 AGTACCCGTACCGCGGTACTCTCCGAAACCGTCCCTCGGTGAGCGCGCGCGATGCCGG 2227
QY 2498 AGCCAGGCGAGCCACGACTACAAAGAGCTGGAGCGGGGACAGAGGCGGACATGGTGT 2557
Db 2228 AGCCGGAACGAAAGAGTACGAGAGCTGG-----CGCGCATCCGAGAAAGTGT 2278
QY 2558 TCATCGGACCATCAACAGCAGCTTCCAGACCATCTCGGSCATCTCGCTCATCGAGATCC 2617
Db 2279 TGTTCGGAACATCAACAGAGATGCGAGGCACTGTTGGGATCTCGCTGCGAGATCC 2338
QY 2618 TCTCAAGCACTCTCCGACGAGGTGTACTCTGGCCAGCTGAACAGGCTGTATCGCTGA 2677
Db 2339 TGTCAAGCACTCTCCGACGAGGTGTACTCTGGACAGCGGACACGCGGA---GTGA 2395
QY 2678 CTTAGAGCGCAAGCGGTGGATGCTTCAAGATTCGGGAGCGGCTGTGCGAGATTG 2737
Db 2396 CTTAGAGCGGAGCGGTGGAGGCTTCAAGCGTTTCGGCGCGGCTGACGAGATCG 2455
QY 2738 AGAATCGGATCAAGACGATGAACGACGATTCGAGACTTGAAGAACCGGAGGCGCTGTGG 2797
Db 2456 AGAGCGGCTGCTGCCATGAACAGGACCCCAACGCAAGAACCGTGTCCGCGCGACCA 2515
QY 2798 AATCGCTGATGCTGTGCTGTACCCCAACAGCTGGAGCTTACCGGCGAGAGGCGGAGG 2857
Db 2516 ATTTCCCTTACAGCTGTCTTACCCAAACACTCCGACCTCAAGGCG---ACGCTGCCG 2572
QY 2858 GGCTTACTCGCATGGGCTTCCCAACGACATCTCCATATGA 2898
Db 2573 GCCTTCCGCGAGGCGCATCCCAACAGCATCTCCATCTGA 2613

RESULT 7

AAQ24492
ID AAQ24492 standard; cDNA; 2830 BP.

XX AC AAQ24492;

XX DT 24-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 12-FEB-1993 (first entry)

XX DE Rice lipoxigenase gene.

XX KW Disease resistant; breeding; wheat flour bleaching; storage; ss.

XX OS Oryza sativa; (Nihon-bare).

XX FH Key Location/Qualifiers
98..2695

XX FT CDS /*tag= a

XX PN JP04094687-A.

XX PD 26-MAR-1992.

XX PF 13-AUG-1990; 90JP-00211469.

XX PR 13-AUG-1990; 90JP-00211469.

XX PA (MITS-) MITSUI GYOSAI SHOKU.

XX DR WPI; 1992-156057/19.

XX DR P-PSDB; AAR23797.

XX PT Rice lipoxigenase gene useful in breeding disease-resistant plant -
PT prepd. by introducing phage or plasmid into host microorganism pref.
FT escherichia coli.

XX PS Claim 1; Fig 1; 7pp; Japanese.

XX CC The rice variety Nihon-bare was allowed to germinate in a dark place and
the RNA isolated from it used to create a cDNA library which was screened

CC to produce a lipoxigenase clone. Lipoxigenase has disease resistant
 CC activity in rice and is useful in producing disease resistant transgenic
 CC plants. Expression of the gene in microorganisms enables mass prodn. of
 CC the enzyme, which can be used for various purposes e.g. wheat flour
 CC bleaching etc. Use of the antisense gene for rice lipoxigenase enables
 CC the breeding of lipoxigenase-reduced or deleted rice, thereby allowing
 CC long term storage of rice free from bad odour characteristics. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)
 XX
 SQ. Sequence 2830 BP; 546 A; 992 C; 846 G; 446 T; 0 U; 0 Other;
 Query Match 36.6%; Score 1148.2; DB 2; Length 2830;
 Best local Similarity 68.6%; Pred. No. 2e-194;
 Matches 1795; Conservative

QY 302 TCCGCGCAGCGGTGAGCTGGTCAAGAGAGGTGTGGACGTGCGGAGCTTCAACGCT 361
 DB 147 TCAAGGCTCCCTCGTCTCATCGCAAGAACGCCCTCGACATCAACGACTTCGGCGCCA 206
 QY 362 CGCTCTCGACGGCGTCCACAGGATCCTCGGCTGGGACGACGCGTGGCTTCCAGCTCG 421
 DB 207 CCGTCATCGAGCGATCTCCGAGTCTCTCGGCCG-----CGGCGTCACTGCGAGCTCG 260
 QY 422 TCAGCGCCACCGCGCGGCGGACCCAGCAACGCGGCGCGTGGCAAGGTGGGGAAGCGCGCC 481
 DB 261 TCAGCTCTCTCTCGTCTGACGCCCAACATGGGAACAGGGGGAGGGTGGGAGCGGAGCGA 320
 QY 482 ACCTGGAGGAGCGGTGGTGTCTCTCAAGTCCACGCGCGGACGCGGAGACCGTGTACCGGG 541
 DB 321 GCCTGGAGCAGTGGCTGACGAGCTCGCTGCTGACGACGCGGAGTCCAAGTTCGGGG 380
 QY 542 TGAGCTTCGAGTGGGA---CGATCGAGGCGATCCCGGGCGCGTCTGTGTCAGAAACC 598
 DB 381 TGAAGTTCGAGTGGGAGGTGGGAAGATGGGATACCCGCGCGCCATCATCTGTCAGAAACA 440
 QY 599 TGCAGACGCGCGGAGTCTTCTCTCAAGAGCTCAACCTCGAGGCGTCCAGCAAGGGCA 658
 DB 441 ACCACGCGCGGAGTCTTCTCTCAAGAGCTCAACCTCGAGAGTCTCCCGCGCGCAGCGG 500
 QY 659 CCGTGTCTTCGTCGCGAATCTGCGGCTACCGGCAAGCTCTACTCCAGGAAACGCA 718
 DB 501 CCGTGTCTTCTGTCGCGCAATCTCTGATCTACCGGCTTCCAGTATCTGCTACAAACCGCG 560
 QY 719 TCTTCTTCGCAACGACACTATCTCCGAGCAAAATGCGGCGGTGGTGGTCTTATC 778
 DB 561 TCTTCTTCTCAACGACATCTACTCCGAGCAAGATGGCGGCGGTGAAGCCGTACC 620
 QY 779 GCGAAGATGAGCTCAAGATCTCCGTGGCGACGATTAATCTCGACCATACAGGAGCATG 838
 DB 621 GCGACGACGAGCTCCGCAACCTCGCGGCGGACGACGACGAGGCGCGGTACAGGAGCAG 680
 QY 839 ATCGCTCTACGTTACGACTACTACAATGACCTTGGTATCCGACAGGGCGGAGAGC 898
 DB 681 ACCGCTGTACCGCTACGAGCTTCAAGAGCTCGGAGCGCCAGCTCCCGC-----A 734
 QY 899 ACCTCGCGCGATCTCTGCTGGGAGCAACACCGGTATCCCGTGTGCTCGAGAACTG 958
 DB 735 ACCCTCGCTGTCTCGCGGCTCCCGGACGCGCCCTACCTCGCGCGCGCGCACCG 794
 QY 959 GCGCGCACCAACAAAGAACCCAAATTCGAGAGAGGCTTTCTGCTGAACCTGA 1018
 DB 795 GCGCGCAACCCACCAAACTGACCCACCGCGGAGAGCGGTGTCTTGTCTGGA---GA 851
 QY 1019 ACATCTACGTCGCGCGTACGAACTGTTGGGATCTCAAGATGTGCGACTTCTTGGGT 1078
 DB 852 ACATCTACGTCGCAACGAGCGAGCGGTTCGGGCACTTGAGATGGCGGACTTCTGGGCT 911
 QY 1079 ACTCGCTGAAGAGATCATCGAGGCTGTCTTCTCAACACTGGGGACTTCTGTGATGACA 1138
 DB 912 ACTTCATCAAGGCGCTCTGTCGAGCGCATCTGTCGCGCGATCGCACCTACGTCGACCTCA 971
 QY 1139 CGGCCCAAGAGTTCGATTCTGTTGAGGATATCTCTCGGCGCTCTACGAGCTGGGCCCGAGAG 1198

DB 972 CACCGCGGAGTTCGACTCTCTTCAAGGACATCTCTCAAGCTCTAGAGGGGCGCTCAAGC 1031
 QY 1199 CACCACCAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGGAGTTCCTTCGAA 1258
 DB 1032 TGCCAGCATCCCGCGCGTGGAGAGCTCGAAGCGCTTCCCTCTCCAGCTGTCAAGG 1091
 QY 1259 GCATTCTCGCAACGCTAGCATCACCGCTTAAGATGCCCTTCCAAATGTCTATCA 1318
 DB 1092 ACCTCATCCCGCGCG-----CGACTACTCTCTCAAGCTCCCATCCGCGACGCTCATC- 1144
 QY 1319 AATCAGATGTGTGAAAAGGCTCCGAGTTTAAGTTTGGCTGGAGGACTGACGAAGT 1378
 DB 1145 -----CGGAGGACAAAGAGCGTGTGATCACCAGCAGT 1181
 QY 1379 TCGGAGAGAGACACTTTCAGGCGTGAACCCAGTAAATCATCAACGCTTACGCGAGTCC 1438
 DB 1182 TCGCCCGGAGATCTCGCGGCGTCAACCCCATGGTTCATCGCCCGCTCACCGAGTTC 1241
 QY 1439 CCGCTAAAGCACCTTGGAACCCAGGAGTACGAGACACACACGACAAATCACTGAAG 1498
 DB 1242 CGCCGGA---GCCGCTCGACCCCGGCGAGGTACGCGACACAGAGCACCATCAAGCGCG 1298
 QY 1499 CTACATCCGGCAATAATCGGAGGCTGTGGTGGAGAGGACTGAGAGAAACAGAGGC 1558
 DB 1299 CGCAGTGGAGCGCGGCTCGAGGGGCTCACCGTGCAGAGGCGATCGACGGCAACCTTC 1358
 QY 1559 TCTTCATCTAGACACCATGACCATTTTCATGCGCTACCTCGACGAGATCAAGAGCTGG 1618
 DB 1359 TCTACGTTGGTGGACACCATGATCTTTCATGCGCTACTTGTGGATATCAATAGCTCG 1418
 QY 1619 AGGGAACTTCATCTACCGCAGCAGACCCCTACTGTTCCTGAAAGGAGTGGACGCTGA 1678
 DB 1419 ACGAACTTTCATCTACGCGCACGCGAGCGTGTGTTCCTGCGCGGCGACGCGCTGG 1478
 QY 1679 AGCCCTCGGCTCGAGCTGAGCTGCGCCACCTGACGCGGCGGCGGCGCTCA 1738
 DB 1479 CGCTCGCATCGAGCTGAGCTTGGCGACCTGAGAGGAGCGGCTGATCACCGCAGGA 1538
 QY 1739 GCAAGTGTATACCCCGGCTCAACCGGG-----TCGAGGGCAAGTCT 1783
 DB 1539 GCAAGTGTATACCGCGCGCGCGCGGCGGCGGCGCGCGCTGGAGTGGTGGTGT 1598
 QY 1784 GGAGCTCGGCAAGGCTTATGCTGGTAAACGACTCTGCTGCGCATCAGCTCATCAGCC 1843
 DB 1599 GGCAGCTCGGCAAGGCGTACTCAAGTGAACGACTCTGCTGGCACGACTGATCAGCC 1658
 QY 1844 ACTGGCTGAACACGACGCGGCTGATCGAGCGCTTCTGTAATTCGCGACAAACCGGCACTCA 1903
 DB 1659 ACTGGCTCAACACGACGCGGCTGATGAGGCGCTTCTGTCATCGCCACCAACCGGCACTCA 1718
 QY 1904 GCGTGTGCTATCCGTCGACCAAGCTGCTGAGCGCGGCTACCTGAGACGCTGAACATCA 1963
 DB 1719 GCGTGGCGCACCGCGTGCACAGCTGCTGCTGCGGCACTACCGGACACCATGACCATCA 1778
 QY 1964 ACGCCCTGGCACCGCGGAGACTCATCAACGCGCGGCGGCTTCTTCGAGCGCACCGCTTCC 2023
 DB 1779 ACGCCCTGGCGCGGAGAGCTCATCAACGCGCGGCGGCTTCTTCGAGAGTGAACGCTTCC 1838
 QY 2024 CTGCAAGTACGCGCTGGGATGTGGGAGAGTGTGCGGAGAGTGTACAGAGCTGGAAATTCAGCAGC 2083
 DB 1839 CGCGAACGAGCGCTCGCATGCTGCGGCGTCTTCAAGGAGTGGAGCTTGGCGGCGC 1898
 QY 2084 AGGCTCTCCGAGCAGATCTCGTCAAGAGAGGCTGTGCTGTGCGGACCAAGCTCAAGGCCAT 2143
 DB 1899 AGGCGCTCCCGAGCAGACTTGTCAAGCGCGGCTCGGT---ACGGACCCCGCGAGCCGT 1955
 QY 2144 ATGCTGTCGAGCTGTGATCAAGAGACTACCCCTATCGCTGCGGCTGCTGCTCATCTGCT 2203
 DB 1956 ACAAGGTGCGGCTGCTCATCGAGGACTACCCGTACCGCAACGAGCGGCTGGCGCTCGCA 2015
 QY 2204 GGGCGATCGAGGCGGTCAAGAGTCACTGAGCATCTACTACCTTAACGAGCGGAGC 2263

Db 2016 CGCAATCGAGCAGTGGGCGACCGAGTACCTGCCATCTACTACCCCAACGAGCGGTGC 2075
QY 2264 TCCAGCGTGCAGTGGAGTGCAGCGGTGGTGGAGAGGTGCGTGGAGGCGCAGCGG 2323
Db 2076 TCCAGGCGGCGGAGCTGCAGCGGTGGTGGAGAGGTCCGCGAGTGGCGCATGGCG 2135
QY 2324 ACCTCAAGAGCCGAGACTGGTGGCCAGAGATGGACACCGTCCAGAGAGTGGTGGCGGT 2383
Db 2136 ACATCAAGAGCCGAGCTGGTGGCGGAGATGAAGCGTGGCGGAGCGTGTCAAGGCGT 2195
QY 2384 GCAGGACCATCATCTGGTGGCATCCGCGTGCAGCGGCTGTCAACTTTGGGCGATACC 2443
Db 2196 GCGCCACCATCATCTGGTGGCATCCGCGTGCAGCGGCTGTCAACTTTGGGCGATACC 2255
QY 2444 CATACGCGGAGTACTCCGAAACCGCGCAGCGGCGCGCCGCGATCCCGAGCCAG 2503
Db 2256 CGTACGCGGAGTACTCCGAAACCGTCCGCGTGGAGCGCGCGGATCCCGGAGCGG 2315
QY 2504 GCAGCCAGCATCAAGAGCTGGAGCGGCGGCGAGAGGAGGCGGATGTTTCATCC 2563
Db 2316 GAAGGAGGAGTACGAGAGCTGG-----CGCGGATCCGGAAGGTGTTGCTCC 2366
QY 2564 GCACCATCAGCAGGAGTCCAGACCATCTGGGCGATCTCGCTCATCGAGATCTCTCCA 2623
Db 2367 GGACAATCAGCAGCATGCAGGCCATCTGGGAGTCTCGCTGGAGATCTCTCCA 2426
QY 2624 AGCACTCTCGAGAGTGTACTCGCGCAGCTGACGAGCTGATCGTGGAGCTAG 2683
Db 2427 AGCACTCTCGAGAGTGTACTCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2483
QY 2684 ACGCCAGGCGGTGGATGCGTTCAGAAAGATTCGGGAGCGGCGTGGTGCAGATTGAGAAATC 2743
Db 2484 ACGCCAGGCGGTGGAGCGTTCAGCGGTTCGCGCGCGGCTGACGAGATCGAGGCC 2543
QY 2744 GGATCAAGAGCATGAAGCAGTCCGAGCTTGAAGAACCGGAAGGCGCTGTGGAATGC 2803
Db 2544 GCGTGTGCGCATGAACAGAGCCGCCACCGCAAGAACCGTGTGCGGCGGAGCAACCAATTTCC 2603
QY 2804 CGTACATGCTGTGATACCCCAACAGCTGCGAGCTTACCGGCGAGAGGCGGAGGCTTA 2863
Db 2604 CCTACAGCTGTCTTACCCCAACACTCCGACCTCGACCTCAAGGCG---ACGCTGCGGCGCTCT 2660
QY 2864 CTGCCATGGGATTCACCAAGCATCTCCATATGAGC 2900
Db 2661 CCGCCAGGCGCATCCCCAACAGCATCTCCATCTGATC 2897

RESULT 8

AAQ24234
ID AAQ24234 standard; DNA; 2830 BP.

AC AAQ24234;

XX 24-OCT-2003 (revised)

DT 04-NOV-1992 (first entry)

XX Lipoxigenase gene.

DE Lipoxigenase gene.

XX Temperature; denaturation; rice; pRLC11; enzyme; ss.

XX Oryza sativa; (Nihonbare).

XX Key Location/Qualifiers

FT CDS 98..2695

FT /*tag= a

FT /label= lipoxigenase

XX JP04094681-A.

XX 26-MAR-1992.

XX 13-AUG-1990; 90JP-00211470.

XX

XX

XX

XX

XX

XX

XX

PR 13-AUG-1990; 90JP-00211470.
XX (MITS-) MITSUI GYOSAI SHOKU.
XX WPI; 1992-156052/19.
XX P-PSDB; AAR20670.
PT Prodn. of protein in E.coli without denaturation - by culturing
PT transformed E.coli at low temp.
XX Disclosure; Fig 1 (1-4); 5pp; Japanese.
XX mRNA was extracted from a rice plant and used to prepare a cDNA library.
CC A clone contg. cDNA encoding the full length lipoxigenase gene was
CC isolated (pRLC11) and used to transform E.coli. The transformant was
CC deposited as FERM P-11635. pRLC11 was then ligated with an expression
CC vector to obtain clone ET3/RLOX2, which was used to transform E.coli
CC BL21(DE3). The obtained clone was deposited as FERM P-11636. This clone
CC was inoculated to ampicillin contg. LB medium, and cultured at 37 degrees
CC C overnight. IPTG was then added, and the mixt. cultured below 20 degrees
CC C, e.g. 18 or 15 degrees C for 16 hrs. Cells were collected and disrupted
CC by ultrasonification to recover the enzyme solution. (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX Sequence 2830 BP; 546 A; 992 C; 846 G; 446 T; 0 U; 0 Other;
QY Query Match 36.6%; Score 1148.2; DB 2; Length 2830;
Best Local Similarity 68.6%; Pred. No. 2e-194;
Matches 1795; Conservative 0; Mismatches 738; Indels 84; Gaps 12;
QY 302 TCCGCGGACGCGTGGGCTGCTCAAGAGGAGGTGCTGGAGCTGGCGACTTCAACGGCT 361
Db 147 TCAGGGGTCCCTCGTCTCATGCGCAAGACGCCCTCGACATCAACGACTTCGGGCGCA 206
QY 362 CGTCTCTCGAGCGGCTGCACAGGATCTCTGGCTGGAGCGACGCGGTGCGCTTCCAGTCTG 421
Db 207 CGTTCATCGAGCGCATCTCCGAGTTCCTCGGCGG-----CGGCGTCACTGCCAGTCTG 260
QY 422 TCAGCGCCACCGCGCGCGACCCCGAGCAACCGGGCGCTGGCAAGTGGGGAGCGGCGCG 481
Db 261 TCAGTCTCTCTCTGTCGACCCCAACATGGGAACAGGGGAGGGTGGGGAGCGAGCGCA 320
QY 482 ACCTGGAGAGCGGTGGTGTCTCAAGTCTACGCGGCGAGCGGGAGACCGTGTACCGGG 541
Db 321 GCCTGGAGCAGTGGCTGACGAGCCTGCGTGCCTGACGACGCGGAGAGTCCAAAGTTCGGG 380
QY 542 TGAGCTTCGAGTGGGA---CGAGTGCAGGCGATCCCGGCGCGCTCTGCTCAGGAACC 598
Db 381 TGAGCTTCGAGTGGGAGTGGAGAGATGGGCATACCCGCGGCCCATCATCTGTCAGGAACA 440
QY 599 TCGAGCAGCGCGAGTTCCTTCTCAAGAGCGTCAACCTCGAGGGCGTCCCGAGGCGCA 658
Db 441 ACCAGCGCGCGAGTTCCTTCTCAAGAGCCATCACCTCGACCAACGTCCTCCGCGCACGGCG 500
QY 659 CGTGTCTCTGTCGCCAACTGCTGGGTCTACCGGCAAGAGTCTACTCCAGGAAGCGCA 718
Db 501 CCGTGTCTTCTGTCGCCAACTCTCTGGATCTACCCCGCTCCAAATATCGCTACCAACCGCG 560
QY 719 TCTTCTTCGCCAACGACACCTATCTGCGGAGCAAAATGCGGCGCGCTTGTGCTTATC 778
Db 561 TCTTCTTCGCAACGACACTTCACTGCGGAGAGATGGCGGCGCTGAGCCGTACC 620
QY 779 GCGAAGATGAGCTCAAGATTCTCGTGGCGACAGTAATCTTGACCATATACAGAGGATG 838
Db 621 GCGACGAGAGCTCCGCAACCTGCGCGCGGACGACACGAGAGGCGCCGTACAGAGGACG 680
QY 839 ATCGGTCTACCGTTACGACTTACTACATGACTTGTGTGATCCCGCAAGCGGCGAGAGC 898
Db 681 ACCCGTCTACCGTACGAGTCTACCAACGACCTCGCGAGCGCCGATCTCGGC-----A 734
QY 899 ACCTCGGCGGATCTCTCGGTGGAGCCAGAACACCGGTATCCCGCTGCTGAGAGACTG 958
Db 735 ACCCTCGCGCTGTCTCTCGGCGGTCTCCCGGACCGCGCTACCTCTCGCGCGCGCGCACCG 794

QY 959 GCCGGCACCCAAAGAAAGACCCAAATTCGAGAGCAGGCTTTTCCTGCTGAACCTGA 1018
Db GCGCAAAACCCAACTGACCCACCGCGAGAGCAGGCTGTCTATTGCTGGA---GA 851
QY 1019 ACATCTACGTCCCGCGTACGACGCTTTGGGATCTCAGATGTCGGACTTCCTTGGGT 1078
Db 852 ACATCTACGTCCCGCGTACGACGCTTTGGGATCTCAGATGTCGGACTTCCTTGGGT 911
QY 1079 ACTCGTGAAGACGATCATCGAGGCTGTTCTTCCAACTCTGGGACTTTCTCGATGACA 1138
Db 912 ACTCCATCAAGGCGCTCGTCAAGGATCGTCCGCGCATCGCACCTACGTCGACCTCA 971
QY 1139 CGCCCAAGGAGTTCGATTCGTTGAGGATATCTCGGCTCTACGAGCTGGGCCACAGG 1198
Db 972 CACCCGCGAGTTCGACTCTCTTCAAGGACATCTCAAGCTCTACGAGGCGGCTCAAGC 1031
QY 1199 CACCCAAACACCTGATAGACGATCAGGAAGATGCCAGGAGTTCCTTCGAA 1258
Db 1032 TGCCAGATCCCGCGCTGGAGAGCTCGGAGCGCTTCCCTCTCAGCTCGTCAAGG 1091
QY 1259 GCATTCGCGAAGGTAGCCATGACACCCGCTAAGATGCCCTTCCAAATGTCATCA 1318
Db 1092 ACCTCATCCCGCGG-----CGACTACTCTCAAGCTCCCATGCGCGACGTCATC- 1144
QY 1319 AATCAGATGTGTTGAAAAAGGCTCCGAGTTCCTGCTGGAGACTGACGAAGAT 1378
Db 1145 -----CGGAGACAAAGAGCGTGGATGACCGACGACGAT 1181
QY 1379 TCCGAGAGACACTTTCAGGCGTGAACCCAGTAAATCATCAAGCTCTGACGAGTTC 1438
Db 1182 TCCCGCGGAGATTCCTCGCGCGGTCAACCCATGCTCATCGCCGCTTCAACGAGTTC 1241
QY 1439 CCCTAAAGACACCTGGACCCAGGAGTACGAGACACACAGCAAGATCACTGAAG 1498
Db 1242 CGCCGA---GCGCTCGACCCGCGCAGGTA GGGGACCGACGAGCACCATCACGGCG 1298
QY 1499 CTCAATCCGCGATACATGGAGGCTGTTCGCTGAGAAACCGATGAGGAACAGAGGC 1558
Db 1299 CGCAGCTCGAGCGCGGCTCGAGGGCTCACCGTGCAGCAGCGCATCGACGCAACCTTC 1358
QY 1559 TCTTCACTCTAGACACCATGACCATTTCTATCGCTGACCTCGACGAGATCAACGAGCTGG 1618
Db 1359 TCTAGCTGAGACACCATGATATTTCTATGCTGATCTGTTGATATCAATAGCTCG 1418
QY 1619 AGGGAACTTCTATAGCCAGCAGGACCTACTGTTCTGAGGACGATGCGACGCTGA 1678
Db 1419 ACACAACTTCTATACGCAACGCGGACGCTGTTCTGCGCGGACGCGACGCTGG 1478
QY 1679 AGCCCTGGCCATCGAGCTGAGCTGCCACCCCTGAGCGGCGCAGCGCGCGGCTCA 1738
Db 1479 CGTCCGATCGAGCTGAGCTTGCAGCACTGCGAGCAGCGGCTGATCACCGCAGGA 1538
QY 1739 GCAAGGTGTACACCCCGGTCAACCGG-----TCGAGGGCCACGCTCT 1783
Db 1539 GCACCGTGTACACCGCGCGGCGCGCGCGGCGCACCGCGCTGAGTGGTGGGTGT 1598
QY 1784 GCGAGCTCGCCAGGCTTATGCTGGTAAAGATCTGCTGCGCATCAGCTGATCAGCC 1843
Db 1599 GCGAGCTCGCCAGGCGTACGTCAGCTGAACGATCTGCTGGCACCCAGCTGATCAGCC 1658
QY 1844 ACTGGTGAACCGCACGCGGTGATCGAGCGCTTGTAAATCGGACAAACCGGAGCTCA 1903
Db 1659 ACTGGCTCAACACGACGCGGTGATGAGGCCCTTCTGTCATCGCCACCAACCGGAGCTCA 1718
QY 1904 GGTGTGTGATCCGTGCAAGAGTGTCTGAGCCGCGACTACCGTGAACGCTGAACATCA 1963
Db 1719 GGTGTGCGCACCGGTGCAAGAGTGTCTGCTCGGCACTTACCGGACACCATGACCATCA 1778
QY 1964 AGCCCTGCGCAGCCAGACACTCATCAACCGCGGCGGTCTTTCAGCGCACCGGTGTTC 2023
Db 1779 ACGGCTGCGCGGAGACGCTCATCAGCGGCGGCGATCTTCAGATGACCGGTGTTC 1838

QY 2024 CTGCAAGTACGCGTGGGATGTCGCGACGCTGTACAAGAGCTGGAATTTCAACGAGC 2083
Db 1839 CGCGAAGCAGCGCGCTGCCATGTCGTCGCGGTCTTACAAGGACTGAGCTTCGCGAC 1898
QY 2084 AGGCTCTCCAGCAGATCTCGTCAAGAGAGTGTGGCTGTGCGGACCACTCAAGCCAT 2143
Db 1999 AGGCGCTCCCGAGAGACCTTGTCAAGCGCGGCGTCCGT---ACGGACCCGCGAGCCGT 1955
QY 2144 ATGCTGTCGAGTCTCTGATCAAGGACTACCCCTATGCGCTTGACGGGCTCGTATCTGGT 2203
Db 1956 ACAAGTGGGCTCTCTCATCGAGGACTACCGTACGCAACGACGGGCTGCGCTGTGCA 2015
QY 2204 GGGCGATCGAGCGGTGGTCAAGAGTACTTGAACATCTACTACCTTAAAGCAGCGGAGC 2263
Db 2016 CGCCAAATCGAGAGTGGGCCACCGAGTACCTTCGCCATCTTACTACCCCAACGACGCGGTGC 2075
QY 2264 TCCAGCTGAGCTGGAGCTGCGAGCGTGTGGAAGAGGTGCGTGAAGAGCGCAAGCGG 2323
Db 2076 TCCAGGCGGACGCGGAGCTGCGAGCGTGTGGAAGAGGTGCGGAGTCCGGCATGCGG 2135
QY 2324 ACCTCAAGGACCGAGACTGCTGGCCAGGATGACACACCGTCCAGAGCTGGCTAGGGCT 2383
Db 2136 ACATCAAGGACCGGAGCTGCTGGTGGCGGAGATGAAGCGGTGGCGGACGCTGCTCAAGCGCT 2195
QY 2384 GCAGACCATCATCTGGGTGGCATCCGCGCTGCAAGCGGCTGCAACTTTGGGCACTACC 2443
Db 2196 GGGCCACCATCATCTGGATCGGCTCCGCGTGTGCAAGCGGCTCACTTCCGCGAGTACC 2255
QY 2444 CATHAGCGGGTACCTCCGAAACGCGCGAGCGCGAGCGCGGCGCGATCCCGGAGCGAG 2503
Db 2256 CGTACGCGGGTACCTCCGAAACCGTCCGTGGTGAAGCGCGCGGATCCCGGAGCGG 2315
QY 2504 GCAGCCACGACTCAAGAAAGCTGGAGCGGGGAGAGGAGGCGGACATGCTGTTCATCC 2563
Db 2316 GAACGAGGAGTACGACGAGCTG-----CGCGCATCCGGAAGGTGTTGTTCC 2366
QY 2564 GCACCATCAGCAGGATTCAGACCATCTGGGCACTTCGCTCATCGAGATCCTCTCCA 2623
Db 2367 GGACATACCAAGCAGATGAGGCCATCTGCGGGATCTGCTGCTGGAGATCCTGTCCA 2426
QY 2624 AGCATCTCCGAGGAGTGTACTCGGCCAGCGTGCAGGCGCTGATCGCTGAGCGTCA 2683
Db 2427 AGCATCTCCGAGGAGTGTACTCGGACGCGGACGCGGACGCGGCAACCGCGG---GTGAGCTTCG 2483
QY 2684 ACGCCAAGCGCTGGATGCGTTCAAGAGTTCGGGAGCGGCTGGTGCAGATTGAGATC 2743
Db 2484 ACGCCAAGCGCTGGAGCGTTCAAGCGGTTTCGCGCGCGGCTGACGAGATCGAGAGCC 2543
QY 2744 GGATCAGACGATGAACGACGTCGCGATTTGAAGAACGGAAGGCGCTGTGGAATGC 2803
Db 2544 GCGTGTGCGCATGAACAGGACCCCGACCGCAAGAACCGTGTGCGGCGGACCAATTTCC 2603
QY 2804 CGTACATGCTGTGTATCCCCAACACGTCGAGCGTTTACCGCGAGAGGCGGCGCTTA 2863
Db 2604 CTTACAGCTGTCTATCCCCAACACCTCGACCTCAAGGCG---ACGCTGCGGCGCTCT 2660
QY 2864 CTGCGATGGCATTCGCAACGAGCATCTCCATATGAGC 2900
Db 2661 CCGCCAGGGGCTATCCCGAACAGCATCTCATCTGATC 2697

RESULT 9

ADC53127
ID ADC53127 standard; DNA; 3033 BP.

XX ADC53127;

AC
XX
DT 18-DEC-2003 (first entry)

XX 9'-specific lipoxigenase gene.

DE
XX 9-specific lipoxigenase; 9'-specific lipoxigenase activity; microbe;
KW animal; plant; gene; ds.

Db 1675 ACATGCTGTGATGAGCCCTTCGTGATCGCTACAAACCGCCAGCTCAGTGTGACAC 1734
QY 1915 CCGGTGCAAGCTGTGAGCCCGCCTACTACGCTGACACGCTGAACTCAACGCCCTTGCA 1974
Db 1735 CCTGTGTACAACTCTCCAGCCACACTATCGGCACACGATGACATCAATGATGGCA 1794
QY 1975 CGCAGACACTCATCAACGCCCGCGCTTCGAGCGCACCGTGTTCCTCTGCAAGTAC 2034
Db 1795 CGCAGACACTCATCAACGCCCGCTGCAATTTTCGAACAACTGTCTTCTCTGCAACAT 1854
QY 2035 GCCTGGGATGTGGGAGACGCTGTACAGAGCTGGAATTTCAACGAGAGGCTTCCCA 2094
Db 1855 GCTCTGGCAATGTCTTACAGAGTTTCAAGAACTGGAATTCGCGAACAGGCGCTTCG 1914
QY 2095 GCAGATCTCGTCAAGAGAGGTGTGGTGTGCGCGACAGTCAAGCCCATATGCTGCCA 2154
Db 1915 GATGATCTGATAAAGAGAGGCAATTCATCAAGACCCCATCAAGCCCATCCAGGTGA 1974
QY 2155 CTGCTGATCAAGACTACCCCTATGCGGTGTGAGCGGCTGTGATCTGGTGGGAGTCA 2214
Db 1975 CTACTGATCAAGACTACCCCTATGCAACAGATGGGCTGTGGATCTGGCAAGCAATCG 2034
QY 2215 CGTGGGTCAAGAGTACCTGGACATCTACTACCTAAACGAGCGGAGCTCCAGCGTAC 2274
Db 2035 CAGTGGTCACTGAGTACTGTGCACTACTACTACCCAAACGATGGTGTCTCCAGGAG 2094
QY 2275 GTGAGCTGAGCGGTGTGGAGAGGCTGTGAGAGGCGCAGCGCACTCAAGGAC 2334
Db 2095 GTGGCGCTGCAAGCTGTGGAGAGGAGTACGGAAAGTCCGGCATGCTGATCTCAAG 2154
QY 2335 CGAGATGTGTGGCCAGGATGACACCGTCCAGCAGTGGCTAGGCGGTGACAGCCATC 2394
Db 2155 GCGGATGTGTGGCCAGAGTGCAGAGCTTGCCTGAGCTCACCAAGCCTGCACCAATC 2214
QY 2395 ATCTGGGTGCACTCCGCTGTACAGCGGTGTCACTTTGGGAGTACCATACCCCGG 2454
Db 2215 ATCTGGATTGCACTAGCACTTCCAGCAGCGCTCAATTTCCGGCAGTACCATACCG 2274
QY 2455 TACTCCGAACCGCGCGAGCGCACCGCGCGCGCTGAGCGCGGAGCGGAGCGACAGC 2514
Db 2275 TATCTTCCAAACCTGCGACCATAGCCCGCGCGCTGAGCGCGGCTTCCAGGAG 2334
QY 2515 TACAAGAGTGGAGCGGGCGAGAGGAGGCGGAGTGTGTTTCATCGCACCATCAC 2574
Db 2335 TACACAGAGTGG-----ACGAGAACCCAGAGAGTCTTCTATCGCACCATCAC 2385
QY 2575 AGCCAGTTCAGACATCTCTGGCATCTCGCTCATCGAGATCTCTCCAGCACTCTCC 2634
Db 2386 AGCCAAATCCAAACCAATCTCGGTGTCTCGCTCATGAGATTTCTATCAAGCACTCAG 2445
QY 2635 GACGAGTGTACCTCGGCCAGGTGACGAGCGCTGATCGCTGACGCTCAGACGCCAAGCG 2694
Db 2446 GATGAGATCTATCTTGGGAGGTGACACGCCAGA---GTGACATCAGACCCCAAGCA 2502
QY 2695 CTGGATTCGCTTCAAGATTCGGAGCCCGCTGGTGTGAGATTCGATTCGATTCAGAG 2754
Db 2503 CTGGAAGATTCAGAGGTTACAGAGGCTGAGGAGCTGGTGGAGATTGAGAGCAAGTGT 2562
QY 2755 ATGAACGACAGTCCGAGTTCGAAGAACCGGAAGGCGCTGTGGAATGCGTACATGCTG 2814
Db 2563 ATGAACAGAGACCCCTGTCTCAAGACCGGCTCGGTTCAGCCAAATTTCCCTACACTG 2622
QY 2815 CTGTACCCCAACAGCTCGAGCTTACCGCGAGAGAGCGCGAGGCGGTACTGCCATGGC 2874
Db 2623 ATGTTCCCAACACGCTCAGACAAATAGG---GGCGGCTGAGGGGATCACTGCCAGGG 2679
QY 2875 ATTCCCAACAGCATCTCCATATGAGCCTG 2903
Db 2680 ATCCCCAATAGCATCTCAATATGAGACTG 2708

RESULT 10
ADA70433

ID ADA70433 standard; DNA; 2559 BP.
XX
AC ADA70433;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3756.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 3756; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2559 BP; 686 A; 700 C; 641 G; 532 T; 0 U; 0 Other;
Query Match 34.0%; Score 1066.8; DB 7; Length 2559;
Best Local Similarity 66.4%; Pred. No. 5.6e-180;
Matches 1729; Conservative 0; Mismatches 782; Indels 93; Gaps 10;
QY 298 AAGATCCGCGCAGGTGAGGCTGTGTCAGAGGAGGTCTGACGCTCGGACCTTCAAC 357
Db 46 AAGATCAAGGCTTGGCTGTGATGAGCGGAAATTAATCTGATCCAAAGGACTTCACT 105
QY 358 GCCTCGCTCTCGACGCGCTCCACAGGATCTCTGGTGGAGCAGCGGCTCGCTTCCAG 417
Db 106 GCCTCGCTCTCGACACGCTCCATGAGGCTTTGGAA-----ACAGCATCACCTGCCAG 159
QY 418 CTGCTCAGCGCCACCGCGCGGACCCAGCACCGGCGCGTGGCAGGTGGGAGGCG 477
Db 160 CTGTGAGCGCCACTGTTCGCGACCAAAACAATAGGCGAGGGGATAGTGTGATCAGAG 219
QY 478 GCACACCTGGAGAGCGGTGTGTCGCTCAAGTCCACGCGGACCGGGAGAGCCGTGTAC 537
Db 220 GCGAATCTGAGCAGGGTTGACAGATTTACCATCGGTATCAACAGGAGTCCAGCTC 279
QY 538 CGGCTGAGCTTCAAGTGGGA---CGAGTCGAGGCGATCCCGGCGCGCTCTCTGTCAGG 594
Db 280 ACAGTGAGGTTCAACTGGGAGATGGCAAGCATGGTGTGCCAGGGGCCATCATCATCAAG 339
QY 595 AACCTGCAGCACCGCAGTTCCTTCCTCAAGACGCTCACCTCGAGGGCGTCCCGAGCAAG 654

QY 2815 CTGTACCCACACAGTGGAGCTTACCGGCGAGAGCCGAGGGCTTACTGCGATGGG 2874
 Db |||||
 QY 2479 ATGTTCCCAACACAGTCAGCAATAAGG---GGCGCTGAGGGATCATCTGCGAGGGC 2535
 Db |||||
 QY 2875 ATTCCCAACAGCATCTCATATGA 2898
 Db 2536 ATCCCAATAGCATCTCAATATGA 2559
 |||||

RESULT 11

ABX13452
 ID ABX13452 standard; DNA; 2562 BP.

AC ABX13452;

DT 04-JUN-2003 (first entry)

DE A. thaliana LOX5 DNA corresponding to Genbank AJ302043.

XX Expression cassette; transgenic; promoter; LOX5; plant; food production;
 KW animal feed; seed; stress resistance; disease resistance; starch content;
 KW lipid content; dormancy; fibre content; pharmaceutical production;
 KW fine chemical production; sterile plant; vitamin; flavouring; perfume;
 KW dye; cotyledon; embryonic tissue; stress factor; LOX; ds.

XX Arabidopsis thaliana.

XX DE10127882-Al.

XX 12-DEC-2002.

XX 11-JUN-2001; 2001DE-01027882.

XX 11-JUN-2001; 2001DE-01027882.

XX (BADI) BASF PLANT SCI GMBH.

XX Bischoff F, Feussner I, Loyall LP;

XX WPI; 2003-279966/28.

XX Cassette for expressing transgene, useful e.g. in production of
 PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
 PT of Arabidopsis, provides cotyledon-specific expression.

XX Claim 5; Page; 28pp; German.

XX This invention describes a novel cassette for the transgenic expression
 CC of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
 CC thaliana or deletion variants of the LOX5 promoter which are functionally
 CC linked to the nucleic acid of the invention. The cassette is used to
 CC prepare transgenic organisms, especially plants, for production of foods,
 CC animal feeds, seeds (including those with increased resistance to stress
 CC and disease, altered starch/lipid contents or dormancy, or altered fibre
 CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and
 CC pharmaceutical proteins) and fine chemicals (especially enzymes,
 CC vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
 CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter
 CC provides strong and specific expression in cotyledons and/or other early
 CC embryonic tissue, so can degrade, or protect against, stress factors to
 CC which these tissues are particularly sensitive. Since cotyledons are the
 CC main storage organs of seeds, expressing transgenes in them produces
 CC targeted increases/modifications in nutritional value. Expression in the
 CC cotyledons is homogeneous, there are no side effects on other plant
 CC organs (pollen) and the promoter is functional in a wide variety of
 CC plants (ornamentals or crops). This sequence represents a nucleic acid
 CC sequence associated with the Arabidopsis thaliana LOX gene described in
 CC the disclosure of the invention

XX Sequence 2562 BP; 733 A; 624 C; 596 G; 609 T; 0 U; 0 Other;

SQ Query Match 24.8%; Score 777.6; DB 7; Length 2562;

Best Local Similarity 58.9%; Pred. No. 1.2e-128;
 Matches 1539; Conservative 0; Mismatches 1004; Indels 69; Gaps 9;

QY 238 AGATCCCGCGCAGCGTGGTCAAGAGAGGCTGCGAGCTGCGGAGCTTCAAC 357
 Db |||||
 QY 4 AAGATAGAGAGAGTGTGTTGATGAAGAGAAATCTCTTGTATTTCAAGAGCTTATG 63
 Db |||||
 QY 358 GCTCGCTCTCCGACGCGCTCCACAGGATCCTCGGCTGGGACGCGGCTCGCTTCCAG 417
 Db 64 GCTTCTCTTGTGATCGTGTCAATGAGCTTCTTGGTGG-----TCGTGTCTCTCTCCAC 117
 QY 418 CTCGTACGCGCACCGCGCGCGACCCCGAGCAACCGGGGCGCTGGCAAGTGGGAGAGCG 477
 Db |||||
 QY 118 CTCATCAGCTCTCACCAACCGCGACCGCGCAATGAGAAAGAGAGAACTTGGAAAAAGCA 177
 QY 478 GCGCACCTGGAGAGCGGTGTGCTCAAGTCCACGG---CGGACGGGAGACCGGTG 534
 Db 178 GCACATCTGGAAATGGTAACAAATAAAGCTCAGTAACCGCTGAGGAACTGCG 237
 QY 535 TACGGGTGAGCTTCGAGTGGGAGAGTCGCGAGGGCATCCCGGCGCGCTCTCTGTGAGG 594
 Db 238 TTTGAGTAAAGCTTTGATTGGGACGAGTCAATGGGACCCCGGCTGCATTTGTGATCAAG 297
 QY 595 AACCTGACGACGCGGAGTCTTCTCAAGAGCTCACCTCGAGGGGCTCCCAAGCAAG 654
 Db 298 AACACACCAATAGTCAATTTACCTTAAGTCCCTCACCTCCGCGGCTTCTCTGATGGC 357
 QY 655 GGCACCGCTGTC-----TTGCTGCCCAACTGTTGGGTCTACCCGCAACAAGCTC 702
 Db 358 GAAGGTGTGGCACTGCGATACATTTTCATCTGCAATTTCTTGGATTTACCCGAATCATCGA 417
 QY 703 TACTCCAGGAGACGATCTTCTCGCAACGACACCTATCTCGCGAGCAAAATCCCGCG 762
 Db 418 TACCGCTCGGACCGGTTTTCTTCTTAAGAGCATATCTTCCAAGTGAACACCGGAG 477
 QY 763 GCGTTGGTGCCTTATCGCAAGATGAGCTCAAGATTCTCGTGGCGAGTAATCTCTGA 822
 Db 478 CTAATCAAGAGCTAAGAGAGAGAGCTAAGAAATCTAAGAGGCAATGAGAAAGAGGA 537
 QY 823 CCATACGAGGAGCATGATCGCTTACGGTTACGACTACTACATGACCTTGGTGTATCCC 882
 Db 538 GAATTTCAAGAAATGGGACAGAGTTTACGACTACCTTATTACAACGACTTTGGGTGCTCT 597
 QY 883 GACAGGCGGAGAGACGCTCGGCGCATCTCGTGGCGAGCCCAAGAACACCCGATATCCC 942
 Db 598 GACAAGGTCCTGACTCAGTTCTGTCGGTTCTTGGCGGTTCCACCTGAGTGCCTTATCCT 657
 QY 943 CGTCTCTCAGAACTGGCGCGCACCAACAAAGAAAGACCAATTCGGAGAGAGGCTT 1002
 Db 658 CGCGTGGCAAAACCGCGCGTAAATCCACCAATCAGACCCCTAAGTCTGAAGCAGGCTG 717
 QY 1003 TTCTCTGCTGAACCTGAACTCTAGTCCGCGGTGACGAACGCTTTGGGCATCTCAAGATG 1062
 Db 718 GCTTTACTAACTTAACATATAGTGCCAGGAGCAGCGATTTAGCCATGTGAAGTTT 777
 QY 1063 TCGGACTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTTCACAACTCGGG 1122
 Db 778 TCAGACTTCTTCGCTTATGCACTCAAGTCCGTGACTCAAGTGTCTGCTCGAGATCGCC 837
 QY 1123 ACTTTCGTCGATACAGCCCAAGGAGTTCGATTCTGTTTGGAGGATATCTCGGGCTCTAC 1182
 Db 838 TCTGTTCCGACACACCATCAAGATTTGACTCTCTCGAAGATGTTTTTCACCTCTAT 897
 QY 1183 GAGTGGGCCGAGAGGACCCCAACACCCACTGATAGAGATCAGAGAAAGATCCCC 1242
 Db 898 GACGCTAGTATTAAGCTCGCCAAATGGTCACACCAATTTCTAAGCTCCGCTGATGTTATCCG 957
 QY 1243 AGCGAGTCTTTCGAGCATTTCCCGAAGCGTAGCATGACCAACCCCGCTTAAGATGCC 1302
 Db 958 TGGGAGATGTTTAGAGAGCTAGTTTCGCAACG---ACGAGAACCGGTTCTTGAAGATATCCC 1014
 QY 1303 CTTCCAAATGTCATCAAAATCAGATGTGTGAAAAAGGCTCCGGAGTTTAAAGTTTGGCTGG 1362
 |||||

Db	1015	TTGCTGACATCTCAA-----GAGACGAGANTCGGCTGG	1051
Qy	1363	AGGACTGACGAAGAGTTGCGGAGAGAGACACTTGCAGCGGTGACACCCAGTAATCATCAAA	1422
Db	1051	AGGACTGACGAAGAGTTGCTCGAGAAATGCTGCGCGGTCTTAATCCGGTGGTATTAGC	1110
Qy	1423	CGTCTGACGGAGTTCGCGCTAAAGACACCTGAGACCAAGGAGTACGAGAGCCACACC	1482
Db	1111	CGTCTTCAGGAATTTCCACAAAGAGTGCTGAGACTCTGCAAGTAGTATGAAACCAACAC	1170
Qy	1483	AGCAAGATCACTGAAGCTTCATCCGGCATAAACATGGGAGCGCTGTCGGTGCAGAAACGCA	1542
Db	1171	TCCTCCATACGAACAGAGCACATAGATCAACATGAACGCGCTCAATGCTCCAAGAGCT	1230
Qy	1543	CTGAGGAACAGAGGCTCTTCATCCTAGACCAACATGACCATTTTCATGCGGTACTTCGAC	1602
Db	1231	TTGAAACAGAAATAGCTATACATATTGGATCATCAGACGATTTGATGCTTACCTGACA	1290
Qy	1603	GAGATCAACGAGCTGGAGGGAACTTCATCTACGCCAGAGGACCTTACTGTTCTCTGAAG	1662
Db	1291	CGGATAAECTCAACAAACACTAA---AACCTATGCGACCCGAAACCTTGCTTGCTTCAA	1347
Qy	1663	GACGATGGCAGCTGAAGACCCCTTGCCCATCGAGCTGAGCCTGCCCCACCCCTGACGGCCAG	1722
Db	1348	GCAGACGGAACACTGAAGACCTCTCGCCATAGAGCTGAGTCTTCCACAGCCACAAGCGCAA	1407
Qy	1723	CAGCGCGCGCGTACGCAAGGTGTACACCCGCGCTCACACGCGCTGCGAGGCCACGTC	1782
Db	1408	TCATATGGATCGGTACGAAAGTTTTCACACAGCAGAGAAAGGTGCGAGGGATCGGTT	1467
Qy	1783	TGGAGCTGCCAAGGCTTATGCTCGTAAACGACTCTGCCCTGGCATCAGCTGATCAGC	1842
Db	1468	TGGCAACTTGCTAAGGCTTATGCTGCGGTCAATGACTGCTGTTATCATCAGCTTATAAGC	1527
Qy	1843	CAGTGGCTGAACAGCAGCGGCTGATCGAGCGCTGCTGAATCGGCAACACCGGAGCTC	1902
Db	1528	CATTGGTTGCAACGCAATGCGGTGATTGAACCGTTTATAATCGCGTCCAATGAGCAGCTC	1587
Qy	1903	AGCGTGTGATCCGCTGCAAGAGCTGCTGAGCGCCGCACTACCGTGACACGCTGGAACATC	1962
Db	1588	AGCGTGTGTCATCCGATCCATAAATCTTACATCTCTCATTTCCGTGACATATGAACATC	1647
Qy	1963	AACGCGCTGCAAGCCAGACACTCATCAACGCGGGGGGTCTTCGAGCGCACCGGTGTTCC	2022
Db	1648	AACGCAATTAGCGGCTCATGTACTCATAACTCAGACGGAGTCTCTTGAGAGAACAGTCTTC	1707
Qy	2023	CCTGCAAGTACGCGCTGGGATGTCGGCAGACGTTACAAGAGCTGGGAATTCACACGAG	2082
Db	1708	CCTAGTCGATCGCCATGGAAATGTCTTCTCAATTTACAGAAATTTGGTTTTTCCACCGAG	1767
Qy	2083	CAGGCTCTCCAGCAGATCTGCTCAAGAGAGGTGTGGCTGTGCGGACACCAAGTCAAGCCCA	2142
Db	1768	CAGGCTCTCCAAAAGACCTCTCAAACGAGGAGTTGCTGTTGAAGATCCAAACAGTGAC	1827
Qy	2143	TATGGTGTCCGATGCTGATCAAGGACTACCCCTATGCGGTTCGACGGGCTCGTCTATCGG	2202
Db	1828	AACGGCTTAAGCTTCTGATCGAAGATTACCCGTTTTCGGGTGACGCGTTAGAGATTTGG	1887
Qy	2203	TGGGCGATCGAGCGGTGGGTCAAGAGAGTACTTGAGACATCTACTACCGTCAACGACCGGAG	2262
Db	1888	TCAGCGATCAAAACATGGGTACAGAGTACTGCACATTTCTACTACAATAATGACAAACC	1947
Qy	2263	CTCCAGGTGACGTGAGCTGAGGGTGTGTAAGAGGTGTGGTGAGAGGGCGGACGGC	2322
Db	1948	GTCCAACCGGATACAGAGATCCAAATCATGGTGAACCGAGCTCCGAACCAAGGCCACGGC	2007
Qy	2323	GACCTCAAGAGCCGAGACTGGTGGCCGACGATGGACACCGTCCAGCAGCTGGCTAGGGGG	2382
Db	2008	GACAAACGACACAGTCAATGGTGGCTTTCGATGCAAAACCGGCGACGACCTAATCGAAACC	2067
Qy	2383	TGCAGACCATCATCTGGGTGGCATCCGGCTGCACGCGGCTGTCAACTTTGGCGAGTAC	2442
Db	2068	TGACCATCATCATCTGGATCGGCTCTGTCTTTCAGCGAGCAATTAATTCGACAGTAC	2127

RESULT 12
ABZ68210

ABZ68210
ID ABZ68210 standard; DNA; 3390 BP.

AC ABZ68210;

DT 07-APR-2003 (first entry)

DE Nucleotide sequence comprising CamV 35S promoter and tobacco LOX1.

AA
KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;
KW polyunsaturated fatty acid; pentadiene; disease resistance;
KW tobacco; tomato; potato; pepper; gene; ss.

OS Nicotiana tabacum.

XX	Key	Location/Qualifiers
FH		
Ft	promoter	1.532

FT	/cay= a
FT	/note= "CamV 35S promoter"
FT	543. .3131
FT	CDS

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FT /tag= D
FT /product= "LOX1"
FT /note= "6"

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XX
PN
WO200299112-A2.

12-DEC-2002
XX PDXX
PF
06-JIN-2002: 2002WO-ER001943XX
PR 07-TTN-2001: 2001EB-00007470

PR 07-JUN-2001; 2001FR-00007470.
PR 07-NOV-2001: 2001FR-00014358.

XX
PA (RHOB-) RHOBT-

PI Mene-Saffirane L, Esquerre-Tugaye M, Fournier J, Beffa R;
 XX Grosjean-Cournoyer M;
 DR WPI: 2003-156859/15.
 DR P-PSDB; ABP70404.
 XX
 PT Reducing sensitivity of plants to diseases and pathogens, by
 PT overexpressing a lipoxigenase, also vectors and cassettes for the process
 PT and transformed plants.
 XX
 PS Example 2; Page 42-46; 47pp; French.
 XX
 CC The present sequence encodes a lipoxigenase-1 (LOX-1) gene. LOX-1 is an
 CC enzyme that catalyses the dioxygenation of polyunsaturated fatty acids
 CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce
 CC the sensitivity of plants to diseases and attack by pathogens.
 CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi
 CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.
 CC tobacco, tomato, potato and pepper
 XX
 SQ Sequence 3390 BP; 1067 A; 698 C; 742 G; 883 T; 0 U; 0 Other;
 Query Match 23.9%; Score 748.2; DB 7; Length 3390;
 Best Local Similarity 58.5%; Pred. No. 2.1e-123;
 Matches 1481; Conservative 0; Mismatches 998; Indels 54; Gaps 8;
 QY 298 AAGATCGCGGACGGTGGCTGGTCAAGAGGAGGTGCTGGACGTGGCGACTTCAAC 357
 DB 594 AAGGTAAAGGAACAGTGGTGGTGGTGAAGAAATGTTTGGATTTTACTGATATTAAT 653
 QY 358 GCCTCGCTCTCCACCGGCTGCCAGAGATCCTCGGCTGGGACGACGGCGTCCCTTCCAG 417
 DB 654 GCCTCAGTCTTGGATGGAGTCTTGGAGTTCCTTGGTGGG-----AGGTCTCTCTCGAG 707
 QY 418 CTGCTCAGCGCCACCGGCGGACCCAGCAACGCGGGGCGGTGGCAAGTGGGGAGGCG 477
 DB 708 TTGATCAGTCTGTTAATGCTGATCTCTGCAATGCTTTACAAGGGAAACGCAAGCA 767
 QY 478 GCCACCTGGAGAGCGGTGGTGGTGGCTCAAGTCCAGCGGCGGACGGGAGACCGGTGAC 537
 DB 768 GCATATTGGAGAACTGGCTTACAAATAGACACCCCAATAGACGAGGTGAATCAGCATTT 827
 QY 538 CGGCTGAGCTTCAGTGGGACGAGTGGCGAG-----GGCATCCCGGGCGCGTCTCTGTCAGG 594
 DB 828 AGAGTCACATTTGATTTGGGATGATGAGGAATTTGGAGTTCACAGGAGCATTCATTATCAAG 887
 QY 595 AACCTCAGCAGCGCGAGTCTTCTCAAGAGCTCACCTCGAGGCGGTCCAGGCGAG 654
 DB 888 AACTTGCAATTTAGTGAGTCTTCTCAAGTCACTCACCCTTGAAGATGTTCTTAATCAT 947
 QY 655 GGCACCGTCTGCTTCTGCTCCAACTGTTGGGTCTACCCGCAACAAGCTCTACTCCAGGAA 714
 DB 948 GGCAAAAGTTCAATTTGCTGTAAATCTTGGGTTTATCTGCTTAATAATATAAGTCAGAT 1007
 QY 715 CGCATCTTCTCGCAACGACACCTATCTCGGAGCAAAATCCCGGCGCGTGTGCTGCT 774
 DB 1008 CGCATCTTCTCGCAATCAGGCTTATCTTACCAGTGAACACCCAGACACATTTGCGAAA 1067
 QY 775 TATCGCAAGATGAGCTCAAGATTTCTCGTGGCGACGATTAATCTTGGACCATACCAGGAG 834
 DB 1068 TACAGAGAAATGAATTAGTAACCTTAAGAGGAGATGGAA---CTGGAAGCTTGAAGAA 1124
 QY 835 CATGATCGGTCTACCGTTACGACTACTACATGACTTGTGATCCCGACAGAGGGGAA 894
 DB 1125 TGGGATAGAGTTATGACTATGCTTACTACAAATGACTTGGGTGATCCAGACAAAGGGCAA 1184
 QY 895 GAGCAGCTCGGCGGATCTCGTGGCGAGCCAGCAACACCCGATATCCCGCTCGTGCAGA 954
 DB 1185 GATTTCGTAAGGCTGTCTTAGAGGATCTTCTGAGTACCCGTATCTCTGAGGCGAGG 1244
 QY 955 ACTGGCGGACCCCAACAAAGAAAGACCAATTCGAGAGCAGGCTT---TTCTGCTG 1011
 DB 1245 ACAGGCGGCAACCAACCAAAACAGATCCTTAATCCGAGAGCAGGATTCCTATGCTATG 1304

QY 1012 AACCTGAACATCTAGTCCCGCTGACGAAGCGCTTTGGGATCTCAAGATGTGCGACTTC 1071
 DB 1305 AGCTTAGACATATATGTGCCAAGGACGAGCGATTTGGTCAATATAAAGTTGTGACACTTC 1364
 QY 1072 CTTGGGTACTCGCTGAAGACGATCATGAGGCTCTTCTTCCAAACACCTGGGACTTTCCGTC 1131
 DB 1365 TTGACATTTGCTTTGAAATCCATTTGTCAGTTGCTTCTCCCTGAGTTTAAAGCTTTGCTTC 1424
 QY 1132 GATGACAGCCCAAGGAGTTCGATTCTGTTTGAGGATATCTCTGGGCTCTAGGAGCTGGC 1191
 DB 1425 GATGACAGCGCATATAGTTTGTAGTTTGGAGATGTAATAAAGTTGTATGAAGAGGA 1484
 QY 1192 CCAGAGGACCCCAACCAACCCACTCATAGCAGAGATCAGGAAGAGATCCCGCAGCGACTTC 1251
 DB 1485 ATCAAGTTGCTCAAGGCCCTTTGTTGAAGGCCATTAATGATAGCATTTCTTTAGAGATA 1544
 QY 1252 CTTGAGAGCATTTGCGGAGGAGTGGCCATGACACCCGCTAAGATGCCCTTCCAAAT 1311
 DB 1545 CTAAAGAACTCTCTCGAAGTGATGG---TGAAGGCCATTTTAAGTACCCCAACTCTCAG 1601
 QY 1312 GTCATCAAAATCAGATGTTGTAAGAGGCTCCGAGGTTTAAAGTTTGGCTCGAGACTGAC 1371
 DB 1602 GTTAT-----TCAAGAGGATTAAGTGCATGAGGAGCGAT 1637
 QY 1372 GAAGAGTTGCGGAGAGAGACATTTGCGAGGCTGGAACCCAGTAATCATCAAAACGTTGACG 1431
 DB 1638 GAAGAAATTTGGGAGAGAAATGTTGGCGGAGTCAATCTCTGTCAATCAGTAGACTCCAA 1697
 QY 1432 GAGTTCCTCCGCTAAAGCAACCTCGGACCCCAAGCAGTACGAGACACACACAGCAAGATC 1491
 DB 1698 GAATTCCTCGGAAAGCAAGTTGGATCTTAATAATATATGCAACCAAAACAGTACAAAT 1757
 QY 1492 ACTGAAGCTCAATTCGCGCATAACTGGGAGGCTGTCGGTGCAGAACGCACTGAGGAAC 1551
 DB 1758 ACCAGAGAGCAGATAGAGGATAAGTGGATGAGTAACTAACTATGAGGCAATCAAGACT 1817
 QY 1552 AAGAGGCTCTTCACTCTAGACACCATGACCAATTTGATCGGCTACCTCGAGAGATCAAC 1611
 DB 1818 AACGAGCTATTCATTTGAACCATCATGATATCTTATGCCATCTTGGAGAGAAATTAAC 1877
 QY 1612 GAGCTGAGGGGAACCTCATCTACGCGCAGCAGCAACCTACTGTTCTTGAAGGACGATGGC 1671
 DB 1878 ACCTGACAGACACAAACCACTATGCTCAAGAACTCTGCTCTTCTTGAAGATAATGGA 1937
 QY 1672 ACCTGAGAGCCCTGGCCATCGAGCTGAGCTGCCCAACCTCGACGCGCAGCAGCGCGC 1731
 DB 1938 ACTTGAAGCCCATCAGCAATTTGAATTAAGCTTGGCCTATCCAGCAGGAGATCAATTTGGC 1997
 QY 1732 GCGCTCAGCAAGGTGTACACCCCGGCTCACACCGGCTCGAGGGCCACGCTCTGGCAGCTC 1791
 DB 1998 GCTGTTAGCAAAAGTATATACACAGCTGATCAAGGTGTTGAAGGTTCTATCTGGCAGTTG 2057
 QY 1792 GCCAAGCTTATGCTGCGTAAAGACTCTGCTGGCAGTACGCTGATCAGCCACTGGCTG 1851
 DB 2058 GCCAAGCTTATGCGAGTGAATGATTCGGGCTTCACTCAACTCATCAGTCACTGGTTG 2117
 QY 1852 AACACGCAAGCGGTGATCGAGCGGCTTCTGTAATCGCAACAAACCGGAGCTCAGCGTGGTG 1911
 DB 2118 AATACACATGACGAGTGAAGCCATTCGTGATCGCAACAAATAGGCAACTAAGCGCTT 2177
 QY 1912 CATCCGCTGCAAGCTGCTGAGCCCGACTACCGTGAACCGTGAACATCAACAGCCCTG 1971
 DB 2178 CACCTTATTTAAGCTTCTCCACCTCATTTCCGFGAGACGATGAACATAATGCTTTA 2237
 QY 1972 GCAGCGCAGACATCATCAACCGCGCGGCTCTTCGAGGCAACCGTGTTCCTCGCAAG 2031
 DB 2238 GCAAGACAGATCTTGATCAACGGTGGTGGACTTCTTGAGTTGACAGTTTTCGGGCCAA 2297
 QY 2032 TAGCGCTGGGATGTCGGCAGACGCTGATACAGAGCTGGAATTTCAACAGAGCGGCTCTC 2091
 DB 2298 TATTCCATGGAATGTGACGAGTAGTTTACAAAGACTGGGTTTCCCTGAAACAGCACTT 2357

QY 2092 CCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCACTCAAGCCCATATGGTGTG 2151
Db CCTACTGATCTCATCAAAAGAGAGGTAGCTGTGAGGACTCGAGTCCCTCCACTTGGCAAT 2417
QY 2152 CGACTGCTGATCAAGGACTTACCCCTATGCTGCTGAGGGCTCGTCACTGTGTGGCGATC 2211
Db CGATTACTGATTCAGAGCTATCCATGCTGTGTGATGGGTGAAATTTGTTCAGCAAT 2477
QY 2212 GAGCGGTGGTCAAGAGTACCTGACATCTACTACCTTAACGAGCGGAGCTCCAGCGT 2271
Db AAAAGTGGTAACTAATGACTGCAACTACTATTACAAATCAGATGATGCGGTTCAAAA 2537
QY 2272 GAGCTGGAGCTCAGCGCTGTGGAAGAGGTGCTGTGAGGAGCGGACGAGCACTCAAG 2331
Db GACACTGAATCCAGAGCTGTTGGAGGAACCTCCGGAAGAGGAGACAGCGTGTGCAAGAA 2597
QY 2332 GACCGAGACTGTGTCGCCAGGATGACACCCGTCAGCAGCTGGTGTAGGGCTGCACAGCC 2391
Db GATGAGCCTTGTGGCTTAAATGACAGACAGTGCAGAAATTGATAGACTCTTGCACCATC 2657
QY 2392 ATCACTGGGTGGATCCGCTGCACCGGCTGTCAACTTTGGGAGTACCCATAGGCC 2451
Db ACAATATGATAGTTCAGCACTTCATGACGAGTCAATTTGGGCAATACCTTATGCT 2717
QY 2452 GGTACTCTCCGAAACCGGCGGACGCCAGCGGCGCGGATGCCGAGCGAGGCGAGCCAC 2511
Db GGTATCTCCCTATCGCTTACATTAAGCCGAAATTCATGCCAGAGCGAGGAGTCT 2777
QY 2512 GACTACAAAGCTGGGAGCGGGCGAGAGGAGCGGACATGGTGTTCATCCGACCATC 2571
Db GAGTATGAGAGCT-----CAAGACAAATCCGATAGGTATTCCTCAAAACAATC 2828
QY 2572 ACCAGCCAGTTCAGACCATCTCGGGCATCTCGCTCATCGAGATCCCTCCAGCATCC 2631
Db ACTCTAGCTCAGACACTGCTTGGCATTTCCCTCATAGAGATCTTGTCAAGGATCT 2888
QY 2632 TCCGACGAGGTGTACTCTCGGACGCTGACGAGCCTGATCGCTGACGTCAAGCGCAAG 2691
Db TCGGATACACTTTACTCTCGGCAAGGAAATCACTGTA---ATGACAAAGGATCAAGAA 2945
QY 2692 GCGCTGGATGCTTCAAAAGATTCGGAGCGGCTGGTGGAGATTGAGATGAGATCAAG 2751
Db CCACCTTCAGCTTTTGGAGGTTTGGAAAGAGCTGATGATATCGAGGATCAGATTATG 3005
QY 2752 AGCATGAACGACAGTCCGAGCTTGAAGAACCGGAGGGGCTGTGGAAATGCCGTACATG 2811
Db CAGATGAATGCTGAGAAATGGAAGACAGGTGCGGTCTGTAAAGTTCCATACAC 3065
QY 2812 CTGCTGTACCCCA 2824
Db TTGCTCTTCCCA 3078

RESULT 13

ID ABZ13699 standard; DNA; 2580 BP.

XX ABZ13699;

XX AC ABZ13699;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1504.

XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN WO200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026685.

XX XX

PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
PI WPI; 2002-304127/34.
DR
XX
XX
PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 1504; 577pp + Sequence Listing; English.
XX

CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention. Note: The sequence data for this patent is
not represented in the printed specification but is based on sequence
information supplied to Derwent by the European Patent Office

XX
SQ Sequence 2580 BP; 778 A; 541 C; 616 G; 645 T; 0 U; 0 Other;
Query Match 23.3%; Score 729, 6; DB 6; Length 2580;
Best Local Similarity 58.7%; Pred. No. 4e-120;
Matches 1502; Conservative 0; Mismatches 989; Indels 69; Gaps 11;
QY 298 AGATCCGCGGACCGGTGAGGTGTCAAGAGGAGTCTCGACGTCCGCACTTCAAC 357
Db 58 AAGGTGAAGGACCGGTGCTGTGATGAAGAGACGCTCTCGATTCAACGATTCAAT 117
QY 358 GCTCTCTCTCGACGCGCTCCACAGGATCTCGCTGGGACGAGCGGCTCCCTCCAG 417
Db 118 GCTTCTCTCTCGATGCTCTTATGAAATTTCTCGGAA-----ACAAATCACTCTTCT 171
QY 418 CTGCTCAGCGCCACCGCGCCGACCCAGCAACCGGGGCGGTGGCAAGGTGGGAGGCG 477
Db 172 CTGTGAAGCTCTGATGTTACTGATTGAGAAACGGTTCTTAAGGCAAACTAGGAGGCT 231
QY 478 GGCACCTCGAGAGCGGCTGTGCTCAAGTCAACGCGGACGCGGAGACCGTGTAC 537
Db 232 GTCACCTGGAGGATTGGATCAACAATCAGCTGTAAACCGCAGCGGAATCCGCTTC 291
QY 538 CGGCTGAGCTTCGAGTGGGACGAGTCCGAGGCGCATCCCGGGGCGCTCTGCTCAGGAAC 597
Db 292 AAGTCACTTTCGATTACGAAACCGATTTCGGTTACCTGGAGCATTTCTGTACGAAC 351
QY 598 CTGACGACGCGAGTCTTCTCAAGCGTCAACCTCGAGGGCGTCCAGGCAAGGCG 657
Db 352 AGCCATTTTCAGTGAGTTTCTTCAAAAGTCTCACACTTGAAGAGGTTCCAGGCGCATG 411
QY 658 ACCGTGCTCTCTCGCCCAACTCTGGGTCTACCGGCAAGCATCTACTCCAGGACGC 717
Db 412 AGAGTCAATACATCTGTAAATTTTGGATTATACCTGCTAAACACTACACTACAGCCGA 471
QY 718 ATCTTCTTCGCAACGACACCTATCTGCGGAGCAAAATGCGGCGGCTGTGCTTAT 777
Db 472 GTCTTCTTCTCAACAAGACTTATCTTCACATGAACACACGAGCGCTGTCAAGTAT 531
QY 778 CGGACAGTACCTCAAGATTTCTCGTGGGACGATATCTCTGGACCATACCCAGGACAT 837
Db 532 AGAAGAAGAGCTAGTGAGTTTGAGAGCAACCGCGA---AGGAGAGCTTAAAGAAATGG 588
QY 838 GATCGCTCTACCGTTACGACTACTACATGATGCTTGTGTGATCCCGCAAGGGCGAAG 897

Db 589 GACAGAGTATATGACTATGCTTACTCAATGATTTAGGCGTCCC-----ACCAAG 639
Qy 898 CAGCTCGGCGGATCTCTCGGTGGCAGCAAGAACACCCGCTATCCCGTCTCGCGAACT 957
Db 640 AACCCACGGCTGTACTTGGAGGACACACGAGTATCTTACCAAGAGAGGAACACC 699
Qy 958 GCGCGGACCCACAAAGAAAGACCCAAATTCGAGAGCGAGCT---TTTCTGCTGAAC 1014
Db 700 GGGCGGAAACCAACTAAGAAAGATCTCTCAAAACGAGAGCAGGCTACCGATCAATCGAGC 759
Qy 1015 CTGAACATCTACGCTCCCGCTGACGAAACGCTTTGGGCATCTCAAGATGTCGAGCTTCCTT 1074
Db 760 CTAGACATATATGTTCCACGAGATGAGAGATTTGGACACTTGAAGATGCTGATTTCCCTT 819
Qy 1075 GGGTACTCGCTGAAGACGATCTCGAGGCTGTTCTTCCAAACACTGGGGAATTTGCGAT 1134
Db 820 GCTTATGCTCTAAAGAGCGATGTCAGTCTCATCAACCTGCACTTGAGGCTGTATTTCGAC 879
Qy 1135 GACACGCCCCAAGAGTTCGATTCGTTTGAAGATATCTCGGCTCTACGAGCTGGGCCCA 1194
Db 880 GATACTCTTAAGAGTTGATTCCTTTGAAGATGTTCTTAAGATCTATGAAGAGAAATC 939
Qy 1195 GAGGACCCCAACCCACTGATAGCAGAGATCAGGAAGAAATCCCCAGCGAGTTTCCTT 1254
Db 940 GATCTACCAACCAAGCTTTGATGATGATGATCGTTAAGAAATATACCGCTTGAGATGTTA 999
Qy 1255 CGAAGCATCTCGCGAACGCTAGCATGACCAACCGCTAAGATGCGCTTCCAAATGTC 1314
Db 1000 AAGAGATATTCAGACAGATGCGCCAGAAATTC---CTTAAGTTCCAGTGTCTCAGGTC 1056
Qy 1315 ATCAATTCAGATGTGTTGAAAGGCTCCGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1374
Db 1057 ATCAAA-----GAGGACAAACTGCATGGAGAACAGATGAG 1092
Qy 1375 GAGTTCGAGAGAGACACTTGCAGCGTGAACCCAGTAAATCATCAAGCTGTGCGGAG 1434
Db 1093 GAATTTGCTAGAAATGTTGGCTGGACTAAACCCCTGTTGTTATTCACTTCTTAAGGAG 1152
Qy 1435 TTCCCGCTAAAAGCACCTTGACCCCAAGCAGTACGAGACCAACCAAGCAAGTCACT 1494
Db 1153 TTTCTCTCAAGAGTAAAGCTTGACGTGAATCATACGGTAAACAGAACAGTCAATCACT 1212
Qy 1495 GAAGCTCACATCGGCATACATGAGGAGGCGCTGCTGGTCAGNACGCACTGAGGACAG 1554
Db 1213 AAAAGCCACATAGAACAAATTTGGATGGACTCACTGTTGAAGAGGCTCTGGAGAGGAG 1272
Qy 1555 AGGCTCTTCACTAGACCAACCATGACCAATTTTCATGCCGTACTCTGACGAGATCAACGAG 1614
Db 1273 AGGTTGTTTATATTAGACCAACATGACACACTGATGCCATCTTGGACGCGTAACACC 1332
Qy 1615 CTGGAGGGGAACTTCACTACGACGAGGACCCCTACTGTTCTGAAAGCAATGCGACG 1674
Db 1333 ACCACAGCAAG---ACTTATGCAAGCAGGACACTTCTGTTCTTGAAGATGATGGGACC 1389
Qy 1675 CTGAAGCCCTCGCCATCGAGCTGAGCTGCGCCACCCCTGACGGCCAGCAGCGCGCGG 1734
Db 1390 TTGAAGCGGTTGTTGATAGAGCTGAGCTTGCTCTATCTTAATGGAGACAAATTTGGAGCA 1449
Qy 1735 GTGAGCAAGGTGACACCCCGGCTCAACCGGCTGAGGGCCACGCTGCGAGCTGCGC 1794
Db 1450 GTGAGTGAAGTATATACGCTGTGTGA---AGGTGTCTACGACTCGCTATGGCAGTTGCT 1506
Qy 1795 AAGGCTTATCCCTGCGTAAACGACTTGCTGCTGCATCAGCTGATCAGCCACTGGCTGAAC 1854
Db 1507 AAGGCTTTGTGCGTGAATGATCTCGGAATCATCAGCTTATTAGCCACTGGATGCA 1566
Qy 1855 ACCGACCGGTGATGAGCGGTTGTAATCGGACAAACCGGACGCTAGCGTGTGAT 1914
Db 1567 ACACGCGCATCGATTGAACCGGTTTGTGATTGGCCAAACAGACAGCTGAGTGTCTTCCAC 1626
Qy 1915 CCGGTGCACAGCTGCTGAGCCGCGCTACCGCTGACAGCTCAACATCAACGCCCTGCA 1974
Db 1627 CCGGTCTTTAAGCTCTTGAACCTCACTTCCGTGATACGATGAATATCAATGCACTTCT 1686

RESULT 14

ADA67958
ID ADA67958 standard; DNA; 2580 BP.

XX ADA67958;

XX AC

XX DT 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 206.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

Qy 1975 GCACAGACACTCATCAACGCGCGGCTCTTTCAGCGCACCGGTGTTCCCTGCAAAAGTAC 2034
Db 1687 AGGCAATCTTGAATCAATGGTGGTGGTATATTTGAATCACTGTGTTTCTTAAATAC 1746
Qy 2035 GCGCTGGGATGTGGCAGACGCTGTACAAGA---GCTGGAATTTCAACGAGCAGCGCTCTC 2091
Db 1747 GCCATGGAGATGTCTATCTTTCAAAAACCACTGAGCTTCCCTGACCAAGCATTA 1806
Qy 2092 CCAGCAGATCTCGTCAAGAGAGGTGTGCTGTGCGGACCAAGTCAAGCCCATATGTTGTC 2151
Db 1807 CCAGCAGAACTTAAAGAGAGGATGCGCGTGTAGGATCCAGAGACACACAGGATTA 1866
Qy 2152 CGACTGTGATCAAGGACTACCCCTATGCGGTTGACCGGCTGTCATCTGTTGGGCGATC 2211
Db 1867 CGTCTGAGGATAAAGACTATCTTACGCACTGATGGCTTGAGGTTTGGTATCTATT 1926
Qy 2212 GAGCGTGGGTCAAGGAGTACTCTGACATCTACTACCTTAACGACGCGAGCTCCAGCT 2271
Db 1927 GAATCATGGTCCAGACTCATTTTCTTGTCTAAGATAGAGGAGGATATCCAAACC 1986
Qy 2272 GACTGTGAGCTGCAAGGCTGTGGAAGAGGTGCTGAGGAGGCGCAGCGACTCAAG 2331
Db 1987 GACACAGAGCTTCCAAAGCTGTGTGGAAGAGGTGCGCGAGGAAGTCTATGGAGACAAAAG 2046
Qy 2332 GACCGAGACTGCTGCGCCAGGATGACACCGTCCAGCAGCTGCTAGGGGTGCGACACC 2391
Db 2047 TCAGAACCATGCTGCGCTAAATGCAAAACCGTGAAGACTTGTGAGTCTTGACCATC 2106
Qy 2392 ATCATCTGGTGGCATCCGCGCTGACGCGCTGTCAACTTTGGGCAAGTACCCATACGCC 2451
Db 2107 ATTATTTGGTGGCTTCTGCTTCTCATGCACTGTAACTTCGACAGTATCCAGTTGCT 2166
Qy 2452 GGGTACCTCCCGACCGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAC 2511
Db 2167 GGGTACCTCCCGAACAGACCGACTATAAGCGCTCAGTACATGCCAAAGGAAACACTCCA 2226
Qy 2512 GACTACAAGAGCTGGAGCGCGGCGCAGAGGAGCGGACATGTTGTTTCATCCGCGCCATC 2571
Db 2227 GAGTTTGAAGAACTTG-----AGAGAACTCTGATAAAGTGTTTTGAAGCCATC 2277
Qy 2572 ACCAGCAGATCCAGACCATCTCGGCTCATCGAGATCTCTCCAGACTCC 2631
Db 2278 ACAGCTCAGCTTCAGACACTTCTAGGATATCTCTGATTGAGATCTCTCTACTCATCT 2337
Qy 2632 TCCGACGAGTGTACCTCGGCCAGCGTGACGAGCTGATCGCTGGAGCTCAGACGCCAAG 2691
Db 2338 AGCGACGAGTCTATTTTGGGACAGAG---AGATTCTAAAGATGGCGGCTGAGAAAGAA 2394
Qy 2692 GCGTGTGATGGTTCAAAAGATTCGGGAGCGGCTGTCAGATTGAGATCGGATCAAG 2751
Db 2395 GCGTTGAGGCGTTCGAGAAAGTTTGGAGAGAAAGTAAAGAGATTGAGAGAAACATTTGAT 2454
Qy 2752 ACCGATGAACGACAGTCCGGACTTGAAGACCGGAAGGGCGCTGTGAAATGCGGTACATG 2811
Db 2455 GAGAGGAACGACGACGAGACTCTCAAGAACAGACTGGTTGGTTAAGATGCCATACACT 2514
Qy 2812 CTGCTGTACCCCAACAGCTCGGAGCTTACCGGCGAGAAGG 2851
Db 2515 TTATTGTTCCGAGCAGTGAAGGCGGAGTCAACGCGCAGGG 2554

XX	Arabidopsis thaliana.	QY	778	CGCAGATGAGCTCAAGATTCTCCGTGGCAGGATATCTCTGGACCATACCCAGGAGCAT	837
OS		Db	532	AGAGAAGAAGAGCTAGTGAGTTTGAGAGGAAACCGCGA---AGGAGAGCTTAAGGAATGG	588
PN	WO2003000898-A1.	QY	838	GATCGCGTCTACCGTTTACGACTACTACATGACCTTGTGTGATCCCGACAAAGGCGCAAGAG	897
PD	03-JAN-2003.	Db	589	GACAGAGTATATGACTATATGCTTACTACATGATTAGGCGTCC-----ACCAAG	639
PF	22-JUN-2001; 2001WO-IB001105.	QY	898	CAGCTCGCGCGATCTCTCGTGGCAGCCAAAGAACCCGATATCCCGTCTGCGTGAAGT	957
PP	22-JUN-2001; 2001WO-IB001105.	Db	640	AACCCACGCGCTGTACTTGGAGGGAACAGAGGATATCTTACCCAAAGAGAGGAAGAAC	699
PR	(SYGN) SYNGENTA PARTICIPATIONS AG.	QY	958	GGCGGACCCCAACAAAGAAAGACCCAAATTCGGAGAGCAGGT---TTTCTGCTGAAC	1014
XX	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;	Db	700	GGGCGAAACCAACTAAGAAGATCTCAAACGAGAGCAGGCTACCGATCACATCGAGC	759
PI	Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;	QY	1015	CTGAACATCTACGTCCCGCGTGACGAAACGCTTTGGGCATCTCAAGATGCGGACTTCCTT	1074
XX	WPI; 2003-175290/17.	Db	760	CTAGACATATATGTTTCCACGAGATGAGAGATTGGACACTTGAAGATGTTCTGATTCTCTT	819
PT	Identifying at least one gene involved in plant resistance or response to	QY	1075	GGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCAAACACTGGGACTTTCGTCGAT	1134
PT	pathogenic infection for conferring resistance or tolerance to a plant to	Db	820	GCTTATGCTCTAAAGCGATTGCTCAGTTCATCCAACTGCACTTGAGGCTGTATCGAC	879
PT	bacterial, fungal or viral infection by determining or detecting plant	QY	1135	GAACGCCCAAGAGTTCGATTGTTGAGGATATCTCTGGGCTCTACGAGCTGGGCCA	1194
PT	gene expression.	Db	880	GATACTCTCTAAAGAGTTCGATTCTTTTGAAGATGTTCTTAAGATCTATGAAGAGGAATC	939
PS	Claim 6; SEQ ID NO 206; 899pp; English.	QY	1195	GAGGACCCCAACAAACCCACTGATACAGAGATCAGGAGAGATCCCGAGGATTCCTT	1254
XX	The present invention relates to a method (M1) for identifying genes	Db	940	GATCTACCAACCAAGCTTTGATTGATAGTATCTGTTAAGATATACCGTTGAGATGTTA	999
CC	involved in plant resistance or response to pathogenic infection. M1	QY	1255	CGAAGATTCTCCGAACGGTAGCCATGACCAACCGCTTAAAGATGCCCTTCCAAATGTC	1314
CC	comprises identifying a gene whose expression is significantly altered in	Db	1000	AAGGAGATATTCAGAACAGATGCCAGAAATTC---CTTAAGTTTCCAGTGCCTCAGGTC	1056
CC	the incompatible interaction of plant gene expression relative to	QY	1315	ATCAATCAGATGCTGTGAAGAGGCTCGGAGTTCGAGTTCGCTGGAGGACTCACGA	1374
CC	expression of the gene in an uninfected plant, in a mutant plant that	Db	1057	ATCAAA-----GAGGACAAACTGCTATGGAGAACAGATGAG	1092
CC	does not express a gene associated with response to pathogenic infection,	QY	1375	GAGTTTCGGAGAGAGACACTTTCAGGCGTGAAACCCAGTAATCATCAAACTGTGACGGAG	1434
CC	or in a corresponding incompatible or compatible interaction. (M1) is	Db	1093	GAAATTTGCTAGAGAAATGTTGGCTGACTAAACCTGTTGTTATTCAACTTCTTAAGGAG	1152
CC	useful for conferring resistance to resistance or tolerance to a plant to	QY	1435	TTCCCGCTTAAAGCACCTTGAGCCCAAGGAGTAGGAGACCAACAGCAAGATCACT	1494
CC	bacterial, fungal or viral infection. The present sequence was used to	Db	1153	TTTCTCCAAAGAGTAAGCTTGACAGTGAATCATACGTTAAACCCAGAACAGTACAACTCACT	1212
CC	illustrate the invention.	QY	1495	GAAGCTCACATCCGGCATAACATGAGGCGCTGTGCTGCAGAACGCACTGAGGAACAAG	1554
XX	Sequence 2580 BP; 778 A; 541 C; 616 G; 645 T; 0 U; 0 Other;	Db	1213	AAAAGCCACATAGAACAAATTTGGATGACTCACTGTTGAAGAGGCTCTGGAGAGGAG	1272
QY	Query Match	QY	1555	AGGCTCTTCACTCTAGACCAACATGACCAATTTTCATGCGGTACCTCGACAGATCAACGAG	1614
Best Local Similarity	23.3%; Score 729.6; DB 7; Length 2580;	Db	1273	AGTTTGTATATATAGACCAACCATGACACTGATGCTACTTTGGGACCGGTAACACC	1332
Matches 1502; Conservative	58.7%; Pred. No. 4e-120;	QY	1615	CTGGAGGGGAACTTCATCTACCGACGAGGACCTTACTGTTCTCTGAAGAGAGTGACG	1674
	Mismatches 989; Indels 69; Gaps 11;	Db	1333	ACCACGCCAG---ACTTATGCAAGCAGGACACTTCTGTTCTTGMAGATGATGGACC	1389
298	AAGATCCGCGCACGGTGAAGCTGGTCAAGAGGAGGTGCTGAGCGTGGCGACTTCAAC	QY	1675	CTGAAGCCCTTGGCCATCGAGCTGAGCTGCTGCCCAACCTGACCGCAGCAGCGGCGCGG	1734
58	AAGGTGAAGGAACGGTGTCTGATGAAGAGAAACGTCCTCGATTTCACAGATTCAAT	Db	1390	TTGAAGCCGTTGGTGATAGAGCTGAGCTTGGCTCATCTTAATGGAGACAAATTTTGAGCA	1449
358	CGCTCGCTCTCGACGGGTCACAGATCTCGCTGGGACGACGCGCTGCCCTCCAG	QY	1735	GTCAACAAAGGTGTACACCCCGGCTCACACCGCGCTCGAGGGGCCAGCTTGGCAGCTCCG	1794
118	GCTTCGTTCTCGATCGTCTCATGAATTTCTCGAA-----ACAAATCACTCTTCGT	Db	1450	GTGAGTGAAGTATATATACGCTTGGTGA---AGGTGTCTACGACTCGCTATGGAGTTGGCT	1506
418	CTCGTCAAGCGCCACCGCGCGCACCCAGCAACGGGGCGGTGGCAAGGTGGGGAAGCGG	QY	1795	AAGGCTTATGCTCGTAAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAAC	1854
172	CTTGTAAGCTCTGATGTTACTGATTCAGAAAACGGTTCTAAGGCACACTAGGGAAGGCT	Db	1507	AAGGCTTTTGTGCGGTGTAATGACTCCGGAATCATCAGCTTATTAGCCACTGGATGCA	1566
478	CGGCACTGGAGAGGCGGTGGTGTGCTCAAGTCCACGGCGGACGGGAGACCGGTGAC	QY			
232	GCTCACTTGGAGGATTTGGATCACAACAATCACTGCTGTTAAACCGCAGCGGAATCCGTTTC	Db			
538	CGGTTGAGTTCGAGTGGAGCGGTGTCAGGGCATCCCGGGCGCGCTGCTGTCAGGAAC	QY			
292	AAGTCACTTCGATTAGCAACCGATTTCGTTACCTCGAGCATTCCTTGTATCAGAAAC	Db			
598	CTGACGACCGCGAGTTCTTCTCAAGACGCTACCTCGAGGGCGTCCAGGCAAGGGC	QY			
352	AGCCATTTCAGTAGTTTCTCTCAAAAGTCTCACACTTGAAGACGTTCCAGGCCATGGC	Db			
658	ACCGTGTCTTCGTCGCACTCGTGGGTCTACCCGACACAGCTCTACTCCAGGAACGC	QY			
412	AGATTCATTACATCTGTAAATTTTGGATTTACCTCTGAACACTACATACAGACCGA	Db			
718	ATCTTCTTCGCAACGACCTATCTCCGAGCAAAATGCCGGCGGCTTGTGCTTAT	QY			
472	GTCCTTCTCTCCAAACAAGACTTATCTTCCACATGAAACACCGAGCGCTGCTCAAGTAT	Db			

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QY 1855 ACGCACGGGTGATCGAGCGGTTCTGTAATCGCGCAAAACCGCAGCTCAGCGTGTGCAT 1914
Db      |||
QY 1567 ACACACGATCGATTGACCGTTTGTGATTTGCCACACACAGCAGCTGAGTGTCTTCAC 1626
Db      |||
QY 1915 CCCTGACAAAGCTGCTAGCCGCACTACGCTGACAGCTGAACATCAACGCGCTGGCA 1974
Db      |||
QY 1627 CCGGTCTTTAAGCTCCTTTGAACCTCACTTCGCTGATACGATGAATCAATGACACTTGT 1686
Db      |||
QY 1975 CGCCAGACACTCAACACGCGCGGCGTCTTGAGCGCACCGTGTTCCTGCAAAAGTAC 2034
Db      |||
QY 1687 AGCAAAATCTTGAATCAATGGTGGTATATTTGAATCACTGTGTTCTCTTAATAC 1746
Db      |||
QY 2035 GCGCTGGGATGTCGGACAGAGTGTACAAGA---GCTGGAATTTCAACGAGCAGCTCTC 2091
Db      |||
QY 1747 GCCATGAGATGTCTATCTTTCAATTTACAAAACCACTGGACCTTCCTGACCAAGCATTA 1806
Db      |||
QY 2092 CCACGACATCTCGTCAAGAGAGGTGCTGCTGCGGACAGTCAAGCCCATATGTGTG 2151
Db      |||
QY 1807 CCACGACACTTAATAAGAGAGGATGCGCGTTGAGGATCCAGAACACACAGCATTA 1866
Db      |||
QY 2152 CGATCTGTGATCAAGGACTACCCCTATGCGGTTGACCGGCTCGTCTATCTGTGGGCGATC 2211
Db      |||
QY 1867 CGTCTGAGGATAAAGACTATCTCTTACGAGTGTGAGTGGCTTGAGGTTTGGTATGCTATT 1926
Db      |||
QY 2212 GAGCGGTGGGTCAAGGAGTACTCGACATCTACTACCTTAACGACGCGAGCTCCAGCGT 2271
Db      |||
QY 1927 GAATCATGGGTCGAGACTATCTTTCTTCTTCAAGATAGAGGAGTATCCAAACC 1986
Db      |||
QY 2272 GACGTGAGCTGACGAGCGTGTGGAAGAGGTGCTGAGGAGCGGACGCGCACTCAAG 2331
Db      |||
QY 1987 GACACAGAGCTCCAAAGCTGCTGGAAGAGGTGCGCGAGGAGGTGATGAGACAAAAG 2046
Db      |||
QY 2332 GACGAGACTGCTGCGCCAGAGTGGACACACGCTCCAGCAGCTGCTAGGGCGTCACGAC 2391
Db      |||
QY 2047 TCAGAACATGCTGCTTAATTCGAACCCGCTGAGAACTTGTGAGTCTTGACCAATC 2106
Db      |||
QY 2392 ATCATCTGGGTGGCATCCGCGCTGACCGCGCTGTCAACTTTGGGAGTACCCATACGCC 2451
Db      |||
QY 2107 ATATTTGGGTGGCTTCTGCTCTTCTATGACGCTGTTAACTTCGACAGTATCCAGTTGCT 2166
Db      |||
QY 2452 GGTGTACCTCCGACCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2511
Db      |||
QY 2167 GGGTACTCTCCAAACACAGCCGACTATTAAGCGCTGAGTACATGCAAGGAAACATCTCA 2226
Db      |||
QY 2512 GACTACAGAGCTGGGAGCGGGGCGAGAGGCGGACATGCTGTTCATCCGCAACATC 2571
Db      |||
QY 2227 GAGTTTGAAGAACTTG-----AGAAGAACTCTGATAAAGTGTGTTTGAAGACCATC 2277
Db      |||
QY 2572 ACCAGCCAGTTCAGACCACTCTGGGCACTCTGCTCATCGAGATCTCTTCCAGCACTCC 2631
Db      |||
QY 2278 ACAGCTCAGCTTCAGACACTTCTAGGAGATATCTCTGATTGAGATCTCTCTACTCATCT 2337
Db      |||
QY 2632 TCCGACGAGGTGTACTCTCGGCCAGCGTGCAGAGCCTGATCGCTGGACGTGAGACGCCAAG 2691
Db      |||
QY 2338 AGCGACGAGGTCTATTGGGACAGAG---AGATTCTAAGAAATGGCGGCTGAGAAAGAA 2394
Db      |||
QY 2692 GCGCTGATGCTTCAAAAGATTTCGGAGCGCGCTGCTGAGATGAGATGAGATGAGATCAAG 2751
Db      |||
QY 2395 GCGTTGAGGCGGTTTCGAGAAATTTGGAGAGAAATTAAGGAGATTGAGAGAAACATTGAT 2454
Db      |||
QY 2752 ACAGTAAACAGACTGCGGACTTGAAGAACCGGAAGGGCGCTGCTGGAATGCGGTACATG 2811
Db      |||
QY 2455 GAGAGGAAACGACGAGACTCTCAAGAACAGAGCTGCTGTTGTTGATTGATGCCATACACT 2514
Db      |||
QY 2812 CTGCTGTACCCCAACACAGTGGAGGTTTACCGGCGAGAGG 2851
Db      |||
QY 2515 TTATTGTTTCGAGCAGTGAAGCGGAGTCAACCGGCGAGG 2554
Db      |||
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RESULT 15

AAT60429

ID AAT60429 standard; cDNA; 2441 BP.

XX

AC AAT60429;
XX
XX 27-AUG-2003 (revised)
DT 08-JUL-1997 (first entry)

XX Tomato fruit ripening specific lipoxygenase gene fragment.

DE LOX gene; fruit ripening specific lipoxygenase; FRS-LOX; tomato;
KW transgenic plant; ss.

XX Lycopersicon esculentum.

XX WO9713851-A1.

XX 17-APR-1997.

XX 11-OCT-1996; 96WO-US016387.

XX 13-OCT-1995; 95US-0005404P.

XX (PURD) PURDUE RES FOUND.

XX Handa AK, Kausch KD;

XX WPI; 1997-235887/21.

XX New transgenic plants with fruits having improved quality - obtained by transforming plant cells so as to inhibit production of fruit ripening specific lipoxygenase in fruits.

XX Claim 6; Fig 1; 38pp; English.

CC A tomato fruit ripening specific lipoxygenase (FRS-LOX) gene fragment (AAT60429) comprises nucleotides 158-2598 of the FRS-LOX gene (see also AAT60428). It was isolated from partial LOX cDNA clone 8-27-1, and can be inserted into the multiple cloning site present between the CMV 35S promoter and rbc 3' terminator sequences in pTZ35rBS in both orientations, yielding pTZSL (sense) and pTZAL (antisense). These vectors can be used to create transgenic fruit-bearing plants, esp. tomato, in which native FRS-LOX gene expression is inhibited. These transgenic plants can provide fruits having improved quality and texture, greater firmness, longer shelf life, better packaging and storage characteristics and improved processing characteristics. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 2441 BP; 742 A; 496 C; 544 G; 659 T; 0 U; 0 Other;

Query Match 21.2%; Score 664.2; DB 2; Length 2441;

Best Local Similarity 57.7%; Pred. No. 1.6e-108;

Matches 1367; Conservative 0; Mismatches 933; Indels 51; Gaps 8;

QY 460 GGCAGGTGGGAAGCGGCGCACCTGGAGAGCGGTGGTTCGCTCAAGTCCACGGCG 519

Db 89 GGGAACTGAGCAATCCAGCATACTTAGAGAGTTGGCTTACAGACATCACCCCAATAACA 148

QY 520 GACGGGAGACCGGTGTACCGGTTGAGTTCGAGTGGGA---CGAGTGCAGGGGCATCCCG 576

Db 149 GAGGGGAATCAACTTTAGTGTACATTTGACTGGGATCGTGACGAGTTGGAGTTCCA 208

QY 577 GCGCGCTCTCTGGTCAGGAACCTGCAGCACGCCGAGTTCTTCTCAAGAGCTCACCCCTC 636

Db 209 GGAGCATTCATCATCAAGAACTCTTCACTTAATGAGTTCTTCTCAAGTCACTCACACTC 268

QY 637 GAGGCGCTCCAGCAAGGCGACCGTGTCTGCTCGCCACTCGTGGGTCTACCCGCAC 696

Db 269 GAAGATGTTCTTAATTTATGGAATAATCAATTTGTATGCAATCTTGGTTTATCTCTGCT 328

QY 697 AAGCTCTACTCCCGAGAACGATCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATG 756

Db 329 TTATAGTACAAGTCTGACCGCATTTTCTTTGCCAATCAGGCTTATCTCCCAAGTGAACA 388

QY 757 CGGCGGCGTGTGGTCTTATTCGCAAGATGAGTCAAGATCTCTCCGTGGCGCAGTAAT 816

Db 389 CCACACCAATTCGAAATATACAGAAAATGAACCTGGTAGCTTTGGAGGAGATGAA-- 446
Qy 817 CTTGGACCAATACAGGAGCAGATGATCGGHTCTACCGTTACGACTACTACAAATGACCTTGGT 876
Db 447 -CTGAAAGCTTGAAGAAATGGGACAGGGTTTATGATTTATGCTTTGCTACAAATGACTTGGGT 505
Qy 877 GATCCGACAGGCGGAGGAGCAGCTCGGCCGATCCTGGTGGCAGCCAAAGAACACCCG 936
Db 506 GAACAGATAGGGGGAAGATATGCTAGGCCCTATCCTTGGAGGGTCTCTGATGACCCG 565
Qy 937 TATCCCGCTCGCTGACAGACTGGCCGACCCAAACAAAGAAAGACCCAAATTCGGAGAGC 996
Db 566 TATCCTGTAGAGCAGGACAGGCGGCAACCAACAAAGCAGATCTTAATTCGAGAGC 625
Qy 997 AGG---CTTTTCTGCTGAACCTGAACATCTAGTCCCGGTGACGAAAGCTTTGGGCAT 1053
Db 626 AGGAACCAATTCGCTATGAGCTTAGACATATATGTCCTCAAGGACGAGCATTTGGTCAT 685
Qy 1054 CTCAGATGTCGGAATTCCTTGGGTAATCGCTGAAGACGATCATCGAGGCTGTTCTTCCA 1113
Db 686 GTGAGAGATCAGACTTTTGAAGCTCGTCTTAAATCCTCTTTGCAAGCTTCTCCCT 745
Qy 1114 ACATCGGGACTTTCGTCGATGACACGCCCAAGAGTTGATTCGTTTGAAGATATCCTC 1173
Db 746 GCGTTTAAAGCTTTGTGCGATTAACACGCTTAATGAGTTCAATAGCTTTGCGGATGACTT 805
Qy 1174 GGGCTCTACGAGCTGGGCCAGAGGCCACCAACCAACCTGATAGCAGAGATCAGGAAG 1233
Db 806 AATCTTATGAGAGAAATCAGTTGCTGAGGCCCTTGGTTGAAAGCCATTAATGAT 865
Qy 1234 AAGATCCCGAGGAGTTCTTTCGAAGCATTCGTCGGAACGGTATGACCAACCCGCTA 1293
Db 866 AACATTTCTCAGAGATCTAAAGAGACATCTTCAACCGGATGCTCAAG---GCCTACTT 922
Qy 1294 AAGATGCCCTTCCAAATGTCATCAATCAGATGTTGTAAGAGGCTCCGGAGTTTAAG 1353
Db 923 AAGTACCACTCTCAGTTTATCAAGCGA-----TAAA 958
Qy 1354 TTTGGCTGGAGACTGACAGAGTTTCGAGAGAGACACTTCGAGCGTGAACCCAGTA 1413
Db 959 ACTGATGGAGGACGGATGAGAAATTTGGGAGAGAAATTTGGCAGGATCCAATCTCTGTC 1018
Qy 1414 ATCATCAACCTCTGACGGAGTTCCCGCTAAAGACACCTGGACCCAAAGCAGTACGA 1473
Db 1019 TTAATCAGTACCTCCAAAGATTTCTCCGAAGAGCAAGTTGGATCCCAACCATATGGA 1078
Qy 1474 GACCACACCAAGATCACTGAAGCTCACATCCGGCATAACTGAGGAGCCTGTCCGTG 1533
Db 1079 AACCAGAACATACAATTTACCACAGAACATGTCAGGATTAAGTTGAATGAATTAACAGTG 1138
Qy 1534 CAGAACGCACTGAGGAAACAGAGGCTTTCATCTAGACCAACCATGACCAATTCATGCCG 1593
Db 1139 AATGAGGCAATCAAGAGTAAACAGGTTATTCATATTGAACCAACCATGACATCGTGATGCCA 1198
Qy 1594 TACCTCGACGAGATCAACAGCTGGAGGGAACTTCATCTACGCCAGCAGACCTTACTG 1653
Db 1199 CTATTGAGAAATTAACATGTGAGCAAAACAAAAAGCCTATGCTCAAGAACTCTGCTC 1258
Qy 1654 TTTCTGAAAGACGATGGCAGCCTGAAGCCCTGTCCTGACATGAGCTGAGCCTTGCCCAACCT 1713
Db 1259 TTTCTTACAAGATGATAGAACTTTGAAGCCACTAGCAATTTGAACCTTAAGCTTGCCACATCCA 1318
Qy 1714 GACGCCAGCAGCGCGGCTGAGCAAGGTGTACACCCGCTCACACCGGCTCGAG 1773
Db 1319 GACGAGATCAATTTGGTACTGTTAGTAAAGTATATACACAGCTGACCAAGGTGTTGAA 1378
Qy 1774 GGGCAGCTCTGGCAGCTCCCAAGGCTTATGCTCGTAAACGACTCTGCTGGCATCAG 1833
Db 1379 GGTTCATCTGGCAGTTTGCCAAAGCCTATCTAGCAGTGAATGATGATGGGCAATTCATCAG 1438
Qy 1834 CTGATCAGCAGCTGGCTGAACACGCAACCGGCTGATCGAGCGGCTTCTGTAATCGGACAAAC 1893
Db 1439 CTCATTAGCCCACTGGTTGAATATACACCGCGTGTGAACCAATTTGTTGATTCGAACAAAT 1498

Qy 1894 CGGAGCTCAGGTGGTGCATCCCGTGCACAAGCTGTGAGCCCGCACTACCGTGACAG 1953
Db 1499 AGGCATCTAAGTGTGCTTATCCCATCATTAACATCTTCTCATCTCATTTCCGTAACAG 1558
Qy 1954 CTGAACATCAACGCCCTGGCAGCCAGACACTCATCAACCGCGCGGCTTCTGAGGCG 2013
Db 1559 ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGCTGG---TTTTGAGAGC 1615
Qy 2014 ACCGTGTTCCCTGCAAAAGTACGCGCTGGGATGTCGCGAGACGTTGTACAAGAGCTGGAAT 2073
Db 1616 TCTCTTTTCTGCGCAAAATATTCAATGAAATGTACAGCAGCTTACAAGATTTGGTT 1675
Qy 2074 TTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGTGTGGCTGTCCCGACAG 2133
Db 1676 TTCCCTGAACAGCACTTCTCTCTCAAAAGAGAGTGGCTGTGAGGACTTG 1735
Qy 2134 TCAAGCCATATGTTGTCGACTGCTGATCAAGACTACCTCTATCCGTTGACGGGCTC 2193
Db 1736 AGCTCCCAACATGGCAATTCGTTACTGATTCGACTATCATATGCTGTTGATGGCTTG 1795
Qy 2194 GTCATCTGTGGGCGATCGAGCGTGGGTCAAGAGTACCTGGACATCTACTACCTAAC 2253
Db 1796 GAAATTTGGGAGCAATCAAAAGTTGGTAAACAGATATTGCAAGTTCTATTACAAATCT 1855
Qy 2254 GACGCGAGCTCCAGCTGAGCTGAGCTGAGCGTGTGAGAGAGTGTGAGAGGCTGCTGAGAG 2313
Db 1856 GACGAGACAGTAGAAGAAAGACACTGAATCCAAAGCTTGGTGAAGAGACTCCGGAAGAA 1915
Qy 2314 GGGCAGCGGACCTCAAGGACCGGAGACTGTGGCCAGGATGGACACCGCTCAGCAGCTG 2373
Db 1916 GGACATGGCGCAAGAAAGATGAGGCTTGGTGGCTTAACTGCAAACTCGACAGAGCTC 1975
Qy 2374 GCTAGGGGTGCACGACCATCATCTGGTGGCATCCGCTGCGCTGACGCGGCTGTCACTTT 2433
Db 1976 AGAGATTTGTCACCATCATTTATATGATAGCTTCAGCACCTTCATGACAGCACTCCATTT 2035
Qy 2434 GGGCAGTACCCATACGCGGCTACCTCCGACCGGACCGGCGGCGGCGGCGGCGGCGGCGG 2493
Db 2036 GGCCTTACTCTTACGCTGGTTATCTCCCTAATCCGCTTACTTTAGCTGTAAATTTGATG 2095
Qy 2494 CCGGAGCCAGGACGACCACTACAAAGAGCTGGGAGCGGGGCAAGAGGAGCGGACATG 2553
Db 2096 CCAGAGCCAGGAAGTTGAGTATGAAGGCT-----CAAGACAAATCCAGACAAG 2146
Qy 2554 GTGTTCTCCGACCATCACAGCCAGTTCAGACCATCTCGGCACTCTCGCTCATCGAG 2613
Db 2147 GTATTCTTAAACAACTTTGTTCTCAGTTGCAATCAGCTGTGAAATTTCCATCTTTGAG 2206
Qy 2614 ATCCTCTCCAAGCACTCTCCGACGAGGTGTACCTCGGCGGCGGCGGCGGCGGCGGCGG 2673
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Qy 2674 TGGAGCTCAGAGCGCAAGGCGCTGATGCGTTTCAAAAGATTCGGGAGCGGCTGCTGAG 2733
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Search completed: March 22, 2004, 22:20:43
Job time : 1156 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 22:00:16 ; Search time 210 Seconds
(without alignments)
8281.981 Million cell updates/sec

Title: US-10-059-909-15
 Perfect score: 3134
 Sequence: 1 coacgcgtccggccgaggcg.....aaaaaaaaaaaaaaaaa 3134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database :
Issued_Patents_NA:**
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2: /cgm2_6/ptodata/2/ina/5B_COMB.seq:**
3: /cgm2_6/ptodata/2/ina/6A_COMB.seq:**
4: /cgm2_6/ptodata/2/ina/6B_COMB.seq:**
5: /cgm2_6/ptodata/2/ina/POTUS_COMB.seq:**
6: /cgm2_6/ptodata/2/ina/backfiles1.seq:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	1336	42.3	3007	4	US-09-810-268-1	Sequence 1, Appli
2	1334	42.2	2595	4	US-09-810-268-2	Sequence 2, Appli
3	1222.2	39.0	2818	4	US-09-751-687-10	Sequence 10, Appl
4	664.2	21.2	2441	4	US-09-051-465-1	Sequence 1, Appli
5	664.2	21.2	2871	4	US-09-051-465-2	Sequence 2, Appli
6	664.2	21.2	2871	4	US-09-051-465-4	Sequence 4, Appli
7	599.2	19.1	4663	4	US-09-751-687-11	Sequence 11, Appl
8	599	19.1	4663	4	US-09-751-687-8	Sequence 8, Appli
9	270.2	8.6	302	4	US-09-313-294A-3908	Sequence 3908, Ap
10	160.4	5.1	282	4	US-09-313-294A-6360	Sequence 6360, Ap
11	155.8	5.0	298	4	US-09-313-294A-4946	Sequence 4946, Ap
12	135	4.3	340	1	US-08-181-271A-40	Sequence 40, Appl
13	135	4.3	340	1	US-08-449-315-40	Sequence 40, Appl
14	135	4.3	340	1	US-08-444-803-40	Sequence 40, Appl
15	135	4.3	340	1	US-08-449-043-40	Sequence 40, Appl
16	135	4.3	340	1	US-08-456-265A-40	Sequence 40, Appl
17	135	4.3	340	1	US-08-455-416-40	Sequence 40, Appl
18	135	4.3	340	1	US-08-455-244-40	Sequence 40, Appl
19	135	4.3	340	1	US-08-454-876-40	Sequence 40, Appl
20	135	4.3	340	2	US-08-457-364-40	Sequence 40, Appl
21	135	4.3	340	2	US-08-456-263-40	Sequence 40, Appl
22	135	4.3	340	2	US-08-456-240-40	Sequence 40, Appl
23	135	4.3	340	2	US-08-455-738-40	Sequence 40, Appl
24	135	4.3	340	2	US-08-571-217-40	Sequence 40, Appl
25	135	4.3	340	2	US-09-350-600-40	Sequence 40, Appl
26	135	4.3	340	4	US-09-906-234-40	Sequence 40, Appl
27	133.2	4.3	155	4	US-09-313-294A-3677	Sequence 3677, Ap

ALIGNMENTS

RESULT 1

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US-09-810-268-1
; Sequence 1, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxxygenase Po
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1369
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-1

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Query Match	42.3%;	Score 1326;	DB 4;	Length 3007;
Best Local Similarity	71.7%;	Prod. No. 2e-264;		
Matches 1906;	Conservative	0;	Mismatches 680;	Indels 72; Gaps 10
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DB	122	-GGCACGGTGGTCTCATGCGCAAGAACGTGCTGACTTCAAGACTTCGGCGCCACCGT	180	
QY	366	CTTCGACGGGTCCACAGGATCTCTGGCTGGGACGACGGCGTCCGCTTCCAGTCTCGTCAAG	425	
DB	181	CGTTGACAGCATCAGCGAGTTCCTCGGCA-----AGGGGGTCACTGTCGACTCATCAG	234	
QY	426	CGCCACCGCGCCGACCCACGACAAACGGGGCCGTGCGCAGAGTGGGAGGGCGGCGCACT	485	
DB	235	CTCCACCCCTGTCACGCCAACACCGGCAACCGCGGGCGGTTCGGGGCGAGAGCGCAACT	294	
QY	486	GGAGAGAGCGGTGTGCTCAAGTCCACGCGGACGGGGAGACCGGTGTACCGGGTGAAG	545	
DB	295	GGAGCATGTGCTACGAGACTTCCGCTGTGACGACCGCGGAGTCCAGTTTCGGGTCAAC	354	
QY	546	CTTCAGTGGGA---CGAGTCGCAGGGCATCCCGGGCGCCGTCCTGGTCAGAGAACTCGCA	602	
DB	355	CTTCGACTGGAGGTGAGGAAGCTGGGAGTGCCTGGGGCGCGTTCGTGTCAGAGAACTCA	414	

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Db 415 CGCGCGAGGTTCTTCTCAAGACATCACTCTCGACGAGTGGCCGCGCGCGCGT 474
QY 663 GGTCTTGTGCGCAACTGTGGGTCTACCGGCAAAAGCTCTACTCCAGGAACGATCTT 722
Db 475 CACCTTGTGCGCAACTGTGGGTCTACCGGCGGCAAGTACCGCTACAACCGGCTT 534
QY 723 CTTGCGCAAGCACACTATCTCGGAGCAAAATGCGGCGGCGTGGTCCCTTATCGCA 782
Db 535 CTTCTCAAGATACGATCTGCTCAAGCCAGATGCGCGGCGGCTGAAGCCGTACCGGA 594
QY 783 AGATGAGCTCAAGATTTCTCGTGGCGACGATATCTTGACCATACAGGAGCATATCG 842
Db 595 CGACGAGCTCGCAACTCTCGCGGCGACGACGAGCAGGCGCCCTACAGGAGCAGACCG 654
QY 843 GGTCTACCGTTACGATCTACATGACCTTGTGATCCGACAGGCGGAGAGCAGCG 902
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QY 903 TCGGCCGATCTCGGTGGCGACGCAAGAACACCCGCTATCCCGCTCGCTGAGAACTGGCG 962
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Db 769 CAAGCCCAACAAACCGACCCAACTCGGATAGCCGACTGTGCTGGTGA-----GCAGAT 825
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QY 1263 TCTCGGAAAGGTAGCATGACCAACCGCTTAAGATGCCCTTCCAAATGTCTCAATC 1322
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Db 1579 TGTGCGCTCAAGACTTCTGGTGGCACCAACTCGTCAGCACTGGCTGAACACCCACGC 1638
QY 1863 GGTGATCAGCGCTTCTGATTCGGCAAAACCGGCTCAGGCTGATCCCGTGCA 1922
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QY 1923 CAAGCTGTAGCGCGCTACCTGTCAGCGCTGAACATCAACCGCCCTGCGACGCCAGAC 1982
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QY 2043 GATGTGCGGACGCTGTACAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCT 2102
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Db 1939 CGAGGACTTACCCGTACCGGAGCGACGCGCTGGCCATCTGCGACGCCATCGAGCAGTGGT 1998
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QY 2283 CGAGCGGTGTGAAGAGGTGCTGAGGAGCGCGACGCGGACCTCAAGGACCGAGACTG 2342
Db 2059 CGAGCGGTGTGAAGAGGTGCGGAGGTGCGGAGCGCGGACCGGACCAAGAGCGCGCGCTG 2118
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RESULT 2

US-09-810-268-2
; Sequence 2, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-2

Query Match 42.2%; Score 1324; DB 4; Length 2595;
Best Local Similarity 71.7%; Pred. No. 5e-264;
Matches 1904; Conservative 0; Mismatches 680; Indels 72; Gaps 10;

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Qy 366 COTCAGCGGCTCCACAGGATCTCTGGTGGGACGAGCGGCTCGCTTCCAGTCTGTCAG 425
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Qy 723 CTTGCGCAACGACACTATCTGCGAGCAAAATGCGCGCGGCTTGTGCTTATCGCA 782

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Db 1002 CTTCC---CGCGCGCGGAGCTACTGCTCAAGCTCCCATCCACAGATCATCCAA-- 1056
Qy 1323 AGATGTGTTGAAAGGCTCCGAGTTCGAGTTTAAAGTTTGGTGGAGGACTGACGAGAGTTCG 1382
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Db 1095 GCGGAGGTGCTCGCGCGGTCAACCCGATGTGATCAGCGCTTCAAGGAGTTCCTCCG 1154
Qy 1443 TAAAGACCTCTGAGCCCAAGGAGTACGGAGACACACAGCAGACATGATCACTGAAGTCA 1502
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Qy 1503 CATCCGGCATAACATGGGAGGCTGTGCGGTGAGAAACGACCTGAGGAAACAAGAGCTCTT 1562
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Qy 1743 GGTGTACACCGGCTCACACCGGCTGAGGGCGACGCTTGTGAGCTCGCGCAAGGCTTA 1802
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Db 1515 TGTGCGCGTCAACGACTCTGGCTTGGCACCACTCGTCAAGCCACTGGTGAACACCCAGC 1574

QY 1863 GGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGACGCTCAGGGTGGTGCATCCCGTGCA 1922
Db 1575 GGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGACGCTCAGGGTGGTGCATCCCGTGCA 1634
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Db 1635 CAAGCTCTGAGCTCGCACTTCGCGACACCATGACCATCAAGCCGCTGCGCGCGAGAC 1694
QY 1983 ACTCATCAAGCCCGCGCGCTTCGAGCGACCGCTGTTCCCTGCAAGTACCGCTGGG 2042
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QY 2103 CGTCAAGAGAGGCTGAGCTGTGCGGACCAAGCTCAAGCCCATATGTTGTCGATCTGAT 2162
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QY 2163 CAAGGACTACCTATCCGTTGAGCGGCTGCTGATCTGTTGGGCGATGAGCGGTGGT 2222
Db 1875 CGAGGACTACCTATCCGTTGAGCGGCTGCTGATCTGTTGGGCGATGAGCGGTGGT 1934
QY 2223 CAAGGAGTACTGACATCTACTACCTCAAGCGGAGCTCCAGCGTCAAGCGTGGAGCT 2282
Db 1935 GGGCGAGTACTGACATCTACTACCTCAAGCGGAGCTCCAGCGTCAAGCGTGGAGCT 1994
QY 2283 GCAGGCTGTGGAAGAGTGTGCTGAGGAGCGCGACCTCAAGGACCGAGCTG 2342
Db 1995 GCAGGCTGTGGAAGAGTGTGCTGAGGAGCGCGACCTCAAGGACCGAGCTG 2054
QY 2343 GTGGCCGAGATGACACCGCTCCAGAGCTGGTTCAGGCGTTCAGGCGTTCAGGCGT 2402
Db 2055 GTGGCCGAGATGACACCGCTCCAGAGCTGGTTCAGGCGTTCAGGCGTTCAGGCGT 2114
QY 2403 GGCATCCGCTGCAAGCGCTGTGCACTTTGGGAGTATCCATACCGGCTACCTCC 2462
Db 2115 CGGCTCGGCTCCAGCGCTGTGCACTTTGGGAGTATCCATACCGGCTACCTCC 2174
QY 2463 GACCGCGCAGCGCAGCGCGCGCGGATGCGGAGCGCAGGCGCAGCTACAGAA 2522
Db 2175 GACAGCGCCACCGTGAAGCGCGCGGATGCGGAGCGCGCAGGAGTACAGAA 2234
QY 2523 GCTGGAGCGGGCAGAGGAGCGGACATGTTGTTTCATCCGACCATCAGGCGAGTT 2582
Db 2235 GCTGG-----AGCGGACCGGAGCGCGGCTTCATCCACCATCAGGCGAGT 2285
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QY 2883 CAGCATCTCCATAGA 2898
Db 2580 CAGCATCTCCATAGA 2595

RESULT 3
US-09-751-687-10
; Sequence 10, Application US/09751687
; Patent No. 660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Ameke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhaug, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-751-687-10

Query Match 39.0%; Score 1222.2; DB 4; Length 2818;
Best Local Similarity 69.0%; Pred. No. 5.2e-243;
Matches 1868; Conservative 0; Mismatches 758; Indels 81; Gaps 11;
QY 210 GGAGCGAAGCGAAGAGCGGCCATGTTCTGGCACGGGTCCGACCGGCTGATCGA 269
Db 32 GGAGCAGTGAAGCGAGAGAGGAGGCGCAAGATGCTGTGGAGGGCTGATCGA 91
QY 270 AAAGAACAAAGAGAGCGGTGGAGCGAGGCAAGATCCGCGGACCGTGGTCAAGAA 329
Db 92 CACCTTCACGGGGCGCAACAGAGCGCGCTCAAGGACCGTGTCTATGCGCA 151
QY 330 GGAGGTGCTGACGTCGCGGCACTTCAACGCTCTCTCGAGCGCTCCAGAGATCT 389
Db 152 GAACGTGTGACCTCAACGACTTCGCGGCGCACCATCATCGACGCGATCGCGAGTTCCT 211
QY 390 CGGCTGGGAGACGACGCGCTTCGAGCTCGTCAAGCGCGCACCGCGCGCGAGCA 449
Db 212 CGG-----CAGGGCGCTTACCTCGAGCTTATCAGTCTCACCGCGCTCGACCAAGCAA 265
QY 450 CGGGGGCGTGGCAAGGTGGGAGGCGCGCACCTCGAGGAGCGCGTGTGTCTCA 509
Db 266 CGGCGTTCGCGGAAAGTGGGCGCGAGCGGAGCTGGAGCAGTGGGTGACGAGCTGCC 325
QY 510 GTCCACGCGGACGCGGAGACCGTGTACCGGGTCAAGTGGGA---CGAGTCGA 566
Db 326 GTCCTGACGACGCGGGAGTCCAAAGTTCGCGCTCACCTTCGAGCTGGGAGTGGAGAGCT 385
QY 567 GGGCATCCCGGCGCGCTCTCTGTCAGGAACTCGACGACCGCGAGTTCCTTCTCAAGAC 626
Db 386 CGGGGTGCGGGCGCCATCGTGTCAACAACTACCAAGCTCCGAGTTCCTGCTTAAAC 445
QY 527 GCTCACCTCGAGGGCGTCCAG---GCAAGGCGAGCTGTCTTTCGCGCAACGACACCTATCT 683
Db 446 CATCACCTTCAGACGCTCCCGCGCGAGCGGCAACCTCACCTTCGTTCGCGCAACTATG 505
QY 684 GGTCTACCTCGCACAAAGCTCTACTCCAGGAAACGATCTTCTTCGCGCAACGACACCTATCT 743
Db 506 GATCTACCCCGCGCAACTTACCGATACGCGCGCTTCTTCGCGCAACGACACCTATCT 565
QY 744 GCGGAGCAAAATGCGCGCGCGTGTGGTCCCTTATCGGCAAGATGAGTCAAGATTCG 803
Db 566 GCGGAGCAGATGCGCGCGCGCTGAGCGCGTACCGGAGCGAGCTCCGGAACCTTCG 625
QY 804 TGGCGAGATATCTCGACCATACAGAGGAGTATCGGCTTACCGTTCAGGACTACTA 863
Db 626 TGGCGAGCAGCAGGCGCGCTACAGAGAGCAGCGGATCTACGCTACGAGCTCTA 685
QY 864 CAATGACCTTGGTATCCCGACAAAGGGCGAAGAGCAGCTTCGCGCGAGTCTCGGTGGCAG 923

;; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting

;; FILE OF INVENTION: Production of Lipoxigenase in Fruits

;; CURRENT APPLICATION NUMBER: US/09/051,465A

;; PRIOR FILING DATE: 1998-07-31

;; PRIOR APPLICATION NUMBER: PCT/US96/16387

;; PRIOR FILING DATE: 1996-10-11

;; PRIOR APPLICATION NUMBER: 60/005,404

;; PRIOR FILING DATE: 1995-10-13

;; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: ASCII

;; SEQ ID NO 1

;; LENGTH: 2441

;; TYPE: DNA

;; ORGANISM: Lycopersicon esculentum

US-09-051-465-1

Query Match 21.28; Score 664.2; DB 4; Length 2441;
Best Local Similarity 57.78; Pred. No. 6.6e-128; Indels 51; Gaps 8;
Matches 1367; Conservative 0; Mismatches 953;

Qy	460	GGCAAGGTGGGAAAGCGGCGCACTGGAGAGGCGGTGGTGCCTCAAGTCCACGGCG	519
Db	89	GGGAACTGACATCCAGCATCTTAGAGAGTTGGCTTACAGACATCAACCAATAACA	148
Qy	520	GACGGGAGACCGTGTACCGGTGAGCTTCGAGTGGGA----CGAGTCGAGGCGATCCG	576
Db	149	GCAGGGGAATCAACTTTTAGTGTACATTTGAGCTGGGATCGTACGAGTTTGAGTTCCA	208
Qy	577	GGCCCGCTCTGGTTCAGAAACCTGACGACGCGGAGTTCTTCTCAAGACGCTCAACCTC	636
Db	209	GGAGCATTCATCAAGAAATCTTCACTTAATAGATTCTTTCTCAAGTCACTCACTC	268
Qy	637	GAGGGCTCCAGGCAAGGACCGTGTCTTCTGTCGCAACTCGTGGGTCTACCGGAC	696
Db	269	GAAGATGTTCTAATTAATGAAATAATCCATTTGTATGCAATTTCTTGGGTTATCTGCT	328
Qy	697	AAGCTCTACTCCAGGAACGATCTCTTCGCAACGACACCTATCTGCGGACAAATG	756
Db	329	TTTAGATACAGTCTGACCGCATTTCTTTGCCAATCAGGCTTATCTCCAGTGAACA	388
Qy	757	CCGGCGGCTGTGGTCCCTTATCGCAAGATGAGTCAAGATTCTCCGTGCGGACGATAAT	816
Db	389	CCACAACATTCGAAATAACAGAGAAATGAACTGGTAGCTTTTGGCAGGAGATGAA--	446
Qy	817	CTCGGACCATACAGGAGCATGTCGGTCTACCGTTACGTTACACTACTACATGACCTTGT	876
Db	447	-CTGGAAGCTTGAAGATGGACAGGGTTTATGATTATGCTTGTCTACATGATGAGT	505
Qy	877	GATCCGACAAAGGCGAAGACGACGCTCGGCCGATCCTCGGTGGCAGCCAAAGAACCCG	936
Db	506	GAACAGATAAGGGGGAAGATGATGCTPAGGCTTATCCTTGGAGGGTCTCTGAGTACCG	565
Qy	937	TATCCCGTCTGACAACTGCGCCGACCCCAACAAAGAAAGAACCTCAATTCGGAGAGC	996
Db	566	TATCCTCGTAGAGCAGCAGGCGCGAACCACAAAGCAGATCCTAATTGCGAGAGC	625
Qy	997	AGG---CTTTTCTGCTGAACCTCAACATCTAGCTCCCGGTGACGAAAGCTTTGGGCAT	1053
Db	626	AGGAACCATTTGCCATAGCTTAGACATATATGTCCCAAGGACGAGCAATTTGGTCAAT	685
Qy	1054	CTCAAGATTCGGACTTCTTGGGTACTCGCTGAGACGATCATCGAGGCTGTCTTCCA	1113
Db	686	GTGAAGAAGTCAGACTTTTGGAGTCTGCTCTTAAATCTCTTTTGAACACGCTTCTCCCT	745
Qy	1114	ACACTGGGACTTTTCGTGATGACACGCCCAAGAGTTTCGATTCTGAGGATATCTCTC	1173
Db	746	CGGTTTAAGGCTTTGTCGATACACGCCCTAATAGATTCAATAGCTTTGCGGATGACTT	805
Qy	1174	GGGCTCTACAGCTGGGCGCCAGAGGCAACCAACAAACCACTGATAGACGATCAGGAAG	1233
Db	806	AATCTCTTAAGAGGAGGAATCAAGTTGCTTGAAGGCGCTTGGTTGAAAGCCATTACTGAT	865

Qy	1234	AAGATCCCGCAGCGAGTTCCTTTCGAAGCATTTCTCGCAACCGTAGCCATGACCAACCCGCTA	1293
Db	866	AACATTTCTCAGAGATACATAAAGACATCTCTTCAACCGGATGTCAG---GCCACTT	922
Qy	1294	AAGATGCCCTTCCAAATGTCTCAATTCATCAATTCAGATGTGTGAAAAAGGCTCCGGAGTTAAG	1353
Db	923	AAGTACCAACTCTCTCAGGTTATTCAAGGCA-----TAAA	958
Qy	1354	TTTGCTGGAGGACTGACGAAGAGTTGCGAGAGAGACACTTTCAGGCGTGAACCCAGTA	1413
Db	959	ACTGCATGAGGACGGATGAAGAATTTGGGAGAGAAATGTTGGCAGGATCCAATCTCTGTC	1018
Qy	1414	ATCATCAAAACGTCTGACGAGTTCCTCCGCTAAAGACACCTTCGACCCCAAGGACGATCAGGA	1473
Db	1019	TTAATCAGTAGACTCCAGAAATTTCTCCGAAAGACAAAGTTGGATCCCAACCATATATGGA	1078
Qy	1474	GACCACACCAAGATCACTGAAGCTCACATCCGATCAACATGCGGAGTGAACGAGGCTGTCGCTG	1533
Db	1079	AACCAAAACAGTACAATTTACCAAGACATGTACAGGTAAGTTGAATGATTAACAGTG	1138
Qy	1534	CAGAACGCACTGAGGAAACAAAGAGCTTTCTATCTAGACCAACCATGACCATTTTCATGCCG	1593
Db	1139	AATGAGGCAATCAAGAGTAAACAGGTTATTCATATTGAACCAACCATGACATCGTGAAGCA	1198
Qy	1594	TACCTCGACGAGATCAACGAGCTCGAGGGAACCTTCATCTACGCGCAGCAGACCCCTACTG	1653
Db	1199	CTATTGAGGAAATTAACATGTACAGCAAAACAAAAAGCTTATGCTCTCAAGACTCTGCTC	1258
Qy	1654	TTCTTGAAGGACGATGGCAGCTGAAGCCCTGCGCCATCGAGCTGAGCCTGCCCCACCT	1713
Db	1259	TTCTTCAAGATGATAGAACTTTGAAGCACTAGCAATTTGAATTAAGCTTGCCACATCCA	1318
Qy	1714	GACGCCAGCAGCGCGCGGTGACGAAAGTGTACACCCGCTCACACGGGCTCGAG	1773
Db	1319	GACGGAGATCAATTTGGTACTGTTAGTAAAGTATATACACGAGCTGACCAAGGTGTTGAA	1378
Qy	1774	GGCCACGCTCTGGCAGCTCGCAAGGCTTATGCTTCGCTGAACAGCTCTGCTGCGCATCAG	1833
Db	1379	GGTTCTATCTGCGAGTTTGCCAAAGCTTATGTACAGTGAATGACATGGGCTTATCATCAG	1438
Qy	1834	CTGATCAGCCTCTGCTGAACACGACGCGGTGATCGAGCGGTTCTGTAATCGGACAAAC	1893
Db	1439	CTCATATGCCACTGGTTGAATACACACGCGGTGATCGAAACCAATTTGTGATGCAACAAAT	1498
Qy	1894	CGGAGCTCAGCGTGTGCTCCCGTGACAAAGCTGCTGAGCCGCGCTACTCCGCTGACACG	1953
Db	1499	AGGCACTTAAGTGTGCTTCACTCCCATTAACATCTTCTCATCTCTATTTCCGTTAAACG	1558
Qy	1954	CTGAACATCAACCCCTGGCAGCCGACACTCATCAACCGCGCGGCTTCTCGAGCGC	2013
Db	1559	ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTTATGATGTTGG---TTTTGAGACG	1615
Qy	2014	ACCGTGTTCCTGCAAAAGTACGCGCTGGGATGTGCGCAGACGTTACAGAGCTGGAAT	2073
Db	1616	TCTCTTTTCTGCAAAATATTCATGGAATGTTCAGCAGCGTTTCAAGATGTTGGTT	1675
Qy	2074	TTCAACGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGTGTGCGCGACGAG	2133
Db	1676	TTCCCTGAACAAGCACTTCCTGTGATCTCTCTCAAAAGAGAGGTGGCTGTGAGGACTTG	1735
Qy	2134	TCAAGCCCATATGTTGTCGACTCTGATCAAGCACTACCCCTATGCGGTGAGCGGCTC	2193
Db	1736	AGCTCCCCACATGGCATTCGTTTACTGATTCGAGCTATCCATATGCTGTGTGAGGCTG	1795
Qy	2194	GTCACTGTGGGCGATCGAGCGGTGGGTCAAGAGGTACCTGGACATCTACTACCTTAAC	2253
Db	1796	GAAATTTGGGCGAGCAATCAAAAGTTGGTAAACAAATATTGCAAGTTCTTATCAAAATCT	1855
Qy	2254	GACCGGAGCTCAGCGTGTGAGCTGCGAGCGTGTGGAGAGGAGGTGCGTGGAGAG	2313
Db	1856	GACGAGCAGTAGAAGAACACTGAACTCCAGCTTTGGTGAAGAGGAGCTCCGGAAGAA	1915
Qy	2314	GCGACGCGGACCTCAAGGACCGAGACTGTGTGGCCGAGGATGGACACCGTCCAGAGCTG	2373

Db 1916 GGACATGCGGCAAGAAAGATGAGGCTTGGTGGCTTAACTGCAAACTCGACAGAGCTC 1975
QY 2374 GCTAGGGCGTGCACGACCATCATCTGGGTGCATCCGCGTGCACGCGGTGTCAACTTTT 2433
Db 1976 AGAGATTGTTGCACCATCATATATATGATAGCTTTCAGCAGCTTCACTTTT 2035
QY 2434 GGGCAGTACCATACGCGGTACTCTCCGAAACGCGGCGGCGGCGGCGGCGGCGG 2493
Db 2036 GGCCTTACTCTTACGCTGGTGTATCTCCCTAATCGCCCTACTTTAAGCTGTAAATTTGATG 2095
QY 2494 CCGGAGCAGGACGACGACACTACAAGAAAGTGGGAGCGGGGCGAAGAGGCGGCGGCAATG 2553
Db 2096 CCAGAGCAGGAAGTGTGAGTATGAAGAGCT-----CAAGACAAATCCAGACAAG 2146
QY 2554 GTGTTCATCCGACCATACGACGAGTTCAGACCACTCTGGGCACTCTGCTCATCGAG 2613
Db 2147 GTATTCCTAAAGACATTTGCTCCTAGTTCCTCAGTTCGAACTCACTGTGAAATTTCACTTTTGA 2206
QY 2614 ATCTCTCCAAAGCACTCTCCGACGAGGTGTACCTCGGCGAGCGGTGACGAGCTGTATCGC 2673
Db 2207 GTCTCGTCAAGGCATGCTTCAGATGAGGTTTACTTGGGACAAAGGAGTCAATTGA---A 2263
QY 2674 TGGAGCTCAGACGCGCAAGCGCTGATGCTTCAAAAGATTTCGGGAGCGCGCTGGTGCAG 2733
Db 2264 TGGCAAAAGGATAAAGAACCACTTGTAGCTTTTGGAGAGTTTGGAAAGATGCTAAAGTAT 2323
QY 2734 ATTGAGAAATCGGATCAAGACGATGAACACAGTCCGAGCTTGAAGAACCGGAAAGGCGCT 2793
Db 2324 ATCGAGAAATCGAATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 2383
QY 2794 GTGGAATGCGGTACATGCTGCTGTACCCCA 2824
Db 2384 GTTAACGTTCCATATACGTTGCTCTTTCCCA 2414

RESULT 5

US-09-051-465-2
; Sequence 2, Application US/09051465A
; Patent No. 635862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; APPLICANT: Kausch, Kurt D.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051.465A
; CURRENT FILING DATE: 1998-07-31
; PRIOR FILING DATE: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR FILING DATE: 60/005.404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 2
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-2

Query Match 21.2%; Score 664.2; DB 4; Length 2871;
Best Local Similarity 57.7%; Pred. No. 6.9e-128;
Matches 1367; Conservative 0; Mismatches 953; Indels 51; Gaps 8;
QY 460 GGCAAGTGGGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519
Db 246 GGGAACTGAGCAATCCAGCATATCTAGAGGTTGGTTTACAGACATCACCCCAATAACA 305
QY 520 GACGGGAGACCGGTGTACCGGCTGAGCTTCAGTGGGA---CGAGTCGCGAGGCGCATCCCG 576
Db 306 GCAGGGGAATCAACTTTTAGTGTATACATTTGCTGGATCGTGCAGGTTTGGAGTTTCCA 365
QY 577 GCGCGCTCTGCTGCTCAGAACCTGCGACGCGGCGGCTTCTTCTCAGAGGCTCACCCCTC 636

Db 366 GGAGCATTCATCATCAAGAAATCTTATCTTAATGATTTCTTCTCAAGTCATCTCACTC 425
QY 637 GAGGGCGTCCAGGCAAGGCGCACCGTCTGCTTCGTCGCAACTCGTGGGTCTACCGCGAC 696
Db 426 GAAGATGTTCTTAATATGAAATAATCCATTTTGTATGCAATTTCTTGGTTTATCTGCT 485
QY 697 AAGCTTATCTCCAGGAAGCGATCTTTTCGCAACGACACCTATCTGCGGAGCAAAATG 756
Db 486 TTTAGATACAAGTCTGACCGCAATTTCTTTGCGCAATCAGGCTTATCTCCCAAGTGAACA 545
QY 757 CCGGCGGCTTGGTGTCTTATCGCAAGATGAGCTCAAGATTCTCGTGGCGACGATAT 816
Db 546 CCACACCATTCGGAATAATACAGAGAAATGACCTGAGTCTTTCGAGGAGATGGA--- 603
QY 817 CTGAGACCATACAGAGAGATGATCGGTCTACCTCTAGCTACTAGTACTAGTACTGCT 876
Db 604 -CTGGAAGCTTTGAAGAAATGAGGAGGTTTATGATTTATGCTTTGCTTACAAATGACTTGGT 662
QY 877 GATCCCGCAAGGGCGAAGAGACGCTCGGCGGATCTCTCGTGGCGAGCAAGAACACCG 936
Db 663 GAACAGATAGGGGAGAGATGCTAGGCTCTCTTGGAGGCTCTCTGAGTACCG 722
QY 937 TATCCCGTCTGCGAATCTGGCGGCAACCAAGAAAGAGCCAAATTCGGAGAGC 996
Db 723 TATCTCTGAGAGGCGAGACAGCGCGGCAACCAAGAAAGAGATCTTAATTCGAGAGC 782
QY 997 AGG---CTTTTCTCTGAACTGAACTCTACGTCCTCGGTCGAGCAAGCGCTTTGGGCGAT 1053
Db 783 AGGAACCATTCCTCTATGAGCTTAGACATATATGTTCCCAAGGAGCGAGATTTGGTCTAT 842
QY 1054 CTCAGATGTGGACTTCTTGGGTACTCTGCTGGAAGAGCATCATCGAGGCTGTCTTCCA 1113
Db 843 GTGAAGAAATCAGACTTTTGTAGCTCTTAAATCTCTTTGCAACGCTTCTCCT 902
QY 1114 ACACCTGGGACTTTCGTCGATCAGCGCCAGGAGTTCGATTCTGTTGAGATATCTCT 1173
Db 903 GCGTTTAAAGCTTTGTGCGATAACACGCTTAATGAGTTCAATAGTTTTCGCGATGACTT 962
QY 1174 GGGCTCTACGAGCTGGGCGGCGAGGCAACCAACCACTGATAGCAGAGATCAGGAAG 1233
Db 963 AATCTCTATGAGGAGGAATCAAGTTGCTGAGGCGCTTGTGTGAAGCCATTACTGAT 1022
QY 1234 AAGATCCCGAGGAGTTCCTTCGAAGCATTTTCGGAAGCGGTAGCATGACACCGCTA 1293
Db 1023 AACATTTCTCAGAGATATAAAGACATCTTCAACGAGTGTCTAAG---GCTACTT 1079
QY 1294 AAGATGCGCTTCCAAATGTCTCAATCAATCAGATGTGTGAAAGAGGCTCCGAGTTTAA 1353
Db 1080 AAGTACCCCACTCTCTCAGGTTATTCAAGGCGA-----TAA 1115
QY 1354 TTTGCTGAGGACTGAGCAAGAGTTCGCGAGAGAGACATTTGAGGCGGTGAACCCAGTA 1413
Db 1116 ACTGCATGAGGAGCGGATGAAGAAATTTGGGAGAGAAATGTTGGCAGGATCCAATCTCTC 1175
QY 1414 ATCATCAAAAGCTCTGACGAGTTCCTCGCTAAAGACCTTGGACCCAGGCGGTACCGA 1473
Db 1176 TTAATCAGTACTCCAGAAATTTCTCCGAGAGCAAGTTGGATCCACCATATATGGA 1235
QY 1474 GACCAACACGAGATCACTGAAAGTCACTCCGCGATACATCCGCGATAACTGGGAGGCTGTGCGTG 1533
Db 1236 AACCAAAACAGTACAAATTTACACAGAACATGATACAGGATAGTTGAATGGAATTAACAGT 1295
QY 1534 CAGAACGCACTGAGGAACAAGAGGCTCTTCACTCTAGACCAACCATGACCATTTTCAATCGCG 1593
Db 1296 AATGAGGCAATCAAGATTAACAGGTTTATTAATTTGAACCAACCATGACATCGTGAATGCA 1355
QY 1594 TACCTCGAGAGATCAACAGAGCTGGAGGGAACTTCTATCTACGCGAGCAGGACCTTACTG 1653
Db 1356 CTATTTAGGAAAAATTAATCATGTACGCAAAACAAAAAGCTTATGCTTCAAGAACTTCTGCTC 1415
QY 1654 TTCCTGAAGGAGGATGGACGCTGAAGCCCTTGGCCATCGAGCTGAGGCTGCCCCACCTC 1713

Db 1416 TTCTTACAGATGATAGAACTTTGAAGCCACTAGCAATTTGAACCTTAAGCTTGCCACATCCA 1475
QY 1714 GAGGCGCAGAGCGCGCGGTGACAGAGGTGTACACCCGGCTCACACGGGCTCAG 1773
Db 1476 GACGGAGATCAATTTGGTACTGTTAGTAAAGTATATACACCAGCTGACCAAGGTTTGA 1535
QY 1774 GGCACGCTGGCAGCTGCCAAGGCTTATGCTCGTAAACGACTCTGCTCTGGCATCAG 1833
Db 1536 GGTTCCTATCTGCAGGTTTCCAAAGCCTATGTAGCAGTGAATGACATGGCATTCATCAG 1595
QY 1834 CTGATCAGCCTCTGGTGAACAGCAGCGGCTGATGAGCCCTTGTATTCGCGCAAC 1893
Db 1596 CTCAATAGCCTGTTGAATACACACGCGGTGATCGAACCAATTTGTGATGCAACAAT 1655
QY 1894 CGCAGCTCAGCGTGTGATCCGTCGCAAGCTGCTGAGCCCGCACTACCGTGACACG 1953
Db 1656 AGGCATCTAAGTGTGCTTATCCCATTTATAACTTCTTCATCTCTCAATTCGTTAACAG 1715
QY 1954 CTGAACATCAAGCCCTGGCAGCCAGACACTCATCAACCGCGCGGCGTCTTCGAGCGC 2013
Db 1716 ATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGCTG---ATTTGAGACG 1772
QY 2014 ACCGTGTTCCCTGCAAGTACGCGTGGGATCTCGCAGAGCTGTACAGAGCTGGAAT 2073
Db 1773 TCTCTTTTTCCTGCCAAATATTCATGGAATGTGACAGAGCTTACAAAGATTGGTT 1832
QY 2074 TTCAAGCAGCAGCTCTCCAGCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAG 2133
Db 1833 TTCCCTGAAACAGCACTCTCTGCTGATCTCTCAAAAGAGGAGTGGCTGTGAGACTTG 1892
QY 2134 TCAAGCCATATGTTCCGACTGCTGATCAGAGGACTACCTATGCTGCGTTCAGCGGCTC 2193
Db 1893 AGCTCCCCCATGGCAATGCTTTACTGATCTTGATCTGACTATCCATATGCTGTTGATGCTG 1952
QY 2194 GTCATCTGTTGGCGGATCCAGCGGTGGTCAAGAGTACTGTGACATCTACTACCTAAC 2253
Db 1953 GAAATTTGGCAGCAATCAAAAGTTGGTAAACAGATATTGCAAGTTCTTATTACAAATCT 2012
QY 2254 GAGCGGAGCTCAGCGTGAAGTGTGAGCTGAGCGGTGTGAGAGAGTGTGAGGAG 2313
Db 2013 GACGAGACAGTAGAAGAGCACTGAACCTCGAAGCTTGTGAGAGGAGCTCCGCGAAGAA 2072
QY 2314 GCGCAGCGACCTCAAGGACCGAGACTGGTGCCCGAGGATGACACCGCTCAGAGCTG 2373
Db 2073 GGCATGGCGACAGAAAGATGAGGCTTGGTGGCTTAACTGCAACTCGACAGGCTC 2132
QY 2374 GCTAGGCGTGCACGACATCTCTGGTGGCATCCCGGTGCAACCGGCTGTCAACTTT 2433
Db 2133 AGAATTTGTCACCATCATATATGATAGCTTTCAGCACTTCATGCAAGCACTCCATTTT 2192
QY 2434 GGCAGTACCATACCGCGGTACCTCCGAAACCGCGGACCGGCGGCGCGCGGATG 2493
Db 2193 GGCTTACTCTTACGCTGCTTATCTCCCTTAATCGCCCTACTTTAAGCTGTAAATTTGAG 2252
QY 2494 CCGGAGCCAGGACGCCACTCAAGAACTCGGAGCGGGGAGAGGAGCGGACATG 2553
Db 2253 CCAGAGCCAGGAGTTGAGTATGAGAGCT-----CAAGACAAATCCAGACAG 2303
QY 2554 GTGTTATCCGACCATCACAGCGATTCAGACCATCTCGGCACTCTCGCTCATCGAG 2613
Db 2304 GTATTCTCAAAACATTTGTTCTCTGATGCAATCACTGCTTGAAATTTCCATCTTTGAG 2363
QY 2614 ATCTCTTCCAGCACTCTCCGAGAGGTGTACTCTGGCCAGCGGTGACGAGCTGATCGC 2673
Db 2364 GTCTCGTCAAGCAGTCTTCAGATGAGTTTACTTGGGACAAAGGACTCAATTGA--A 2420
QY 2674 TGGAGCTCAGCGCAAGCGCTGATGCTGCTTCAAGATTCGCGAGCGCGCTGTGAG 2733
Db 2421 TGGACAAAGGATAAAGAACCACTTTGATGCTTTTGGAGAGTTTGGAAAGATGCTAACTGAT 2480
QY 2734 ATTCAGATCGGATCAAGACGATGAACGACAGCTCGGACTTGAAGAACCGGAGGCGCT 2793
Db 2481 ATCAGAAATCGAATTTATGATTAATGATGATCATAGAGTTGGAGAAACAGGTCAGGCT 2540

QY 2794 GTGAAATGCGTACATGCTGCTGTATACCCCA 2824
Db 2541 GTTAAAGTCCATATAGTGTGCTCTTTCCCA 2571

RESULT 6

US-09-051-465-4
; Sequence 4, Application US/09051465A
; Patent No. 6355862
; GENERAL INFORMATION:
; APPLICANT: Handa, Avtar K.
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits
; FILE REFERENCE: 7024-297
; CURRENT APPLICATION NUMBER: US/09/051,465A
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: PCT/US96/16387
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: 60/005,404
; PRIOR FILING DATE: 1995-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: ASCII
; SEQ ID NO 4
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-051-465-4

Query Match 21.2%; Score 664.2; DB 4; Length 2871;
Best Local Similarity 57.7%; Pred. No. 6.9e-128;
Matches 1367; Conservative 0; Mismatches 953; Indels 51; Gaps 8;
QY 460 GCGAAGTGGGGAAGCGCGCACCTGAGAGAGCGGTGCTCAAGTCCACGGCG 519
Db 246 GGGAAATGAGCAATCCAGCATACTTAGAGATTGGCTTACAGACATACCCCAATAACA 305
QY 520 GACGGGAGAGCGGTGACCGGGTACGAGTGGGGA---CGAGTCCGAGGGCATCCCG 576
Db 306 GAGGGGAATCACTTTTAGTGTATCAATTTGACTGGATCGTACGAGTTTGAAGTTCCA 365
QY 577 GCGCGCTCTCTGGTCAAGAACCTGACAGACGCGGAGTTCTTCTAAGACGCTCACCTC 636
Db 366 GGAGCATTCATCATCAAGAAATCTCATCTTAATAGATTCTTCTCAAGTCACTCACACTC 425
QY 637 GAGGGGTCCAGCAGGAGGACCGTCTGCTGCGCCAACTCGTGGGTCTACCGGCAC 696
Db 426 GAAGATGTTCTTAATTTAGGAAATCCATTTGTATGCAATTTCTGGGTTTATCTTGCT 485
QY 697 AAGCTCTACTCCCAAGGAACGATCTTCTCGCCAAACGACACCTATCTGCGAGCAAAATG 756
Db 486 TTTAGATCAAGTCTGACCGCATTTTCTTTGCCAAATCAGGCTTATCTCCCAAGTGAACA 545
QY 757 CCGCGGGGTTGGTCCCTTATCGCAAGATGAGCTCAAGATTCTCCGTGGCGACGATAAT 816
Db 546 CCACAAACCAATTCGAAAATACAGAGAAATGAATGCTAGCTTTGCGAGGAGATGAAA-- 603
QY 817 CCGGACCATACAGGAGGATGATCGGTCTACCGTTACGACTACTACATGACCTTGGT 876
Db 604 -CTGAAAGCTTGAAGATGAGGACAGGTTTATGATTATGCTTGTCTACATGACTTGGT 662
QY 877 GATCCCGAAGCGGAGAGCAGCTGCGCGGATCTCGGTGGGAGCGCAAGAACACCGG 936
Db 663 GAACAGATAAGGGGGAAGAGTATGCTAGGCTTATCTTGGAGGCTCTCTGAGTACCCG 722
QY 937 TATCCCGTCTGCTCAGAACTGGCGGCGACCCCAAGAAAGACCCAAATTCGAGAGC 996
Db 723 TATCTCTAGAGGAGGACAGGCGCGGACCAACCAAGAGATCTTAATTTGCGAGGC 782
QY 997 AGG---CTTTTCTGCTGAACCTGAACATCTACGCTCCCGGTGACGAACGCTTTGGGCA 1053
Db 783 AGGAACCCATTTGCTTATGAGCTTAGACATATATGCTCCCAAGGGACGAGCATTTGGT 842

QY	1054	CTCAAGATGTCGGACTTTCCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCA	1113
Db	843	GTGAAGAAATGCAGACTTTTGGACGTGCTCTTAAATCCTCTTTGCAAAAGCTTCTCCCT	902
QY	1114	ACACTGGGACATTTTCGTGATGACAGCCCAAGGATTCGATTCGTTTCAGGATATCCCTC	1173
Db	903	GCCTTTAAGGCTTTGTGCGATAACAGCCCTAAATGAGTTCAATAGCTTTCCGGATGTACTT	962
QY	1174	GGGCTCTACAGACTGGGCCAGAGGACCCAAACACCCACTGTATAGACAGATCAGGAAG	1233
Db	963	AATCTCTATGAAGAGGAATCAAAGTTGCCTGAAGGCCCTTGGTTGAAAGCCATTACTGAT	1022
QY	1234	AAGATCCCAGACGATTCCTTCGAAGCATTCGCCGAACGGTAGCCATGACACCCCGCTA	1293
Db	1023	AACATTTCTCCAGATATCTAAAGACATCCCTTCAAACGGATGGTCAAG---GCCTACTT	1079
QY	1294	AAGATGCCCTTCCAAATGTCAATAATCAGATGTGTGTAAGAAAGCTCCGGAGTTTAAG	1353
Db	1080	AAGTACCCTACTCTCAGGTTATTCGAAGGGA-----TAAA	1115
QY	1354	TTTGGCTGGAGGACTGACGAAGAGTTCCGACAGAGACACTTTCAGCGGTGACACCAGTA	1413
Db	1116	ACTGCATGGAGGACGGATGAAGAAATTTGGAGAGAAATGTTGGCAGATCCAAATCCTGTC	1175
QY	1414	ATCATCAAAACGCTGTACGGAGTTCCCCCGCTTAAAGACACCCCTGGACCCCAAGCAGTAGCGGA	1473
Db	1176	TTAATCAGTAGACTCCAAGAAATTTCTCCGAGAGCAAGTTGGATCCAACATATATGGA	1235
QY	1474	GACCAACACGACAAAGATCACTGAAGCTCAATCCGGCATTAACATGGAGGCCCTGTCGGTG	1533
Db	1236	AACCAAAACAGTACAATTTACCACAGAACATGTACAGGATAAGTTGAATGGATTAACAGTG	1295
QY	1534	CAGAAACCACTGAGAAACAAGAGCTCTTCATCCTAGACCAACCATGACCAATTTTCATGCCG	1593
Db	1296	AATGAGCCTATCAAGCTTAACAGGTTATTCATTTGAACCAACCATGACATCGTGAATGCCA	1355
QY	1594	TACCTGACGAGATCAACGAGCTGGAGGGGAACTTCATCTATAGCCAGCAGGACCTTACTG	1653
Db	1356	CTATTGAGGAAAAATTAACATGTCTAGCAAAACACAAAAAGCCTATGCCCTCAAGAACTCTGCTC	1415
QY	1654	TTCTGTAAGGACGATGGCAGCTGAAGCCCTTGCCCATCGAGCTGAGCCTGCCCCACCCCT	1713
Db	1416	TTCTCAAGATATAGACTTTTGAAGCCACTAGCAATTGAATAGCTTGCACATCCA	1475
QY	1714	GACGGCAGCAGCGCGCGGCTCAGCAAGGTGTACACCCGGGTACACCGGGGTGCGAG	1773
Db	1476	GACGGAGATCAATTTTGGTACTGTGTAGTAAAGTATATACACACGCTGACCAAGGTGTGA	1535
QY	1774	GGCCACGCTGGCAGCTCGCCAGGCTTATGCTCTCGCTTAAACGACTCTGCTGGCATCAG	1833
Db	1536	GGTTCTATCTGGCAGTTTGCCAAAGCCTATGTAGCACTGAATGACATGGGCATTCATCAG	1595
QY	1834	CTGATACGCCACTGGCTGAACACGCAACGGGTGATCGAGCGGTTCGTAATCGCGACAAC	1893
Db	1596	CTCATTAGCCACTGGTTGAATACACACGCGGTGATCGAACCATTTGTGATTCGAACAAT	1655
QY	1894	CGGCAGCTCAGCGTGGTGCAATCCCGTGCACAAGCTGTGAGCCCGCCTACTACCGTGACCG	1953
Db	1656	AGGCATCTAAGTGTGCTTATCCCAATTCAATAACTTCTTCATCTCATTTCCGTACACG	1715
QY	1954	CTGAACATCAACGCCCTTGGCACGCCACGACACTCAATCAACGCGCGCGCTCTTCGAGCGC	2013
Db	1716	ATGAACATAAATGCTTTAGCAAGAGACCTTGAACCTATGATGGTGG---TTTTGAGACG	1772
QY	2014	ACCGTGTCTCTGAAAGTAGCGCGCTGGGATGTGCGACAGCTGTACAAGAGCTGGAAT	2073
Db	1773	TCTCTTTTCTGCGAAATATTCATGGAATATGACAGCAAGCTTAAGAATTGGGTT	1832
QY	2074	TTCAACGAGCAGGCTCTCCACGAGATCTCGTCAAGAGAGGTGTGGCTGCGCGACCAAG	2133
Db	1833	TTCCCTGAACAAGCACTTCCTGCTGATCTCTCTCAAAAGAGAGTGGCTGTGTGAGGACTTG	1892

Qy	2134	TC AAGGCCCATATGGTGTCCGACTGTCTGATCAAGGACTACCCCTATGTCGCTTGACGGGCTC	2139	
Db	1893	AGCTCCCCACATGGCAATCGTTTACTGATCTTCTGGACTATCCATATGCTGTGTATGCTTG	1952	
Qy	2194	GT CATCTGGTGGCGCATCAGCGGTGGGTCAAGGAGTACTCGACATCTACTACCCATAAC	2253	
Db	1953	GAATTTGGCGACCAATCAAAGTTGGTAAACAGATATTGCAAGTTCTATTACAAATCT	2012	
Qy	2254	GACGGCGAGTCTCAGCGTGTGACGTGTGAGCTGTCCAGCGCTGTGTGAGAGAGGTGCGTGAAGG	2313	
Db	2013	GACGAGACAGTAGAGAAAGACACTGAACCTCCAAGCTTGTGTGAAGAGAGTCCCGCAAGAA	2072	
Qy	2314	GCCACGGCGACCTCAAGGACCAGACTGTGTGCCCCAGGATGGACACCGTCCACGACGCTG	2373	
Db	2073	GGACATGGCGACAAGAAAGATGAGGCTTGGTGGCTTAAACTGCAAACTGCACAAGAGCTC	2132	
Qy	2374	GCTAGGCGGTGCACGACCACTATCTGGTGGGCATCTCGCGCTGTGACGGGCTGTCAACTTT	2433	
Db	2133	AGAGATTGTTGCAACCACTATATATGGATAGCTTCAGCACTTCATGACGACATCCCAATTTT	2192	
Qy	2434	GGCAGTATACCATATACGCGGGTACCTCCGAAACGGCCGACGGCCAGCGCGCCCGATG	2493	
Db	2193	GGCTTATACCTTACCGCTGGTTATCTCCCTATATCGGCCCTACTTTAAGCTGTATTTGATG	2252	
Qy	2494	CCGAGCCAGGCAGCCACGACTCAAGAAGCTCGGAGCGGGCAGAGGAGGCGGACATG	2553	
Db	2253	CCAGGCCAGGAAGTGTGTGATATGAAGACT-----CAAGACAAATCCAGACAAG	2303	
Qy	2554	GTGTTTATCCGCAACCATCACACGCGAGTTCAGACCATCTCTGGGCATCTCGCTCATTCGAG	2613	
Db	2304	GTATTCCTAAAAACATTTGTTTCCTCAGTTCGAATCACTGCTTGAAATTTCCATCTTTGAG	2363	
Qy	2614	ATCCTCTCCAAGACACTCCTCCGACGAGGTGTACTCTGGCCAGCGTGCAGAGCCTGTATCGC	2673	
Db	2364	GTCTCGTCAAGGATGCTTCAGATGAGTTTACTTTGGACAAGGGACTCAATTGA---A	2420	
Qy	2674	TGAGCTGCAGCGCAAGGCGCTGGATGCGTTCAAAGAATTCGGGAGCCCGCTGGTGCAG	2733	
Db	2421	TGGACAAAGGATAAAGAACCACTGTGAGCTTTTGTAGAGGTTTGGAAAGATGCTAAAGTGAT	2480	
Qy	2734	ATTGAGAAATCGGATCAAGACGATGAACGACAGTCCGACCTTGAAGAACCGGAAGGGCGCT	2793	
Db	2481	ATCGAGAAATCGAATTATGATAATGAAATGATCAATAGAGTTTGGAAAGAACAGGTTCAGGCGCT	2540	
Qy	2794	GTGAAATGCCGTACATGCTGTGTACCCCA	2824	
Db	2541	GTAAACGCTTCATATACGTTGCTCTTTTCCCA	2571	

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RESULT 7
US-09-751-687-11
; Sequence 11, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11U501
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2346)..(2348)
; OTHER INFORMATION: "t" is a, c, t, or g encoding

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OTHER INFORMATION: i
US-09-751-687-11

Query Match 19.1%; Score 599.2; DB 4; Length 4663;
Best Local Similarity 59.2%; Pred. No. 2.1e-114;
Matches 1511; Conservative 0; Mismatches 621; Indels 421; Gaps 12;

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QY 734 ACACCTATCTGCGAGCAAAATGCGCGGCGTGTGGTGTCTTATCGGCAAGATGAGCTCA 793
DB 2020 AGAGCTACCTGCGAGCCAGATGCGCGCGCTGAGCGGTACCGGACGAGCTCC 2079
QY 794 AGATTCTCGTGGCGAGCAATATCTTGGACCAATACAGGAGCATGATCGCGTCTACCGTT 853
DB 2080 GGAACCTTGGTGGCGAGCAACAGGAGGCGGTACCGAGGACGACACCGCATCTACCGCT 2139
QY 854 ACAGCTACTACATGATGACCTTGGTGATCCCGACAGGCGGAGAGCAGCGTCCGGCGATCC 913
DB 2140 ACAGCTCTACAGCACTCTGGCG-----AGGCGCGCCCATCC 2178
QY 914 TCGGTGGCAGCAGCAACCCGTATCCCGTCTGCTGACAGACTGGCGCGCACCAACAA 973
DB 2179 TCGCGCGCAACTCCGACCACTTACCGCGCGCGCGCGCACGAGCGCAAGCGCAACG 2238
QY 974 AGAAGACCCAAATTCGGAGGACAGGCTTTCTGCTGCTGACCTGACATCTAGTCCCGC 1033
DB 2239 CCAGGACCCGAGCTGGAGAGCGGCTGTGCTGTGGA---GCAATCTACGTGCCGC 2295
QY 1034 GTGACGAACGCTTTGGGCATCTCAAGATGTGCGACTTCTTGGTACTCGCTGAAGACGA 1093
DB 2296 GGGACGAGAAGTTCCGGCCACCTCAAGAGCTCGACTTCTGGGTACTCCATCAAGGCCA 2355
QY 1094 TCATCAGGCTGTCTTCCAACTCTGGGACTTTCGTGATGACACGCGCCAGAGATTG 1153
DB 2356 TCACGAGGCACTCTTCCGCGCGCTGCGACCTACGTGACACACCCCGCGGAGTTG 2415
QY 1154 ATTCTGTTGAGGATATCTTCCGGCTCTACGAGTGGCGCGCAGGACCAACCAACCCAC 1213
DB 2416 ACTCTTCCAGGACATCACTCTATGAGGCGGCATCAAGTCCCAAGTGGCG 2475
QY 1214 TGATGAGAGATCAGAGAGATCCCGAGGAGTTCCTTGAAGCATCTTGGCGAAG 1273
DB 2476 CCTTGGAGGAGCTCCGTAAGCAGTTCCCGCTCAGCTCATCAAGGACCTCTCCCGCTG 2535
QY 1274 GTAGCATGACCACTCCGCTTAAAGATGCCCTTCCAAATGTCTCAATCAGATGTGTGA 1333
DB 2536 GCGGC---GACTCCCTGCTTAAGTCCCGTCCCGTCCCATCATCTCCAGGAGACAGCAG 2592
QY 1334 AAAAGGCTCGGAGTTAAGTTTGGCTGGAG-----ACTGACGAAGAGTTGCGGA 1384
DB 2593 CGTGGAGGACCGAGGAGTTCCGACGGAGGTCTCGCNCNNNGTCAACCCCGTCA 2652
QY 1385 GAGAGACATTCAGGCGTGAACCCAGTAATCATCAA-----1421
DB 2653 TCAGCGCTTCAGGTGAGTCAGCATTTATTTGTTCTTGTGTGTATGTTGTCATGG 2712
QY 1422 -----ACGTCTGAGC 1431
DB 2713 TGAGAAAGTGCAGATCTTGATTTGGCTTGGGTGCGCATGCAAGCATCTGTCATGCGATG 2772
QY 1432 GAGTTCCCGCTTAAAGCACTTGGACCAAGCAGTACGAGACCAACAGCAAGATC 1491
DB 2773 GAGTTCCCGCAAAAGTAGTCTGGACCTTAGCAAGTTTGGTGAACCAACAGCAAGCATC 2832
QY 1492 ACTGAAGCTCACATCCGGCATACATGGGAGGCTCTCGGTGCAAGACGA 1542
DB 2833 ACCGCGAGCACATAGAGAAGACCTTCGAGGCGCTCACGGTGCAGCAGGTAATTGGTCCA 2892
QY 1543 -----1542
DB 2893 AGCCATGACATCAACTATGATTACCTAGGAGTAATTGGTAGCTGTAGATAATTGGCT 2952
QY 1543 -----1542
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DB 2953 TCGTTGCAATTAATTTGATGCTGCGCGATCAAGTATGATGCTTTGAAATTTGCGAG 3012
QY 1543 ---CTGAGGAACAAGAGGCTCTTCACTCTAGACCAATGATACCATTTTCATGCGGTACCTC 1599
DB 3013 GCGCTGGAAGCAACAGGCTGTATCTTGTATGATCAATGACCGGTTCATGCGGTCTCTG 3072
QY 1600 GACGAGATCAACGAGCTTGGAGGGAATTTCTATGCGCAGCAGGACCTTACTTGTCTCTG 1659
DB 3073 ATCGACGTCAACAACCTGCGCGCACTTCTATCGCCACAGGAGCCCTTCTTCTCTG 3132
QY 1660 AAGGACATGCGACGCTGGAAGCCCTGGCCATCAGCTGAGCTGCTGCCCACTCTGAGCGGC 1719
DB 3133 CGCGGACGCGAGGCTCACGCGCTGCGCATCAGCTGAGCGAGCCCATCATCCAGGCG 3192
QY 1720 CAGCAGCGCGCGCGCTCAGCAAGGTGTACACCCCGCTCACACCGG---CGTCGAGGCG 1776
DB 3193 GGCCTTACCAACGCGCAAGAGGTTTACACGCGGTGCGCCAGCGCTCCGTCGAAGGC 3252
QY 1777 CAGCTGTGGCAGCTCGCAAGGCTTATGCTGTGTAACAGCTCTGCTGCGATCAGCTG 1836
DB 3253 TGGGTGTGGAGCTCGCAAGGCTTACGTCGCCGTCAATGACTCCCGGTGGCACCACTC 3312
QY 1837 ATCAGCCACT-----1846
DB 3313 GTGAGCCACTGCTGCTTCTCCAGCTCGATGTGATTCAGTCAGTCGATGCACACAACT 3372
QY 1847 -----GGCTGAACAACGCGCGGTGATTCAGCGGTT 1877
DB 3373 GATCGAAATATGATTGATTGAAACGCGAGGCTGAACACTCAGCGGTGATGAGGCGTT 3432
QY 1878 CGTAATCGCAACAAACGCGAGCTCAGCGTGTGCTATCCCGTGCACAAGCTGCTGAGGCC 1937
DB 3433 CGTATCTCGACGNAACCGCACCTTAGCTGACGCGCGGTGCAAGCTGCTGAGGCC 3492
QY 1938 GCATACCTGTGACACGCTGAACATCAACGCCCTTGGCAACGACACTCATCAACGCGCG 1997
DB 3493 GCATACCGGACACCATGACCATCAACGCGCTGGCGCGCAGACGCTCATCAACGCGCG 3552
QY 1998 CGGCGCTTCTGAGCGCACCGTGTTCCTGCAAGTACGCGCTGGGATGTCGCGCAGACGT 2057
DB 3553 CGGCATTTTGAAGTACGCTGTTCCCGGCAAGTTCGCGTGGGATGTCGCGCGGTT 3612
QY 2058 GTACAAGCTTGAATTTCAACAGCAGGCTCTCCAGCAGATCTCTGTCAG-----2109
DB 3613 GTACAAGCTTGAAGTTTCAACGAGGAGTCTCCGAGCAGTCTCATCAAGAGTACGT 3672
QY 2110 -----2109
DB 3673 ACCTGTAATGTTATGATGTGTAACAAANTGGGCGTCTCGCTCACTGACAGGAACG 3732
QY 2110 -----AGAGGTGGCTGTGCGGACCCAGTCAAGCCCATATGTTGTCGA 2154
DB 3733 TGGTAAAAAATGCGAGGCGATGGCGTGGAGGACCGCTCGAGCCGTACAAGGTGCGG 3792
QY 2155 CTGCTGATCAAGNCTACCCCTATGCGTTGACGGGCTGCTCATCTGTTGGGCGATCGAG 2214
DB 3793 TTGCTGTGTGCGACTACCGGTACGCGGCGGAGCGGCTGCGATCTGCGACCGCCTTGG 3852
QY 2215 CGGTGGGTCAAGAGTACCTGGACATCTACTACCTTAAACGACGCGCGAGCTTCCAGCGGTGAC 2274
DB 3853 CAGTACGTGAGCGAGTACCTGGCCATCTACTACCGAAGCAGCGCGTGTGTCAGGCGAT 3912
QY 2275 GTGAGCTGACAGGCTGTGAGAGGAGTGTGAGGAGCGCGGACCGGCTCAGGAC 2334
DB 3913 ACAGAGTGCAGCGGTGTGGAAGGAGACCGCGAGGTGGGCAACCGGACCTCAGGAC 3972
QY 2335 CGAGACTGTGTGGCCCGAGATGGACACCGTCCAGCAGCTGCTAGGGGCTGCGACGCATC 2394
DB 3973 GCGCCATGTGTGGCCCAAGATGCAAGTGTCCGAGCTGCGCAAGGCTGCACCCATC 4032
QY 2395 ATCTGGGTGCGATCCGCGCTGCGAGCGGCTGTCACTTTGGGAGTACCCATAGCGCGG 2454
DB 4033 ATCTGGATCGGGTCCGGCTGCGATGCGGCGAGTCACTTCGCGGAGTACCCCTACGCGGG 4092
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Db 3229 GTCCGACGCGCTCCGTCGAGGCTGGGTGGGAGCTCGCCAAAGCCCTACCTCGCGGTC 3288
Qy 1813 AACGACTCTGCTGGCATCAGCTGATCAGCACT----- 1846
Db 3289 AATGACTCCGGGTGGGACAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGAT 3348
Qy 1847 -----GCTGAA 1853
Db 3349 TCAGTCAGTCGATGCAACAACCTGATCGAAATATGATTGATGAAACGCGCAGCTGAA 3408
Qy 1854 CAGCGACGCGGTGATCGAGCCGTTCTGTAATCGCGACAAACCGGCGAGCTCAGCGTGGTGCA 1913
Db 3409 CACTCAGCGGTGATGAGCCGTTCTGTAATCTCGACGAAACCGGCACTTAGCTAGCGCA 3468
Qy 1914 TCCCGTGCACAGCTCTGAGCCCGCACTACCGTGACAGCTGACATCAACGCCCTGCG 1973
Db 3469 CCGGTGGCAAGCTCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCCCTGCG 3528
Qy 1974 AGCCGACACTCATCAACCGCGCGCGCTCTTCGAGCGCACCGTGTTCCTGCAAGTA 2033
Db 3529 GCGGACAGCGTCTCATCAACCGCGCGCGCATCTTCGAGATGACGGTGTCCCGGCAAGTT 3588
Qy 2034 CCGCTGGGATGTCGGGACAGTGTAAGAGCTGGAATTTCAAGAGCGGCTCTCC 2093
Db 3589 CCGTGGGATGTCGGCGGTGTCGAGTGTGTAAGAGCTGGAATTTCAAGAGCGGCTCTCC 3648
Qy 2094 AGCAGATCTCGTCAAG----- 2109
Db 3649 GGACGATCTCATCAAGAGTACGTACCTGGTAAATGTTATGATGTGTAAACAATTTGG 3708
Qy 2110 -----AGAGTGTGGCTGTGCGGAC 2130
Db 3709 GCGTCTCGCTCACTGACAGGAACGTTGTTAAAAAAATGACGGGCGATCGCGTGGAGAC 3768
Qy 2131 CAGTCAAGCCCATATGTTGTCGACTGCTGATCAAGAGTACTCCCTATGCTGCGTTCAGCGG 2190
Db 3769 CCGTCAGCCCGTACAGGTGGTGTGTTGTTGTCGACTACCTGCTGCGGCGGACGG 3828
Qy 2191 CTCGTATCTGTGGCGATGACGCGGTGGTCAAGAGTACTCTGGAATCTTACTACCT 2250
Db 3829 CTGGCATCTGGCACCCATTGACGAGTACGTGACGAGTACTCTGGCCATCTACTACCG 3888
Qy 2251 AACGACGGGAGCTCCAGCGTGCAGTGGAGCTGAGGCGTGTGGAAGAGGTGCGTGAG 2310
Db 3889 AACGACGGGAGTGCAGCGGCGATACGAGGTGTCAGGCGTGTGGAAGAGTACGCGGAG 3948
Qy 2311 GAGGCGACGCGGACCTCAAGGACCGAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2370
Db 3949 GTGGGACGCGGACCTCAAGGACGCGCCATGTTGGGCGCAAGATGCAAGTGTGCGGAG 4008
Qy 2371 CTGGCTAGGCGGTGACGACCATCATCTGGGTGGCATCGCGCTGACGCGGCTGTGAC 2430
Db 4009 CTGGCCAGCGGTGACACCATCATCTGGATCGGGTGGGCGTGCATGCGGCGAGTCAAC 4068
Qy 2431 TTTGGGAGTACCCATACGCGGCTACTCTCCGAAACCGGCGGACGCGGCGGCGCGCG 2490
Db 4069 TTTGGGAGTACCCCTACGCGGCTTCTCCGAAACCGGCGGACGCGTGGGCGGCGCG 4128
Qy 2491 ATGCGGACGAGGACGACCACTACAAAGAGTGGAGGCGGCGGCGGCGGCGGCGGAC 2550
Db 4129 ATGCGGAGCGGCGGACGAGAGTACGCGGAGTGG-----ACGCGGACCGCGGAG 4179
Qy 2551 ATGGTGTTCATCGGACCATCACAGGAGTTCAGAGCATCTCTGGGATCTCGCTATC 2610
Db 4180 CGGGCTTCATCCACCATCACAGGCGGAGATCCAGACCATCATCGGGTGTGCTGCTG 4239
Qy 2611 GAGATCTCTCAAGACTCTCCGAGGAGTGTACTCGGCGGCGGCGGCGGCGGCGGCGGAT 2670
Db 4240 GAGGTGCTGTGCAAGACTCTCTCCGAGGCTGTACTCTCGGCGGCGGCGGCGGCGGCGG 4298
Qy 2671 CGCTGAGCTGACGCGGAGCGGTGATGGTGTCAAAAGATTCGGGAGCGGCTGTG 2730
Db 4299 --GTGACCTCGGACCCAAAGCCCTGAGGTTTCAAGCGGTTTCAAGCGGCTGCTGTG 4356

Qy 2731 CAGATTGAGAATCGGATCAAGAGCATGAACGACAGTCCGACTTGAAGAACCGGAAGGGG 2790
Db 4357 GAGATCGAGAGCAAGGTGGTGGGATGAACCATGACCCGAGCTCAAGAACCGCAACGGC 4416
Qy 2791 CCTGTGAAATGCGGTACATGCTGCTGTACCCCAACACGCTCGGAGCTTACCGGCGAG 2850
Db 4417 CCGGCTAAGTTTCCCTACATGCTGCTGTACCCCAACACCTCCGACCAAGGGCG--CC 4473
Qy 2851 GCCAGGCGGCTTACTGCTATGGGCAATCCCAACAGCATCTCCCATATGAGCTGGGCA 2907
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RESULT 9

US-09-313-294A-3908
; Sequence 3908, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3908
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700282343H2
; NAME/KEY: unsure
; LOCATION: 30, 38, 50, 73, 85, 104, 224, 246, 259, 278, 281, 294
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3908

Query Match

8.6%; Score 270.2; DB 4; Length 302;
Best Local Similarity 94.6%; Pred. No. 6.6e-47;
Matches 283; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

Qy 2545 GCGGACATGGTGTCTATCCGACCATCAACGACGATTCAGACCATCTCGGCGATCTCG 2604
Db 1 GCGGACATGGTGTCTATCCGACCATCAACGACGATTCAGACCATCTCGGCGATCTCG 60
Qy 2605 CTATCGAGATCTCTCCAGCACT--CTCCGACGAGGTGTACCTCGGCGAGTGAAGA 2663
Db 61 CTATCGAGATCTCTCCAGCACT--CTCCGACGAGGTGTACCTCGGCGAGTGAAGA 120
Qy 2664 GCTGATCTGAGCTGACGCGGACGCGGATGCGTTCAAAAGATTCGGGAGCGG 2723
Db 121 GCTGATCTGAGCTGACGCGGACGCGGATGCGTTCAAAAGATTCGGGAGCGG 180
Qy 2724 GCTGATCTGAGATTCGGAATCGGATCAAGAGGTGTACCTCGGCGAGTGAAGA 2783
Db 181 GCTGATCTGAGATTCGGAATCGGATCAAGAGGTGTACCTCGGCGAGTGAAGA 240
Qy 2784 GAAGGCGCTGTGGAATCGGATCAATGCTGTGCTGTACCTCCCAACAGCTCGGAGTTACCG 2842
Db 241 GAAGGCGCTGTGGAATTCGATGCTGTGCTGTACCTCCCAACAGCTCGGCGAGTGAAGA 299

RESULT 10

US-09-313-294A-6360
; Sequence 6360, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6360
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351661H1
; NAME/KEY: unsure
; LOCATION: 55, 64, 68, 85, 241, 246, 250-251, 253-254
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6360

Query Match 5.1%; Score 160.4; DB 4; Length 282;
Best Local Similarity 77.0%; Pred. No. 2.9e-24;
Matches 214; Conservative 0; Mismatches 61; Indels 3; Gaps 2;
QY 2247 CCTAAGCAGCGGAGCTCCAGCGGTGACGTGGAGCTGCAGGCGTGTGGTGAAGGAGGTGG 2306
DB 1 CCCCAACGACGGCGTCTGGCGGCGGACGTGGAGCTGCAGCGTGTGGTGAAGGAGCGCG 60
QY 2307 TGAGGAGCGCAGCGGACCTCAAGACCGAGA--CTGTGGGCCAGGATGACACCGTTC 2364
DB 61 CGANGTCNGGACGCCGACCTCAANAGACCGAACCTGTGGTGGCCCAAGATGACAGCGGTG 120
QY 2365 CAGCAGCTGGCTAGGGGCTGCAGCACCATCATCTGGGTGGCATCTCCGCTGCACGCGGCT 2424
DB 121 GCGGAGCTGTCAAGGCTTCACCAACCATCATCTGGATCGGTCGGGGCTCCACGCGGCC 180
QY 2425 GTCAACTTGGGAGTACCATACGCGGGTACTCTCCGACCGCGGCGGCGGCGGCGGCG 2484
DB 181 GTCAACTTGGGAGTACCATACGCGGGTACTCTCCGACCGCGGCGGCGGCGGCGGCGG 239
QY 2485 CGCCCGATGCGGAGCGGAGCGGCGGAGCTACAGAA 2522
DB 240 ANGCGGTGCGNCGGCGGAGCGGAGTACGCGGA 277

RESULT 11
US-09-313-294A-4946
; Sequence 4946, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4946
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349323H1
US-09-313-294A-4946

Query Match 5.0%; Score 155.8; DB 4; Length 298;
Best Local Similarity 72.3%; Pred. No. 2.6e-23;
Matches 216; Conservative 0; Mismatches 82; Indels 1; Gaps 1;
QY 1993 GCGCGGCGCTCTTCGAGCGCACCGGTGTTCCCTCGAAAGTACGCGTGGGATGTCGGA 2052
DB 1 GCGCGGCGCATCTTCGAGATGACCGGTATTCCCGCGGAAGTACGCCATCGAGATCTCTCC 60

QY 2053 GACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCAGCAGATCTCTGTCAGAGA 2112
DB 61 AAAGTCTAAGCGCAGCTGGAATTTCAACGAGCAGGCGCTCTCCAGCAGATCTCTGTCAGAGA 120
QY 2113 GGTGTGGCTGTGCGGACCACTCAAGCCCATATGGTGTCCGACTGTGTCGATCAAGGACTAC 2172
DB 121 GGCATGGCGGTTCAGATCCGTCGAGGCCCTTACAAGGTGCGGCTGCTGATCGAGGACTAC 180
QY 2173 CCTATGCGGTTGACGGGCTCGTCTATCTGGTGGCGATCCGAGCGGTGGGTCAAGGAGTAC 2232
DB 181 CCGTACGCTCGAGCGGCTGCGCGTGG--CAGCCATCGAGCAGTGGGTGACGCGGATAC 239
QY 2233 CTGGACATCTACTACCTTAAACGAGCGGAGTCCAGGCTGACGTGGAGCTGCGAGCGGTG 2291
DB 240 CTGGCATCTACTACCCCAACGAGCGGCTGTGTGAGCGCGGAGTGTGAGCTGCGAGCGGTG 298

RESULT 12
US-08-181-271A-40
; Sequence 40, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,271A
; FILING DATE: 13-JAN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667

QY 1352 AGTTGCTGAGGACTGACGAGAGTTCCGCGAGAGACACTTGCAGCGTGAAACCCAG 1411
Db 1 AGCTCGNGTGGCGAACGAGGAGTTCCCGGAGAGATGCTCGCGGNGCTCAACCCAC 60
QY 1412 TAATCATCAACGCTCTGACGAGTTCCCGCTAAAGACCCCTGGACCCCAAGCGATAG 1471
Db 61 ACATCATCACCGCTGAAAGTGTTCCTCCGAGGAGCAGNTTGA-----AGGTTAG 114
QY 1472 GAGACACACGAGACGATCACTGAAGCTCACATCCGGGATACATGGAGGCGCTTCGG 1531
Db 115 GTGACACGAGGAGCAGATACGCTGGAGCAGATCAACACACACCTCGGNAAGCTCAACG 174
QY 1532 TGCAAGACGACTGAGGAAACAGAGGCTTTTCCTAGACACCATGACCATTTTCATGC 1591
Db 175 TCGACAGGCAATCGACCGCAGAGGCTTTTCCTAGACACCATGACCATTTTCATGC 234
QY 1592 CGTACCTCGAGAGATCAACGAGCTGGAGGGGAACCTTC--ATCTACGCCAGGAGACCTT 1649
Db 235 CTCACCTGCTAAAGATCAACAGTCTCCCAACACATTCGCTCTAGCNCACCGAGGAGCT 294
QY 1650 ACTGTTCTTGAAGACGATGCGCTGAGCGCCCTGGCCATCGAG 1695
Db 295 GCTCTTCTGCAAGATCGGAGTCTTCAAGNCAATCGNATCGAG 340

QY 1352 AGTTGCTGAGGACTGACGAGAGTTCCGCGAGAGACACTTGCAGCGTGAAACCCAG 1411
Db 1 AGCTCGNGTGGCGAACGAGGAGTTCCCGGAGAGATGCTCGCGGNGCTCAACCCAC 60
QY 1412 TAATCATCAACGCTCTGACGAGTTCCCGCTAAAGACCCCTGGACCCCAAGCGATAG 1471
Db 61 ACATCATCACCGCTGAAAGTGTTCCTCCGAGGAGCAGNTTGA-----AGGTTAG 114
QY 1472 GAGACACACGAGACGATCACTGAAGCTCACATCCGGGATACATGGAGGCGCTTCGG 1531
Db 115 GTGACACGAGGAGCAGATACGCTGGAGCAGATCAACACACACCTCGGNAAGCTCAACG 174
QY 1532 TGCAAGACGACTGAGGAAACAGAGGCTTTTCCTAGACACCATGACCATTTTCATGC 1591
Db 175 TCGACAGGCAATCGACCGCAGAGGCTTTTCCTAGACACCATGACCATTTTCATGC 234
QY 1592 CGTACCTCGAGAGATCAACGAGCTGGAGGGGAACCTTC--ATCTACGCCAGGAGACCTT 1649
Db 235 CTCACCTGCTAAAGATCAACAGTCTCCCAACACATTCGCTCTAGCNCACCGAGGAGCT 294
QY 1650 ACTGTTCTTGAAGACGATGCGCTGAGCGCCCTGGCCATCGAG 1695
Db 295 GCTCTTCTGCAAGATCGGAGTCTTCAAGNCAATCGNATCGAG 340

RESULT 13
US-08-449-315-40
; Sequence 40, Application US/08449315
; Patent No. 5850505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-315-40

Query Match 4.3%; Score 135; DB 1; Length 340;
Best Local Similarity 65.3%; Pred. No. 5.3e-19;
Matches 226; Conservative 0; Mismatches 112; Indels 8; Gaps 2;

QY 1352 AGTTTGGCTGGAGACTGACGAGAGTTCGCGAGAGAGACATTCGAGCGGTGAACCCAG 1411
Db 1 AGCTCGNTGGCGAAGCGGAGGAGTTCGCCGGGAGATGCTCGCGGCTCAACCCAC 60

QY 1412 TAATCATCAAGCTGTGACGAGTTCCTCCGCTAAAGACCTTGGACCCAGGCGAGTAGG 1471
Db 61 ACATCATCACCCGCTGAACGCTGTTCCCTCCGAGGAGCAGNTTGA-----AGGGTAGG 114

QY 1472 GAGACACACACGACAGATCACTGAAGCTCACATCCGGATACATGAGGAGCGCTGTGCG 1531
Db 115 GTGACGAGAGCAGACAGATCACTGAGGAGCAGATCCACACACCTCGGNAAGCTCAAG 174

QY 1532 TGCGAAGCGACTGAGGAGCAAGAGGCTTTCTCTCTAGACACATGACACCTTTCTATGC 1591
Db 175 TCGACAGGCAATCGAGCGGCAAGAGGCTTTCTCTCTAGACACACGACCAACTTCTATGC 234

QY 1592 CGTACCTCGAGGAGTCAACGAGCTGGAGGGGAACTTC--ATCTAGCGCAGGAGCCCT 1649
Db 235 CTACCTGCTAAGATCAACAGTCTCCCAACACATTCGCTTACGNCACGAGAGCT 294

QY 1650 ACTGTTCTTGAAGAGCATGGCAGCTGAGAGCCCTGGCCATCGAG 1695
Db 295 GCTCTTCTTGAAGATGACGGGACTCTCAAGNCAATCGNATCGAG 340

RESULT 14
US-08-444-803-40
Sequence 40, Application US/08444803
Patent No. 5654414
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc

APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO. 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-444-803-40

Query Match 4.3%; Score 135; DB 1; Length 340;
Best Local Similarity 65.3%; Pred. No. 5.3e-19;
Matches 226; Conservative 0; Mismatches 112; Indels 8; Gaps 2;

QY 1352 AGTTTGGCTGGAGGACTGACGAGAGTTCGCGAGAGACACATTGCGGCGGTGAACCCAG 1411
Db 1 AGCTCGGTGGCGAAGCGGAGGAGTTCGCCCGGAGATGCTCGCGGNGCTCAACCCAC 60

QY 1412 TAATCATCAAGCTTGACGGAGTTCGCCCGGTAAAGACACCTGGACCAAGGCGATGCG 1471
Db 61 ACATCATCCCGCGCTGAACGTTGCTCCCTCCGAGGAGCAGCGNTTGA-----AGGGTACG 114

QY 1472 GAGACACACACGACGAGATCACTGAAGCTCACATCGGCGATTAACATGGAGGCGCTGTGCG 1531
Db 115 GTGACACGACGACGACGATCAAGTGGAGCACATCCACACACCTCGNAGGCTCAACG 174

QY 1532 TCAGAACCCACTGAGGAAACAGAGGCTTTCATCTAGACACCATGACCAATTTCTATGC 1591
Db 175 TCACAAGGCAATCGACGCGGAGAGGCTTTCATCTAGACACCATGACCAATTTCTATGC 234

QY 1592 CGTACCTCGACGAGATCAACGAGCTGGAGGGAATTC--ATCTACGCCAGCAGGACCT 1649
Db 235 CTCACCTGCTAAGATCAACAGTCTCCCAACACATTCGCTTACGACCAAGGACGCT 294

QY 1650 ACTGTTCTGAAGGACGATGGACGCTGAAGCCCTTGGCCATCGAG 1695
Db 295 GCTCTTCTGCAAGATGACGGGACTCTCAAGNCAATCGNCAATCGAG 340

RESULT 15
US-08-449-043-40
Sequence 40, Application US/08449043
Patent No. 5689044
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhans, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Sherica C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO. 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-043-40

Query Match 4.3%; Score 135; DB 1; Length 340;
Best Local Similarity 65.3%; Pred. No. 5.3e-19;
Matches 226; Conservative 0; Mismatches 112; Indels 8; Gaps 2;

QY 1352 AGTTTGGCTGAGGACTGACGAGAGTTTCGCGAGAGAGACACTTTCAGGGCGTGAACCCAG 1411
Db |||||
1 AGCTCGNGTGGCGAAACGACGAGAGTTTCGCCGGGAGATGCTCGCGGNTCAACCCAC 60
QY 1412 TAATCATCAACGCTGTACGGAGTTCCCGCTAAAGCACTTGGACCCAGGCAGTACG 1471
Db |||||
61 ACATCATCACCCTGTGACGTGTTCCTCCGAGGACAGNTTGA-----AGGGTACG 114
QY 1472 GAGACCAACAGCAAGATCACTGAAGCTCACATCCGGGCATAACATGGGAGGCTGTTCGG 1531
Db |||||
115 GTGACCAAGACGAGCAAGATCACGGTGGAGCACATCCCAACACAACTCGGNAAGCTCAACG 174
QY 1532 TGCAGACGCACTGAGGAGCAAGAGGCTTTCATCTAGACCAACCATGACCATTTATGC 1591
Db |||||
175 TCGACAGGCAATCGACGCCAAGAGGCTTTCATCTAGACCAACCATGACCAACTTCATGC 234
QY 1592 CGTACCTCGACGAGATCAACGAGCTGGAGGGGAACTTC--ATCTACGCCAGCAGGACCCCT 1649
Db |||||
235 CTCACCTGTAAAGATCAACAGTCTCCAAACACATTCGGTCTTACGNCACCAAGGAGCT 294
QY 1650 ACTGTTCTGAGGACGATGGCAGCTGAGCCCTGGCCATCGAG 1695
Db |||||
295 GCTCTTCTGCAAGATGACGGGACTCTCAAGNCAATCGNCATCGAG 340

Search completed: March 23, 2004, 03:49:15
Job time : 232 secs

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 01:38:07 ; Search time 1266 Seconds
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Title: US-10-059-909-15

Perfect score: 3134

Sequence: 1 ccacgcgtccggccgagggcg.....aaaaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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4	2664	85.0	2664	14	US-10-132-350-23
5	2664	85.0	2664	14	US-10-132-350-27
6	2440.4	77.9	3080	14	US-10-132-350-17
7	2433.4	77.6	3063	12	US-10-425-114-34535
8	2368	75.6	2664	14	US-10-132-350-19
9	1698.4	54.2	7492	14	US-10-132-350-53
10	1499.4	47.8	4483	14	US-10-132-350-56
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14	1268.8	40.5	2874	12	US-10-425-114-17199
15	1267.4	40.4	2622	14	US-10-132-350-3

16	1222.2	39.0	2818	10	US-09-751-687-10
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20	840.6	26.8	2566	15	US-10-360-238-813
21	762.6	24.3	1421	12	US-10-425-114-5888
22	742.8	23.7	2828	12	US-10-425-114-11204
23	738.4	23.6	2867	12	US-10-424-599-70317
24	729.6	23.3	2580	9	US-09-938-842A-1504
25	729.6	23.3	2580	11	US-09-938-842A-1504
26	719.8	23.0	2744	12	US-10-425-114-12761
27	675.2	21.5	1329	12	US-10-425-114-34925
28	674	21.5	2689	14	US-10-132-350-49
29	673	21.5	2529	14	US-10-132-350-51
30	657.6	21.0	2929	14	US-10-059-909-11
31	639	20.4	2990	12	US-10-424-599-99756
32	637.4	20.3	2816	12	US-10-425-114-7942
33	637.4	20.3	2926	12	US-10-425-114-29333
34	635.8	20.3	2929	12	US-10-425-114-11279
35	634.2	20.2	3307	12	US-10-424-599-116102
36	623.8	19.9	2441	12	US-10-425-114-8504
37	622.6	19.9	3037	12	US-10-424-599-96731
38	620	19.8	2718	14	US-10-132-350-47
39	620	19.8	3074	14	US-10-132-350-45
40	610.8	19.5	2782	12	US-10-425-114-7612
41	610.8	19.5	2804	12	US-10-425-114-9323
42	610.8	19.5	2868	12	US-10-425-114-6926
43	610.8	19.5	2940	12	US-10-424-599-73134
44	610.6	19.5	2704	12	US-10-425-114-8087
45	610.6	19.5	2793	12	US-10-424-599-73131

ALIGNMENTS

RESULT 1

US-10-059-909-15
; Sequence 15, Application US/10059909
; Publication No. US20030074693A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Kinney, Anthony
; APPLICANT: Klein, Theodore
; APPLICANT: Lee, Jian Ming
; APPLICANT: Pearlstein, Richard
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Shen, Jennie
; APPLICANT: Thorpe, Cathy
; APPLICANT: Tingey, Scott
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Lipoxigenases
; FILE REFERENCE: B01333 US CIP
; CURRENT APPLICATION NUMBER: US/10/059,909
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: 09/501,422
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,597
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 3134
; TYPE: DNA
; ORGANISM: Zea mays
US-10-059-909-15

Query Match 100.0%; Score 3134; DB 14; Length 3134;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACGCGTCGCGCGAGCGAGCGAGCGCGTCCGCCCTATATATCGCGCGAGGCGAGCA 60

DB 1 CCACGCGTCGCGCGAGCGAGCGAGCGCGTCCGCCCTATATATCGCGCGAGGCGAGCA 60

Db	2221	GTCAAGAGTACCTGGGACATCTACTACCTTAAAGACGGCAGCTCCAGCGTGACGTGGAG	2280
Qy	2281	CTGCAGCGTGTGTGGAAAGAGTGTGCTGAGGAGCGCACGGCGCACTCTCAAGGACCGGAC	2340
Db	2281	CTGCAGCGTGTGTGGAAAGAGTGTGCTGAGGAGCGCACGGCGCACTCTCAAGGACCGGAC	2340
Qy	2341	TGTGGCCCAAGGATGGACACGGTCCAGCACTGGCTAGGGCGTGACGACCATCATCTGG	2400
Db	2341	TGTGGCCCAAGGATGGACACGGTCCAGCACTGGCTAGGGCGTGACGACCATCATCTGG	2400
Qy	2401	GTGSCATCCCGCTGCACGCGGCTGTCAACTTTTGGGCACTACCCATACGCGCGGTACCTC	2460
Db	2401	GTGSCATCCCGCTGCACGCGGCTGTCAACTTTTGGGCACTACCCATACGCGCGGTACCTC	2460
Qy	2461	CCGAACGGGCGGACGGCCAGCCGGCGCCGATCCCGGAGCCAGCGACGACGACTACAAG	2520
Db	2461	CCGAACGGGCGGACGGCCAGCCGGCGCCGATCCCGGAGCCAGCGACGACGACTACAAG	2520
Qy	2521	AAGCTGGAGCGGGCGAGAAAGGAGCGGACATGCTGTTCATCCGCACTATCACCGCCAG	2580
Db	2521	AAGCTGGAGCGGGCGAGAAAGGAGCGGACATGCTGTTCATCCGCACTATCACCGCCAG	2580
Qy	2581	TTCAGACCACTCTGGGCATCTCGCTCATCGAGATCTCTTCCAGCACTCTCTCCGACGAG	2640
Db	2581	TTCAGACCACTCTGGGCATCTCGCTCATCGAGATCTCTTCCAGCACTCTCTCCGACGAG	2640
Qy	2641	GTGTACTCTCGGCCACGCGTGACGACCTGTATCGCTGGACGTGACGCGCAAGGCGCTGGAT	2700
Db	2641	GTGTACTCTCGGCCACGCGTGACGACCTGTATCGCTGGACGTGACGCGCAAGGCGCTGGAT	2700
Qy	2701	GCCTTCAAAAGATTCCGGGACCGGCTGGTGACAGATTGAGAAATCGGATCAAGACGATGAAC	2760
Db	2701	GCCTTCAAAAGATTCCGGGACCGGCTGGTGACAGATTGAGAAATCGGATCAAGACGATGAAC	2760
Qy	2761	GACAGTCCGACATTGAAGAACCGGAAGGGCGCTGTGGAAATGCCGTACATGCTGCTGAC	2820
Db	2761	GACAGTCCGACATTGAAGAACCGGAAGGGCGCTGTGGAAATGCCGTACATGCTGCTGAC	2820
Qy	2821	CCCAACACGTCGGAAGCTTACCGGCGAAGAGCGCGGGGCTTACTGCGCATGCGGCATCCC	2880
Db	2821	CCCAACACGTCGGAAGCTTACCGGCGAAGAGCGCGGGGCTTACTGCGCATGCGGCATCCC	2880
Qy	2881	AACAGCATCTCCATATGAGCTCGGCGAGATTGTGTCTCGTAGTAAATTTGTGTGCTGCGC	2940
Db	2881	AACAGCATCTCCATATGAGCTCGGCGAGATTGTGTCTCGTAGTAAATTTGTGTGCTGCGC	2940
Qy	2941	CGTGCAGATGTTCTTCAATTTGTTGTCAGTCTCAGGCTAGGGGATGAGATCATACC	3000
Db	2941	CGTGCAGATGTTCTTCAATTTGTTGTCAGTCTCAGGCTAGGGGATGAGATCATACC	3000
Qy	3001	ATGATCTTTGTAGGGTTGAGAGAGGATCCACGCTTGAATTTGTTGTCATGTATGTAAT	3060
Db	3001	ATGATCTTTGTAGGGTTGAGAGAGGATCCACGCTTGAATTTGTTGTCATGTATGTAAT	3060
Qy	3061	TCCTGGTTAATAATAAAGTTCTGTCAGTTCACTTCTTAAAAAACAACAAAAA	3120
Db	3061	TCCTGGTTAATAATAAAGTTCTGTCAGTTCACTTCTTAAAAAACAACAAAAA	3120
Qy	3121	AAAAAAAAAAAAAG 3134	
Db	3121	AAAAAAAAAAAAAG 3134	

RESULT 2		
US-10-132-350-21		
; Sequence 21, Application US/10132350		
; Publication No. US20030166855A1		
; GENERAL INFORMATION:		
; APPLICANT: Acevedo, Pedro A. Navarro		
; APPLICANT: Duivick, Jonathan P.		
; APPLICANT: Kolomiets, Mikhailo V.		
; APPLICANT: Simmons, Carl R.		


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Db 1530 CTGCCCCACCTGACGGCCAGCAGCGCGCGCGGTGAGCAAGGTGTACACCCCGGCTCAC 1589
Qy 1762 ACCGGCTCGAGGGCCACGCTCTGGCAGCTGCGCAAGGCTTATGCTTGCCTTAACGACTCT 1821
Db 1590 ACCGGCTCGAGGGCCACGCTCTGGCAGCTGCGCAAGGCTTATGCTTGCCTTAACGACTCT 1649
Qy 1822 GCTTGGCATCAGCTGATCAGCCACTGGCTGAACACAGCAGCGGTGATCGAGCGTTTCTGTA 1881
Db 1650 GCTTGGCATCAGCTGATCAGCCACTGGCTGAACACAGCAGCGGTGATCGAGCGTTTCTGTA 1709
Qy 1882 ATCCGCAAAACCGGACGCTCAGCGTGGTGCATCCCGTGCACAAGTCTGTGAGCCGCGAC 1941
Db 1710 ATCCGCAAAACCGGACGCTCAGCGTGGTGCATCCCGTGCACAAGTCTGTGAGCCGCGAC 1769
Qy 1942 TACCGTACACGCTGAACATCAACGCGCTCGGACGCCAGACATCTCAACGCGCGCGC 2001
Db 1770 TACCGTACACGCTGAACATCAACGCGCTCGGACGCCAGACATCTCAACGCGCGCGC 1828
Qy 2002 GTCTTGAGCGCACCGTGTTCCTTGC- AAAGTACGCGCTGGGATCTCGGACAGCTGTA 2060
Db 1829 GTCTTGAGCGCACCGTGTTCCTTGC- AAAGTACGCGCTGGGATCTCGGACAGCTGTA 1888
Qy 2061 CAAGAGCTGAATTTCAAGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGGC 2120
Db 1889 CAAGAGCTGAATTTCAAGAGCAGGCTCTCCAGCAGATCTCGTCAAGAGAGGTGGC 1948
Qy 2121 TGTGCGGACGCTCAAGCCCATATGCTGTCCGACTGCTGATCAAGACTACCCCTATGC 2180
Db 1949 TGTGCGGACGCTCAAGCCCATATGCTGTCCGACTGCTGATCAAGACTACCCCTATGC 2008
Qy 2181 GGTGACGGCTGTCATCTGTGGGGGATCGAGCGGTGGTCAAGAGTACTCGGACAT 2240
Db 2009 GGTGACGGCTGTCATCTGTGGGGGATCGAGCGGTGGTCAAGAGTACTCGGACAT 2068
Qy 2241 CTACTACCTTAAAGACGGGAGCTCCAGCGTACGCTGAGCTGACGCGTGTGGAAGA 2300
Db 2069 CTACTACCTTAAAGACGGGAGCTCCAGCGTACGCTGAGCTGAGCTGTGGAAGA 2128
Qy 2301 GGTGCTGAGAGGCGCACGGGACCTCAAGACCGAGACTGTGTGCGCCAGATGACAC 2360
Db 2129 GGTGCTGAGAGGCGCACGGGACCTCAAGACCGAGACTGTGTGCGCCAGATGACAC 2188
Qy 2361 CGTCCAGCAGCTGGCTAGGGCGTGACGACCATCTGTGGTGGCATCGCGCTGCACGC 2420
Db 2189 CGTCCAGCAGCTGGCTAGGGCGTGACGACCATCTGTGGTGGCATCGCGCTGCACGC 2248
Qy 2421 GGCTGTCAACTTTGGGAGTACCCATACGCGGGTACCTCCCGAACCGGCGCAGCCAG 2480
Db 2249 GGCTGTCAACTTTGGGAGTACCCATACGCGGGTACCTCCCGAACCGGCGCAGCCAG 2308
Qy 2481 CCGGCGCCGATCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2540
Db 2309 CCGGCGCCGATCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2368
Qy 2541 GGAGCGCGCATGGTGTTCATCCGCGCACCATCACGACGCGCTCCAGACCATCTCGGCAT 2600
Db 2369 GGAGCGCGCATGGTGTTCATCCGCGCACCATCACGACGCGCTCCAGACCATCTCGGCAT 2428
Qy 2601 CTGCTCATCGAGATCTCTTCAAGACATCTCTCCGACGAGGTGTACTCTCGCGCAGCGTGA 2660
Db 2429 CTGCTCATCGAGATCTCTTCAAGACATCTCTCCGACGAGGTGTACTCTCGCGCAGCGTGA 2488
Qy 2661 CGAGCCTGTGCTGGACGCTCAGACGCGCAGGCGCTGGAATCGCTTCAAAGATTTCGGAG 2720
Db 2489 CGAGCCTGTGAGCTGACGCTCAGACGCGCAGGCGCTGGAATCGCTTCAAAGATTTCGGAG 2548
Qy 2721 CCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACGCTCGGACTTGAAGAA 2780
Db 2549 CCGGCTGGTGCAGATTGAGAAATCGGATCAAGACGATGAACGACGCTCGGACTTGAAGAA 2608
Qy 2781 CCGGAGGGGCGCTGTGAATGCGGTACATGCTGTACCCCAACACGCTCGGAGTTAC 2840
Db 2609 CCGGAGGGGCGCTGTGAATGCGGTACATGCTGTACCCCAACACGCTCGGAGTTAC 2668
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RESULT 4

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US-10-132-350-23
; Sequence 23, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duviok, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10132.350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2664)
US-10-132-350-23
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Query Match 85.0%; Score 2664; DB 14; Length 2664;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 ATGTTCTTGGCACCGGGTTCGGGACCGGCTGACGGGAAAGAACAAAGGAGCGTGGAGCGAG 294
Db 1 ATGTTCTTGGCACCGGGTTCGGGACCGGCTGACGGGAAAGAACAAAGGAGCGTGGAGCGAG 60

Qy 295 GGCAGATTCGCGCACCGGTGAGCTGGTCAAGAGAGGTGCTGACGTCGCGGACTTC 354
Db 61 GGCAGATTCGCGCACCGGTGAGCTGGTCAAGAGAGGTGCTGACGTCGCGGACTTC 120

Qy 355 AACGCTCTGCTCTCGACGGCTCCACAGGATCTCGGCTGGGACGACGCGCTCGCCTTC 414
Db 121 AACGCTCTGCTCTCGACGGCTCCACAGGATCTCGGCTGGGACGACGCGCTCGCCTTC 180

Qy 415 CAGTCTGTGAGCGCCACCGCGCGGACCCCGACAAACGGGGCGCTGGCAAGGTGGGGAAG 474
Db 181 CAGTCTGTGAGCGCCACCGCGCGGACCCCGACAAACGGGGCGCTGGCAAGGTGGGGAAG 240

Qy 475 GCGGCGCACTGGAGGAGCGGTGGTGTCTCAAGTCCACGCGGACGGGGAGACCGTG 534
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Db 241 GCAGCGCACCTGGAGAGGCGGTGGTTCGCTCAAGTCCACGGCGGACGGGAGACCGGTG 300
Qy 535 TACCGGGTGAAGCTTCGAGTGGGACGAGTCCAGGGGATCCCGGGCGCGCTCTGTCGTCAGG 594
Db 301 TACCGGGTGAAGCTTCGAGTGGGACGAGTCCAGGGGATCCCGGGCGCGCTCTGTCGTCAGG 360
Qy 595 AACCTGCAGCAGCCGCGAGTTCTTCTCAAGACGCTCACCTTCGAGGGCGTCCAGGCGAAG 654
Db 361 AACCTGCAGCAGCCGCGAGTTCTTCTCAAGACGCTCACCTTCGAGGGCGTCCAGGCGAAG 420
Qy 655 GGACCGTCTCTTCGTGCGCAACTCGTGGGTCTACCCGCAAGAAGCTCTACTTCCAGGAA 714
Db 421 GGACCGTCTCTTCGTGCGCAACTCGTGGGTCTACCCGCAAGAAGCTCTACTTCCAGGAA 480
Qy 715 CGATCTTCTTCGCAACGACACTATCTCCGAGCAAAATGCGGGCGGTTCGTGCGCT 774
Db 481 CGATCTTCTTCGCAACGACACTATCTCCGAGCAAAATGCGGGCGGTTCGTGCGCT 540
Qy 775 TATCGGCAAGATGAGCTCAAGATTCCTCGTGGCGAGATATCTCTGGAACATACAGGAG 834
Db 541 TATCGGCAAGATGAGCTCAAGATTCCTCGTGGCGAGATATCTCTGGAACATACAGGAG 600
Qy 835 CATGATCGGTCTACCGTTAGGACTACTCAATGACCTTGGTGTATCCCGACAGGGCGAA 894
Db 601 CATGATCGGTCTACCGTTAGGACTACTCAATGACCTTGGTGTATCCCGACAGGGCGAA 660
Qy 895 GAGCAGCTCGGCGGATCTCGTGGGAGCAAGAACACCCGATCCCGCTCGCTCGAGA 954
Db 661 GAGCAGCTCGGCGGATCTCGTGGGAGCAAGAACACCCGATCCCGCTCGCTCGAGA 720
Qy 955 ACTGGCGGACCCCAACAAAGAGAGCCAAATTCGAGAGAGGCTTTTCGTGCTGAAC 1014
Db 721 ACTGGCGGACCCCAACAAAGAGAGCCAAATTCGAGAGAGGCTTTTCGTGCTGAAC 780
Qy 1015 CTGAACATCTACGCTCCGCGGTGAGCAAGCTTTGGGCACTCTCAAGATGTCGAGCTTCCTT 1074
Db 781 CTGAACATCTACGCTCCGCGGTGAGCAAGCTTTGGGCACTCTCAAGATGTCGAGCTTCCTT 840
Qy 1075 GGGTACTCGCTGAAGAGATCATGAGCGCTGCTTCCAACTCTGGGACTTTCGTCGAT 1134
Db 841 GGGTACTCGCTGAAGAGATCATGAGCGCTGCTTCCAACTCTGGGACTTTCGTCGAT 900
Qy 1135 GACAGCGCCAGGAGTTTCGATTCGTTGAGGATATCTCGGGCTCTACAGAGCTGGGCCCCA 1194
Db 901 GACAGCGCCAGGAGTTTCGATTCGTTGAGGATATCTCGGGCTCTACAGAGCTGGGCCCCA 960
Qy 1195 GAGGCAACCAACCACTGATAGCAGAGATCAGGAAGAAGATCCCGACGAGTTTCCTT 1254
Db 961 GAGGCAACCAACCACTGATAGCAGAGATCAGGAAGAAGATCCCGACGAGTTTCCTT 1020
Qy 1255 CGAGCATTCGCGAGAGCTAGCATGACCAACCGCTAAGATGCCCTTCCAAATGTC 1314
Db 1021 CGAAGCATTCGCGAGAGCTAGCATGACCAACCGCTAAGATGCCCTTCCAAATGTC 1080
Qy 1315 ATCAAAATCAGATGTTGAAAGAGCTCCGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1374
Db 1081 ATCAAAATCAGATGTTGAAAGAGCTCCGAGTTTAAAGTTTGGCTGGAGGACTGACGAA 1140
Qy 1375 GAGTTCCGAGAGAGACACTTGCAGGCGTGAACCCAGTATCATCAACGCTCTGACGGAG 1434
Db 1141 GAGTTCCGAGAGAGACACTTGCAGGCGTGAACCCAGTATCATCAACGCTCTGACGGAG 1200
Qy 1435 TTCCCGCTAAAGCAACCCCTGGAACCCAGGCGATGACGAGACCAACACAGCAAGATCACT 1494
Db 1201 TTCCCGCTAAAGCAACCCCTGGAACCCAGGCGATGACGAGACCAACACAGCAAGATCACT 1260
Qy 1495 GAAGTCACTCCGGGCAATACATGGGAGGCTGTCGCTGAGAGACGACATGAGAGCAAG 1554
Db 1261 GAAGTCACTCCGGGCAATACATGGGAGGCTGTCGCTGAGAGACGACATGAGAGCAAG 1320
Qy 1555 AGGCTCTTCACTTAGACCACTGACCATTTTCATGCGGTACCTTCGAGAGATCAACGAG 1614
Db 1321 AGGCTCTTCACTTAGACCACTGACCATTTTCATGCGGTACCTTCGAGAGATCAACGAG 1380

Qy 1615 CTGAGGGGAACTTTCATCTACGCCAGAGGACCTACTGTTCCTGAAAGGACGATGGCAGC 1674
Db 1381 CTGAGGGGAACTTTCATCTACGCCAGAGGACCTACTGTTCCTGAAAGGACGATGGCAGC 1440
Qy 1675 CTGAAGCCCTTGGCCATCTGAGCTGAGCCTGCCCCACCTGACGGCCAGCAGCGGGCGG 1734
Db 1441 CTGAAGCCCTTGGCCATCTGAGCTGAGCCTGCCCCACCTGACGGCCAGCAGCGGGCGG 1500
Qy 1735 GTGAGCAAGGTGTACACCCCGGCTCACACCGGGCTCGAGGGCCACGCTCTGGCAGCTGCC 1794
Db 1501 GTGAGCAAGGTGTACACCCCGGCTCACACCGGGCTCGAGGGCCACGCTCTGGCAGCTGCC 1560
Qy 1795 AAGGCTTATGCTCGTAAACGACTCTGCTTGGGCAATCAGCTGATCAGCCACTGGCTGAAC 1854
Db 1561 AAGGCTTATGCTCGTAAACGACTCTGCTTGGGCAATCAGCTGATCAGCCACTGGCTGAAC 1620
Qy 1855 ACGCAGCGGGTGTGAGCGGCTCGTAAATCGCAGCAAAACCGGACGCTCAGCGTGGTGCAT 1914
Db 1621 ACGCAGCGGGTGTGAGCGGCTCGTAAATCGCAGCAAAACCGGACGCTCAGCGTGGTGCAT 1680
Qy 1915 CCGGTGCAAAAGCTGCTGAGCCCGCAGCTTACCGTGAACACGCTGAACATCAACCGCCTGGCA 1974
Db 1681 CCGGTGCAAAAGCTGCTGAGCCCGCAGCTTACCGTGAACACGCTGAACATCAACCGCCTGGCA 1740
Qy 1975 GCGCAGACACTCATCAACCGCGGGCGGTCTTTCGAGCGCACCGTGTTCCTGCAAGGTAC 2034
Db 1741 GCGCAGACACTCATCAACCGCGGGCGGTCTTTCGAGCGCACCGTGTTCCTGCAAGGTAC 1800
Qy 2035 GCGCTGGGGATGTGGGAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 2094
Db 1801 GCGCTGGGGATGTGGGAGACGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA 1860
Qy 2095 GCAGATCTCTGTCAGAGAGGTGTGGCTGTGCGGACCACTCAAGCCCATATGTTGTCGA 2154
Db 1861 GCAGATCTCTGTCAGAGAGGTGTGGCTGTGCGGACCACTCAAGCCCATATGTTGTCGA 1920
Qy 2155 CTGCTGATCAAGGACTACCCCTATGCGGTGACCGGCTCGCTCATCTGTGGGCGCATCGAG 2214
Db 1921 CTGCTGATCAAGGACTACCCCTATGCGGTGACCGGCTCGCTCATCTGTGGGCGCATCGAG 1980
Qy 2215 CCGTGGGTCAAGGAGTACCTGGACATCTATACCTTAACGACGGGAGCTCCAGCGTGAC 2274
Db 1981 CCGTGGGTCAAGGAGTACCTGGACATCTATACCTTAACGACGGGAGCTCCAGCGTGAC 2040
Qy 2275 GTGAGACTGCAAGGCGTGGTGAAGAGGTGGTGAAGAGGCGCACGGGACCTCAAGGAC 2334
Db 2041 GTGAGACTGCAAGGCGTGGTGAAGAGGTGGTGAAGAGGCGCACGGGACCTCAAGGAC 2100
Qy 2335 CGAGACTGTTGGCCCGCAGGATGGAACACCGTCCAGCAGCTGGCTAGGGGCTGACAGCACCATC 2394
Db 2101 CGAGACTGTTGGCCCGCAGGATGGAACACCGTCCAGCAGCTGGCTAGGGGCTGACAGCACCATC 2160
Qy 2395 ATCTGGTGGCATCCGCGCTGCAAGCGGCTGCACTTTGGGCGAGTACCCATAGCGGG 2454
Db 2161 ATCTGGTGGCATCCGCGCTGCAAGCGGCTGCACTTTGGGCGAGTACCCATAGCGGG 2220
Qy 2455 TACCTCCGCAACCGGCGCACGGCGCCGATGCGCGGAGCCAGGAGCGACCGAC 2514
Db 2221 TACCTCCGCAACCGGCGCACGGCGCCGATGCGCGGAGCCAGGAGCGACCGAC 2280
Qy 2515 TACAAGAGCTGGGAGCGGGGAGAGGAGCGGACATGTTGTTATCCGACCATCATCC 2574
Db 2281 TACAAGAGCTGGGAGCGGGGAGAGGAGCGGACATGTTGTTATCCGACCATCATCC 2340
Qy 2575 AGCCAGTTTCCAGACCATCTCGGGCATCTCGTCTCATCGAGATCTCTCCAGCACTCTCC 2634
Db 2341 AGCCAGTTTCCAGACCATCTCGGGCATCTCGTCTCATCGAGATCTCTCCAGCACTCTCC 2400
Qy 2635 GACGAGGTGTACCTCGGCGCAGGTGAAGAGCGTGTGATCTGAGACGTCAGACGCCAGGCG 2694
Db 2401 GACGAGGTGTACCTCGGCGCAGGTGAAGAGCGTGTGATCTGAGACGTCAGACGCCAGGCG 2460

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QY 2695 CTGGATCGTTCAAAAGATTCCGGAGCCGGCTGGTGCAGATTGAGATTCGATCAAGACG 2754
Db |||||||
QY 2461 CTGGATCGTTCAAAAGATTCCGGAGCCGGCTGGTGCAGATTGAGATTCGATCAAGACG 2520
Db |||||||
QY 2755 ATGAACGACAGTCGGGACTTGAAGAACCGGAGGGGCTGTGGAAATGCCGTACATGCTG 2814
Db |||||||
QY 2521 ATGAACGACAGTCGGGACTTGAAGAACCGGAGGGGCTGTGGAAATGCCGTACATGCTG 2580
QY 2815 CTGTACCCCAACACGTCGAGCTTACCGCGGAGAGGGCGGAGGGCTTACTGCCATGGC 2874
Db |||||||
QY 2581 CTGTACCCCAACACGTCGAGCTTACCGCGGAGAGGGCGGAGGGCTTACTGCCATGGC 2640
QY 2875 ATTCCCAACAGCATCTCCATATGA 2898
Db |||||||
QY 2641 ATTCCCAACAGCATCTCCATATGA 2664

RESULT 5
US-10-132-350-27
; Sequence 27, Application US/10132350
; Publication NO. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2664)
US-10-132-350-27

Query Match 85.0%; Score 2664; DB 14; Length 2664;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 ATGTTCTGGCACGGGTCCGGACCGGCTGACGGAAAGAACAGGAGGCGTGGAGCGAG 294
Db 1 ATGTTCTGGCACGGGTCCGGACCGGCTGACGGAAAGAACAGGAGGCGTGGAGCGAG 60

QY 295 GGCAGATCCGGGACAGCGTGGAGGTGTCAGAAAGAGAGGTCTGGAGCTGGCGCATTC 354
Db 61 GGCAGATCCGGGACAGCGTGGAGGTGTCAGAAAGAGAGGTGTCGGAGCTGGCGCATTC 120

QY 355 AACGCTCGCTCTCTCGAGCGGCTGCACAGGATCTCTCGGCTGGAGACGGGCTGCCTTC 414
Db 121 AACGCTCGCTCTCTCGAGCGGCTGCACAGGATCTCTCGGCTGGAGACGGGCTGCCTTC 180

QY 415 CAGCTGTGTCAGGCCCAACCGCGGCGGACCCAGCAACCGGGGCGGTGGCAAGTGGGGAG 474
Db 181 CAGCTGTGTCAGGCCCAACCGCGGCGGACCCAGCAACCGGGGCGGTGGCAAGTGGGGAG 240

QY 475 GGGGCGCAGCTGGAGAGCGGTGTGTCGCTCAAGTCCAGGCGGCGGAGGACCGTG 534
Db 241 GGGGCGCAGCTGGAGAGCGGTGTGTCGCTCAAGTCCAGGCGGCGGAGGACCGTG 300

QY 535 TACCGGCTGAGCTTCGAGTGGGACAGGTGCGAGGCGCATCCCGGGCGCGCTCTGTCAGG 594
Db 301 TACCGGCTGAGCTTCGAGTGGGACAGGTGCGAGGCGCATCCCGGGCGCGCTCTGTCAGG 360
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QY 595 AACCTGCAGCAGCGCGAGTTCTTCTCAGACGCTCAACCTCGAGGGGCTGCCAGGCAAG 654
Db |||||||
QY 361 AACCTGCAGCAGCGCGAGTTCTTCTCAGACGCTCAACCTCGAGGGCTGCCAGGCAAG 420
Db |||||||
QY 655 GGCACCGTCTGTTCTGTCGCCAACTCTGTTGGTCTACCCGCAAGCTCTTACTCCAGGAA 714
Db |||||||
QY 421 GGCACCGTCTGTTCTGTCGCCAACTCTGTTGGTCTACCCGCAAGCTCTTACTCCAGGAA 480
QY 715 CGCATCTTCTGCGCAACGACACCTTATCTGCGAGCAAAATGCGGCGGCTTGTGCTCT 774
Db |||||||
QY 481 CGCATCTTCTGCGCAACGACACCTTATCTGCGAGCAAAATGCGGCGGCTTGTGCTCT 540
QY 775 TATCGGCAAGATGAGCTCAAGATTCTCCGTGCGAGCAATAATCTCTGAGCAATACAGGAG 834
Db |||||||
QY 541 TATCGGCAAGATGAGCTCAAGATTCTCCGTGCGAGCAATAATCTCTGAGCAATACAGGAG 600
QY 835 CATGATCGGCTTACCGTTACGACTACTACATGACTTGGCTGATCCCGCAAGGCGAA 894
Db |||||||
QY 601 CATGATCGGCTTACCGTTACGACTACTACATGACTTGGCTGATCCCGCAAGGCGAA 660
QY 895 GAGCAGCTCGGCGGATCTCTCGGTGCGAGCAAGCAACCCCGTATCCCGTCTGCTGCA 954
Db |||||||
QY 661 GAGCAGCTCGGCGGATCTCTCGGTGCGAGCAAGCAACCCCGTATCCCGTCTGCTGCA 720
QY 955 ACTGGCGGCAACCAAGAAAGAACCCCAATTCGAGAGCAGGCTTCTCTGCTGAC 1014
Db |||||||
QY 721 ACTGGCGGCAACCAAGAAAGAACCCCAATTCGAGAGCAGGCTTCTCTGCTGAC 780
QY 1015 CTGAACATCTACGTCCCGGTGCGAGCAACGCTTGGGCTCTCAAGATGTCGAGATTCCT 1074
Db |||||||
QY 781 CTGAACATCTACGTCCCGGTGCGAGCAACGCTTGGGCTCTCAAGATGTCGAGATTCCT 840
QY 1075 GGCTACTGCTGAAGACGATCATCTGAGGCTGTTCTTCAACACTGGGAGCTTCTGCTGAT 1134
Db |||||||
QY 841 GGCTACTGCTGAAGACGATCATCTGAGGCTGTTCTTCAACACTGGGAGCTTCTGCTGAT 900
QY 1135 GACACGCCCAAGGAGTTCGATTCTGTTGAGGATATCTCTCGGCTCTACAGCTGGGCCA 1194
Db |||||||
QY 901 GACACGCCCAAGGAGTTCGATTCTGTTGAGGATATCTCTCGGCTCTACAGCTGGGCCA 960
QY 1195 GAGGCAACCAACCACTGATGAGAGATCAGAGAAAGATCCCGAGGAGTTCCT 1254
Db |||||||
QY 961 GAGGCAACCAACCACTGATGAGAGATCAGAGAAAGATCCCGAGGAGTTCCT 1020
QY 1255 CBAAGCATTCGCGAAGCTGACCACTGACCCCGCTAAAGATGCCCTTCCAAATGTC 1314
Db |||||||
QY 1021 CBAAGCATTCGCGAAGCTGACCACTGACCCCGCTAAAGATGCCCTTCCAAATGTC 1080
QY 1315 ATCAATCAGATGTTGAAAGGCTCCGGAGTTTAACTTTGGTGGAGGACTGACGAA 1374
Db |||||||
QY 1081 ATCAATCAGATGTTGAAAGGCTCCGGAGTTTAACTTTGGTGGAGGACTGACGAA 1140
QY 1375 GAGTTCCGAGAGAGACACTTCGAGCGGTGAACCCAGTAAATCATCAACGCTCTGAGGAG 1434
Db |||||||
QY 1141 GAGTTCCGAGAGAGACACTTCGAGCGGTGAACCCAGTAAATCATCAACGCTCTGAGGAG 1200
QY 1435 TTCCCGCTTAAAGCAACCTTGGACCCCAAGGCTGACGAGACCAACCAAGGATCACT 1494
Db |||||||
QY 1201 TTCCCGCTTAAAGCAACCTTGGACCCCAAGGCTGACGAGACCAACCAAGGATCACT 1260
QY 1495 GAAGCTCAATCCGGGATTAACATGGAGGCGCTGTCGTCAGAACGCACTGAGGAGCAAG 1554
Db |||||||
QY 1261 GAAGCTCAATCCGGGATTAACATGGAGGCGCTGTCGTCAGAACGCACTGAGGAGCAAG 1320
QY 1555 AGGCTCTTATCTAGACCAACCATGACCATTTTATGCTCCCTTCTGACGAGATCAACGAG 1614
Db |||||||
QY 1321 AGGCTCTTATCTAGACCAACCATGACCATTTTATGCTCCCTTCTGACGAGATCAACGAG 1380
QY 1615 CTGAGGGGAACTTCAATCTAGCGCAGGACCCCTTCTGTTCTTCTGAGGACGATGCGAG 1674
Db |||||||
QY 1381 CTGAGGGGAACTTCAATCTAGCGCAGGACCCCTTCTGTTCTTCTGAGGACGATGCGAG 1440
Db |||||||
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QY	557	ACGAGTTCGACGGGCATCCCGGGCGCGTCTTGGTCAAGAACCTTCGACGACGCCGAGTTCT	616
Db	474	ACGGGTCCGACGGGGTCCCTCGCGCGGTCTTGGTGAGGAACCTTCGACGACGCCGAGTTCT	533
QY	617	TCCTCAAGACGCTCACCTCTCAGGGCGTCCACAGCAAGGGCACCGTCGTCTTCGTCCGCCA	676
Db	534	TCCTCAAGTCGCTCACCTCGAGGGGTCCTCCGAGGGGACCGTCGTCTTCGTCCGCCA	593
QY	677	ACTCGTGGGTCTACCCGCAACAGCTCTACTCCCAAGAACGCACTTCTTCGCCCAACGACA	736
Db	594	ACTCGTGGATCTACCCGCACAATCTCTACTCCCAAGAACGGCTCTTCTTCGCCCAACGACA	653
QY	737	CCTATCTCCGACGCAAAATCGCGGGCGTTGGTGCCTTATCCGCAAGATGAGCTCAAGA	796
Db	654	CTTATCTCCAAAGCAAAATGCTCGGGCATTTGGTGCCTTACCGCGACGAGCTCAAGA	713
QY	797	TTCTCCGTGGCAGGATAATCTTCGACCATACAGGACATGATCGGGCTTACCGTTACG	856
Db	714	TTCTCCGGCGGACGATAATCTTCGACCATACAGGACGACGCGGTCTTACCGTTACG	773
QY	857	ACTACTACAATGACCTTGGTGATCCGACAAAGGGCGAAGACAGCTCGGCCGATCTCTCG	916
Db	774	ACTACTACAACGACCTCTCGTGAGCGACGAAGAGGTGAAGCAATGSCCGCGCTGTCTCTCG	833
QY	917	GTGGCAGCCAAAGAACACCCGTATCCCGTCCCTCGACGAATCGGCCGCGCACCCCAACAAAGA	976
Db	834	GGGGCAGCCAAAGAACACCCGTATCCCGTCCCTCGACGAACCGGCCGCGGTCCACAGAGA	893
QY	977	AAGACCCAAATTCGGAGACGAGGTTTCTGTGTGAACCTTGAAACATCTACGTCCCGGTG	1036
Db	894	CAGACCCCAACTCGGAGACGAGGTGTTCTGTGTGAACCTTGAAACATCTACGTCCCGGTG	953
QY	1037	ACGAACGCTTTGGCATCTCAAGATGTCGGAATCTTCTGGTACTCTCGTGAAGACGATCA	1096
Db	954	ACGAGCGTTTGGGCATCTCAAGATGTCGHAATCTCTCGGTACTACTGAAGCGATCA	1013
QY	1097	TCGAGGCTGTGTTTCCAACTCTGGGACCTTTTCGTGATGACACGCCCAAGAGTTCGATT	1156
Db	1014	TCGAGGCTGTCTTCCGACGCTGGGACGTTTCTGTGTGACGATACGCCCAAGAGTTCGATT	1073
QY	1157	CGTTTGAGGATATCTCTGGGCTCTACGAGCTGGGCCCGACAGGCAACCAACCCACTGA	1216
Db	1074	CGTTTCGAAGACATCTTCTGGGCTCTACGAGCGGGTCCAGAGGCCGCCCAACCCACTGG	1133
QY	1217	TAGCAGAGATCAGGAAGAAGATCCCAAGCGAGTTCTCTCGAAGCATTTCTGCCGACGGTA	1276
Db	1134	TAGCAGAGTTCAGGACGAGATCCCAAGCGAGTTCTTCAGAGCATTTCTGCCGATGTA	1193
QY	1277	GCAATGACACCCGCTAAGATGCCCTTCCAAATGTCATAAATCAGATGTGTGAAAA	1336
Db	1194	GCAATGACACCCGCTAAGATGCCCTTCCAAATATCATCAGATCAGATGTGTGAAAA	1253
QY	1337	AGGCTCCGAGTTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACCTTG	1396
Db	1254	AGGCTCCAGTTTTAAGTTTGGCTGGAGGACCGACGAAGAGTTTTCGAGGAGACCGTTG	1313
QY	1397	CAGCGGTGAACCCAGTAAATCATCAACGCTGTGACGGAGTTTCCCGCTTAAAGACCCCTGG	1456
Db	1314	CAGCGGTGAACCCAGTGTCTCATCAACGCTGTGACGGAGTTTCCCAAGTAAAGTACCCCTGG	1373
QY	1457	ACCAAGGCAGTACGGACACACACGACGAGATCATGAGCTCATCATCCGCGATCAACA	1516
Db	1374	ACCAAGTCAATACGGAGACCATACGAGCAAGATCACCGAAGTCAATCCAGCATCAACA	1433
QY	1517	TGGAGGCGCTGCGGTGAGAACGCACTGAGGAACAAGAGCTCTTCATCTTAGACCAACC	1576
Db	1434	TGGAAGGCGCTGCGGTGAGAAATGCATGAAGAAAGACAGGCTCTTCATCTTAGACCAATC	1493
QY	1577	ATGACCAATTTCAATGCGGTACTCGACGAGATCAACGAGCTGGAGGGGAACTTCATCTTACG	1636
Db	1494	ATGACCAATTTCAATGCGGTACTCAACAGATCAACGAGTTTGGAGGGGAACTTCATCTTACG	1553

Qy	1537	CCAGCAGGACCCCTACTCTTCTCTGAAGGACGATGGCAGCGTGAAGACCCCTCTGGCCATCTGAGC	1591
Db	1554	CCAGCAGGACCCCTACTCTTCTCTGAAGGACGATGGCAGCCCTCTGAAGACCCCTCTGGCGTCTGAGC	1613
Qy	1697	TGAGCTGCCCCCACTTCTGAGCGGCAGCAGCGCGCGCGCGGTCTAGCAAGAGTGTACACCCCGG	1756
Db	1614	TGAGCTGCCCCCACTTCTGAGCGGCAGCAGCGCGCGGTCTAGCAAGAGTGTACACCCCGAG	1673
Qy	1757	CTCACACCGCGCTCGAGGGCCACGTCTGGCAGCTTCGCAAGGCTTATTCCTCTGGTGTAAACG	1816
Db	1674	CTCACTCCGCGCTTGAGGGCCACGTCTGGCAACTTTCGAAGGCTTATTCCTCTGGTGTAAACG	1733
Qy	1817	ACTCTGCTCGCATCAGCTGATCAGCACTTGGCTGTGAACACGACGCGGTGTATCGAGCCGT	1876
Db	1734	ACTCTGCTCGCATCAGCTGATCAGCACTTGGCTGTGAACACGACGCGGTGTATCGAGCCGT	1793
Qy	1877	TCGTAAATCGCGACAAACCCGACGCTCAGCGTGTGTATCCCTGTGCACAAAGCTCTCTGAGCC	1936
Db	1794	TCGTATCGCAACGAACCCGACGCTGAGCGTGTGTATCCCTGTGCACAAAGCTCTCTGAGCC	1853
Qy	1937	CGCACTACCGGTGACCGCTGAACATCAACGCCCTCTGCACGCGCAGACACATCATCAACGCCG	1996
Db	1854	CACACTACCGGTGACCGCTGAACATCAACGCCCTCTGCACGCGCAGACACATCATCAACGCCG	1913
Qy	1997	CGCGCGCTTTCGAGCGCACCGTGTTCCTTCGAAAGTACGCGCTGGGGATGTCCGCGAGACG	2056
Db	1914	ACGGCATCTTCGAGCGCACCGTGTTCCTTCGAAAGTACGCGCTGGGGATGTCTCTCCGACG	1973
Qy	2057	TGTACAAGAGCTGGAAATTTCAACGAGGAGGCTCTCCAGCAGATCTCTGTCMAAGAGAGTG	2116
Db	1974	TGTACAAGAGCTGGAAATTTCAACGAGGAGGCTCTCCAGCAGACCTCTGTCMAAGAGAGTG	2033
Qy	2117	TGGCTGTGCGGACCAAGTCAAGCCCATATGCTGTCCGACTGCTGTGATCAAGGACTACCCCT	2176
Db	2034	TGGCTGTGCGGACCAAGTCAAGCCCATATGCTGTCCGACTGCTGTGATCAAGGACTACCCCT	2093
Qy	2177	ATGCGGTTGACGGGCTCGTCACTCTGTGGCGCATTCAGAGCGGTGGGTCAAGGAGTACCTGG	2236
Db	2094	ACGCGGTGGACGGGCTCGTCACTCTGTGGCGCATTCAGAGCGGTGGGTCAAGGAGTACCTGG	2153
Qy	2237	ACATCTACTACCTTAACGACGGCGAGCTCCAGCGTGCAGCTGGAGCTTCGAGGCGTGTGGGA	2296
Db	2154	AGTCTCTACTACCTTAACGACGGCGAGCTCCAGCGCGCATTCGAGGCGTGTGGGA	2213
Qy	2297	AGGAGGTGCGTAGGAGGGCGCACGGGCACTCAAGGACCGAGACTGGTGCCCGCAGATGG	2356
Db	2214	AGGAGGTGCGTAGGAGGGCGCACGGGCACTCAAGGACCGAGACTGGTGCCCGCAGATGG	2273
Qy	2357	ACACGCTCCAGCAGCTTGGCTAGGGCGTGCACGACATCATCTGGGTGGCATTCGCGCGCTGC	2416
Db	2274	ACGCGGTCCAGCGGCTGGCCAGGGCGTGCAGACCGTCACTCTGGGTAGCGTTCGCGCTGC	2333
Qy	2417	ACGCGGCTGTCAACTTTGGCGAGTACCCATACGCCGGGTACCTCCGCAACCGGCGCCAGCGG	2476
Db	2334	ACGGGCGGTCAACTTTGGCGAGTACCCGTAACCGCGGTACCTCCGCAACCGGCGCCAGCGG	2393
Qy	2477	CCAGCGCGGCCCGATGTCGCGAGCCACGCGACGCCAGTACAAGAAAGCTTGGAGCGGGGC	2536
Db	2394	TGAGCGCGGGCCGATGTCGCGAGCCGCGGACGCAACACTACAGAAAGCTTGGAGCGGGGC	2453
Qy	2537	AGAAGAGGGCGGACATGGTGTTCATCCGACCATCACACGCGATTCAGACCATCTCTGG	2596
Db	2454	AGAAGAGGGCGGACATGGTGTTCATCCGACCATCACACGCGATTCAGACCATCTCTGG	2513
Qy	2597	GCATCTCGCTCATTCGAGATCTCTTCAAGCACTCTCTCCGACGAGGTGTACCTCGGCGACG	2656
Db	2514	GCATCTCGCTCATTCGAGATCTCTTCAAGCACTCTCTCCGACGAGGTGTACCTCGGCGACG	2573
Qy	2657	GTGACGAGCTGTATCTCTGAGCTGTACAGCGCAGGCGCTGGATGCTTCAAAAGATTCTG	2716
Db	2574	GCACGAGCTGTATCTCTGAGCTGTACAGCGCAGGCGCTTGAACGCGCTTCAGAAAGTTCTG	2633
Qy	2717	GGAGCGCGCTTGTGTGCAGATTGAGAAATTCGATCAAGACGATGAACGACAGTTCGCGACTTGA	2776

Db 2634 GAAGCGGCTGTTGGAGATCGAGACGGATCAGGACGATGAGACGACGCCGCGAGTTGA 2693
Qy 2777 AGAACCGGAAGGGCTGTGGAAATCCGCTACATGCTGTGTACCCCAACACGTCGGAGC 2836
Db 2694 AGAACCGGAAGGGCGCGGTGGAGATCCGCTACATGCTGTGTACCCCAACACGTCGGAGT 2753
Qy 2837 TTACCGCGGAGAGGCGCGGGGCTTACTGCCATGGGCATTCGCCACACATCTCCATAT 2896
Db 2754 TCACCGCGGAGAGGCGGGGCTTACTGCCATGGGCATTCGCCACACATCTCCATAT 2813
Qy 2897 GAGCCTGGGCGAGATTGT-----GTCTCGTAGTAATTTGTGTGTCGCGCGTGGCA 2947
Db 2814 GAGCCTCCTCACTGCTGAGCGGATGTTGTAGATGCTCTGTACTGCTGTGTAAATGT 2873
Qy 2948 TGTGTTTCTCATTGTTTGTGCTCAGTCTCAGGTAGGGATGAGATCATACCATGATC- 3006
Db 2874 GTCGTTATTTCGTTGTTTGTGCTCT---GGTAGGGAATGGAGATTTGATTTGATCC 2930
Qy 3007 ----TTTGTAGGGTTGAGAGAGAGTCCAGCTTTGAATATTGTTGTCATGTATG--TAAT 3060
Db 2931 ATGATCTGTAGGGTTGAGAGAGAG--CCAGCTCTGGTAATGTTGTCAATGTGTTCTT 2989
Qy 3061 TCTTGGTTATATAT-AAAATTCTAGTTCATTTCTTAAAAAACAACAAAAA 3119
Db 2990 TCTTGGTTAGAAATAAAATTCGTCTGCTCAAAAAA 3049
Qy 3120 AAAAAAAAAAAAAA 3133
Db 3050 AAAAAAAAAAAAAA 3063

RESULT 7

US-10-425-114-34535
; Sequence 34535, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 34535
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZWELM017282G11_FLI
US-10-425-114-34535

Query Match 77.6%; Score 2433.4; DB 12; Length 3003;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 2652; Conservative 0; Mismatches 297; Indels 16; Gaps 3;

Qy 147 GCGAGGACGAGCGAGCGAGGAGCCATCCACGAGCCAGCCAGCCGCTTCTGAGAG 206
Db 32 GCAGGCGAGCGGAGGCGATCCACCCACCCACCGGACACTCCCTGAGAGCGAGA 91
Qy 207 CGAGGAGCGAGAAAGCGAGCGGCGATTTCTGGCAAGGGGTCGCGGACCGGCTGAC 266
Db 92 AGCGAGAGCGAGAGCGGCGGCGCCACCATTTCTGGCAAGGGGTCGCGGACCGGCTGAC 151
Qy 267 GCGNAGAACAGAGCGGTCGAGCGGAGGCGAGATCCCGGACACGGTGGCTGTCTCA 326
Db 152 GGGAGAGAACAGAGGCGGTGGAAACGAGGGAAGATCCCGGACCGGTGAGGCTGTCTCA 211

Qy 327 GAAGGAGGTGCTGACGCTCGGCGACTTTCAAGCCTCGCTCCTCGACGGCGCTCCACAGGAT 386
Db 212 GAAGGAGGTGCTGACGCTCGGCGACTTTCAAGCCTCGCTCCTCGACGGCGCTCCACAGGAT 271
Qy 387 CCTCGGCTGGAGCGAACGCGGCTGCGCTTTCCAGCTGCTGAGCGCCACCGCGCGCGACCCCGAG 446
Db 272 CCTCGGCTGGAGCGAACGCGGCTGCGCTTTCCAGCTGCTGAGCGCCACCGCGCGCGACCCCGAG 331
Qy 447 CAACGGGGCGGTGGCAAGGTGGGGAAGGCGGCGCACCTCGAGGAGCGGTGGTGTGCT 506
Db 332 CAACGGGAGCGCGCGCAAGGTTCGGGAAGGCGGCGCACCTCGAGGAGCGGTGGTGTGCT 391
Qy 507 CAAGTCCACGCGCGACGCGGAGACCGGTATACCGGGTGAAGCTTCAGATGGAGCGAGTCCGA 566
Db 392 CAAGTCCACGCGACGCGGAGACCGGTATACCGGGTGAAGCTTCAGATGGAGCGAGTCCGA 451
Qy 567 GGGCATCCCGGCGCGCTCTGCTGCTCAGGAACCTCGACGACGCGAGTCTTCCTCAAGAC 626
Db 452 GGGCGTCCCGGCGCGCTCTGCTGCTCAGGAACCTCGACGACGCGAGTCTTCCTCAAGTC 511
Qy 627 GCTCACCTCGAGGCGCTCCAGGCAAGGCGACCGCTGCTCTTCGTCCGCCAACTCGTGGGT 686
Db 512 GCTCACCTCGAGGCGCTCCCGGCAAGGCGACCGCTGCTCTTCGTCCGCCAACTCGTGGGT 571
Qy 687 CTACCCGCAAGCTCTACTCCAGGAAAGCAATCTTCTTCGCGCAACGACACCTATCTGCC 746
Db 572 CTACCCGCAATCTCTACTCCAGGAAAGCGCTCTTCTTCGCGCAACGACACTTATCTGCC 631
Qy 747 GAGCAAAATGCGGCGGCTTGTGCTTATCGGCAAGATGAGCTCAAGATTTCTCCGTGG 806
Db 632 AAGCAAAATGCTCGGCGATTTGCTCTTACCGGCAAGCGAGCTCAAGATTTCTCCGCG 691
Qy 807 CGACGATAATCCTGACCATACGAGGACATGATGCGCTTACCGTTACGACTACTCAAA 866
Db 692 CGACGATAATCCTGACCATACGAGGACGACGCGGCTTACCGTTACGACTACTCAAA 751
Qy 867 TGACCTTGTGATCCCGCAAGGCGGAGGACGCTCGCGCGATCTCGTGGCGAGCA 926
Db 752 CGACCTCGGTGAGCCAGCAAGGCTGAGACCATGCGCGGCTCTCTCGGGGCGAGCCA 811
Qy 927 AGAACACCGGTATCCCGTCTGCTGCAAGACTGGCGCGCACCCCAAAAGAAAGACCCAAA 986
Db 812 AGAACACCGGTATCCCGTCTGCTGCAAGCGCGCGGCTCCAAACAGAGACAGACCCCAA 871
Qy 987 TTCGAGAGGAGGCTTTCTGCTGAACTGAACTAGCTCCCGGCTGACGACGCTT 1046
Db 872 CTCGAGAGGAGGCTGTTCTGCTGAACTGAACTAGCTCCCGGCGAGCGGCTT 931
Qy 1047 TGGCATCTCAAGATGTCGGAATTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGT 1106
Db 932 TGGCATCTCAAGATGTCGGAATTTCTTGGGTACTCGCTGAAGACGATCATCGAGGCTGT 991
Qy 1107 TCTTCCAACTGGGGACTTTGCTGATGACACGCCCAAGAGTTCGATTGCTTTGAGGA 1166
Db 992 CTTTCCGACGCTGGGAGCGTTGCTGCGAGATACGCCCAAGAGTTCGATTGCTTTGAGGA 1051
Qy 1167 TATCTCGGCTTACGAGCTGGGCGCGAGAGGCGCCCAACCAACCACTGATAGAGAGAT 1226
Db 1052 CATCTTTGGGCTTACGAGCGGGTTCAGAGGCGGCCCAACCAACCACTGATAGAGAGT 1111
Qy 1227 CAGGAAGAAGATCCCGAGCGAGTTCTTTCGAAAGCATTTCTCCGAAACGGTATGACCA 1286
Db 1112 CAGGAAGAAGATCCCGAGCGAGTTCTTTCGAAAGCATTTCTCCGAAACGGTATGACCA 1171
Qy 1287 CCCCTAAAGATGCCCTTCCAAATGTCATCAATCAGATGTTGTGAAAGGCTCCGGA 1346
Db 1172 CCCCTAAAGATGCCCTTCCAAATGTCATCAATCAGATGTTGTGAAAGGCTCCGGA 1231
Qy 1347 GTTTAAGTTTGGCTGGAGGACTGACGAAGAGTTTCGCGAGAGAGACACTTGCAGCGCTGAA 1406
Db 1232 GTTTAAGTTTGGCTGGAGGACCGAGAGAGTTTTCGAGGGGAGACGCTTGCAGGCGTGA 1291
Qy 1407 CCCAGTAATCATCAACGCTGTGACGAGTTTCCCGCTTAAAGACACCTTGGAGCCCAAGCA 1466

1292 CCCAGTGTCTATCAAAAGTCTGACGAGTTCAGCTAAAGTACCTTGGACCCAGTCA 1351
1467 GTACGAGACCAACACGACCAAGATCACTGAAGCTCACATCCGGGATAAACATGGAGGCT 1526
1352 ATACGAGACCAATACGACCAAGATCACGGAAGCTCACATCCAGATTAACATGGAAGGCT 1411
1527 GTCCGTGAGACGACCTGAGGAAACAGAGGCTCTTCACTCTAGACCAACATGACCATTT 1586
1412 GTCACTGAGATGACCTGAGGAAACAGAGGCTCTTCACTCTAGACCAACATGACCATTT 1471
1587 CATGCCGTACCTGACGAGATCAACGAGCTGAGGGAACCTTCACTCTAGACCAACGAGAC 1646
1472 CATGCCGTACCTCAACAGATCAACGAGTGGAGGGAACCTTCACTCTAGACCAACGAGAC 1531
1647 CTAATCTTCTGAGAGGAGTGGACAGCTGAGGAGGCTTGGCCATCGAGCTGAGGCTGCC 1706
1532 CTAATCTTCTGAGAGGAGTGGACAGCTGAGGAGGCTTGGCCATCGAGCTGAGGCTGCC 1591
1707 CCACCTGTACGCGGACGAGCGCGGCGGTGACGAGGCTGACACCCCGGCTCACACCGG 1766
1592 CCACCTGTGACGAGCAGCAGCGCGGCTGACGAGGCTGACACCCCGGCTCACACCGG 1651
1767 CGTGAGGCGCAGCTGTGAGCTGCGCAAGGCTTATGCTGCTGCTGAAAGCTCTGCTG 1826
1652 CGTGAGGCGCAGCTGTGAGCTGCGCAAGGCTTATGCTGCTGCTGAAAGCTCTGCTG 1711
1827 GCATCAGCTGATCAGCCTGCTGACACGACGCGGTGATGACGAGGCTTCTGTAATCGC 1886
1712 GCATCAGCTGATCAGCCTGCTGACACGACGCGGTGATGACGAGGCTTCTGTAATCGC 1771
1887 GACAAACCGGACGCTGAGCTGCTGATCCGCTGACAAAGCTGACGAGGCTTCTGTAATCGC 1946
1772 AACAAACCGGACGCTGAGCTGCTGATCCAGTGCACAAAGCTGACGAGGCTTCTGTAATCGC 1831
1947 TCACGCTGATCAGCTGAGCTGCTGATCCAGTGCACAAAGCTGACGAGGCTTCTGTAATCGC 2006
1832 TCACGCTGATCAGCTGAGCTGCTGATCCAGTGCACAAAGCTGACGAGGCTTCTGTAATCGC 1891
2007 CGAGCGCACCGTGTCCCTGCAAGTACGCGTGGGATGTCGCGAGACGCTGTACAAGAG 2066
1892 CGAGCGCACCGTGTCCCTGCAAGTACGCGTGGGATGTCCTCCGACGCTGTACAAGAG 1951
2067 CTGGAATTCACGAGCAGCTCTCCAGCAGATCTCGTCAAGAGAGTGGCTGTGCC 2126
1952 CTGGAATTCACGAGCAGCTCTCCAGCAGATCTCGTCAAGAGAGTGGCTGTGCC 2011
2127 GGACCACTCAAGCCATATGCTGCTGATCAAGGACTACCCCTATGCCGTTGA 2186
2012 GGACCACTCAAGCCATATGCTGCTGATCAAGGACTACCCCTATGCCGTTGA 2071
2187 CGGCTCGTCACTGTGTGGGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTA 2246
2072 CGGCTCGTCACTGTGTGGGATCGAGCGGTGGTCAAGGAGTACCTGGACATCTACTA 2131
2247 CCTCAACGAGCGGAGCTCCAGCTGAGCTGAGCTGAGGCGGTGGTGAAGAGGCTGC 2306
2132 CCTCAACGAGCGGAGCTCCAGCTGAGCTGAGCTGAGGCGGTGGTGAAGAGGCTGC 2191
2307 TGAGGAGCGCAGCGGACCTCAAGACCGAGACTGCTGGGCGGACGAGTGAACCGCTCA 2366
2192 CGAGGAGCGCAGCGGACCTCAAGACCGAGACTGCTGGGCGGACGAGTGAACCGCTCA 2251
2367 GCAGCTGCTAGGCGGTGACGAGCAGCTATCTGGGTGGGATCGGCTGACGCGGCTGT 2426
2252 CGGCTGCGCAGGCGGTGACGAGCAGCTATCTGGGTGGGATCGGCTGACGCGGCGGT 2311
2427 CAACTTTGGGAGTACCTACGCGGTACCTCCCGAACCGGCGGACGCGGCGG 2486
2312 CAACTTTGGGAGTACCTACGCGGTACCTCCCGAACCGGCGGACGCGGCGG 2371
2487 CCGGATGCCGAGCGCAGGACCACTACAGAGCTGGAGCGGCGGACGAGGCG 2546

2372 GCCGATGCCGAGCGGCGAGCAGCTACAAGAAGCTGGAGCGGCGGACAGAGGAGC 2431
2547 GGCATGTGTTCATCCGCAACCATCACAGCCAGTTCCAGACCATCTCTGGGATCTCGCT 2606
2432 GGACGCGGTGTTATCCGCAACCATCACAGCCAGTTCCAGACCATCTCTGGGATCTCGCT 2491
2607 CATCGAGATCTCTCCAGCACTCTCCGCAACCATCACAGCCAGTTCCAGACCATCTCTGGGATCTCGCT 2666
2492 CATCGAGATCTCTCCAGCACTCTCCGCAACCATCACAGCCAGTTCCAGACCATCTCTGGGATCTCGCT 2551
2667 TGATCCTCGAGCTGAGCCCAAGCGCTGATGCTTCAAAAGATTCGGAGCGGCT 2726
2552 TGAGCGCTGAGCTGAGCCCAAGCGCTGATGCTTCAAAAGATTCGGAGCGGCT 2611
2727 GGTGAGATTCGAGATTCGAGATCAAGACGATCAAGACGATTCGAGCTTGAAGAACCGGAA 2786
2612 GGTGAGATTCGAGATTCGAGATCAAGACGATCAAGACGATTCGAGCTTGAAGAACCGGAA 2671
2787 GGGGCTGTGGAATGCCCTATGCTGTACCCCAACACGTCGAGCGTTACCGGCGA 2846
2672 GGGGCTGTGGAATGCCCTATGCTGTACCCCAACACGTCGAGCGTTACCGGCGA 2731
2847 GAGGCGGAGGCGCTTACTGCCATGGCATTCCCAACGATCTCCATATGAGCTGGGC 2906
2732 GAGGCGGAGGCGCTTACTGCCATGGCATTCCCAACGATCTCCATATGAGCTCTCTC 2791
2907 AGATTGT-----GTCTCGTAGTAAATTTGTGTGCGCGCTGGAGATGTTTCTT 2957
2792 ACTGCTGAGCGGATGGTTTGTAGATGTTCTGTACGCTGTGTAAATGTGCTGTTTAT 2851
2958 CATGTTTTGTGAGCTCTAGGCTAGGAGTGGATGAGATCATACCATGATC-----TTTGA 3012
2852 CGTGTGTTGTGAGCTCTAGGCTAGGAGTGGATGAGATGTTGATGATCCATGATCTGTA 2911
3013 GCGTTGAGAGAGGAGTCCACGCT--TGAATATTTGTGTGATGATGATGATTTCTTGGTTAA 3070
2912 GCGTTGAGAGAGGAGTCCACGCTCTGGAGATGTTGTCATGTTGTTCTTCTTCTTTAAG 2971
3071 TAATAAGTTCTGCTCAGTTCACTTCT 3095
2972 AATAAAGTTCTGCTCAGTTCACTTAT 2996

RESULT 8

US-10-132-350-19
; Sequence 19, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duviols, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT FILING DATE: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2664)
US-10-132-350-19

Query Match 75.6%; Score 2368; DB 14; Length 2664;

Best Local Similarity 93.1%; Pred. No. 0;
Matches 2479; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy	235	ATGTTCTGGACAGGGTTCGGGACCGGCTGACGGGAAGAACAAAGAGGGGTGGAGCGAG	294
Db	1	ATGTTCTGGACAGGGTTCGGGACCGGCTGACGGGAAGAACAAAGAGGGGTGGAGCGAG	60
Qy	295	GGCAAGATCCGGCGCACCGGTGAGGCTGGTCAAGAAGAGAGGTGTGGACGTGCGCGACTTC	354
Db	61	GGAAAGATCCGGCGCACCGGTGAGGCTGGTCAAGAAGAGAGGTGTGGACGTGCGCGACTTC	120
Qy	355	AACGCTCGTCTCGACAGGGTCCACAGGATCTCTGGCTGGGACGACGGCGTTCGCTTC	414
Db	121	AACGCTCGTCTCGACAGGGTCCACAGGATCTCTGGCTGGGACGACGGCGTTCGCTTC	180
Qy	415	CAGTCTGTGACGGCCACCGGGCGGACCCAGCAAAAGGGGGCGGTGGCAAGGTGGGGAAG	474
Db	181	CAGTCTGTGACGGCCACCGGGCGGACCCAGCAAAAGGGGGCGGTGGCAAGGTGGGGAAG	240
Qy	475	GGCGCGACCTGGAGGAGGGTGTGTCTCAAGTCCACGGCGGACGGGGAGACCGGTG	534
Db	241	GGCGCGACCTGGAGGAGGGTGTGTCTCAAGTCCACGGCGGACGGGGAGACCGGTG	300
Qy	535	TACCGGTGAGTTCGAGTGGGACGAGTCCGAGGSCATCCGGCGCGCTCTGCTGCTCAGG	594
Db	301	TACCGGTGAGTTCGAGTGGGACGAGTCCGAGGSCATCCGGCGCGCTCTGCTGCTCAGG	360
Qy	595	AACCTGACGACGCGGAGTTCCTCTCAAGACGCTCACCTCTGAGGGCGTCCAGGCAAG	654
Db	361	AACCTGACGACGCGGAGTTCCTCTCAAGTCTGCTCACCTCTGAGGGCGTCCCGGCGAG	420
Qy	655	GGACCGTGTCTGCTGCGCACTCTGCTGGGTCTACCGGACAAAGCTCTACTCCGAGGAA	714
Db	421	GGACCGTGTCTGCTGCGCACTCTGCTGGGTCTACCGGACAAAGCTCTACTCCGAGGAA	480
Qy	715	CGCATCTTCTCGGCAACGACCTATCTCGCGAGCAAAATCGCGGGCGTGGTGGCT	774
Db	481	CGCGTCTTCTCGGCAACGACCTATCTCGCGAGCAAAATGCTGGGATTTGGTGGCT	540
Qy	775	TATCGGCAAGATGACTCAAGATTCCTCGTGGGACGATTAATCTCTGGACCATACGAGGAG	834
Db	541	TACCGGAGGACGAGCTCAAGATTCCTCGGCGGACGATTAATCTCTGGACCATACGAGGAG	600
Qy	835	CATGATCGCTTACCGTACGACTACTCAAGTACCTTGGTGTATCCCGACAGGGCGGA	894
Db	601	CACGACCGCTTACCGTACGACTACTCAAGTACCTTGGTGTATCCCGACAGGGGTGAA	660
Qy	895	GAGCACGCTCGGCGATCTCTCGTGGGACGACCAAGAACACCCGTATCCCGTCTGCTGAGA	954
Db	661	GACCATGCCGGCTGCTCTCGGGGCGAGCCAGAACACCCGTATCCCGTCTGCTGAGG	720
Qy	955	ACTGGCGGACCCCAAAAGAGACCCAAATTCGGAGAGCAGGCTTTCTGCTGTAAC	1014
Db	721	ACCGGCGGCGTCCAAAGAGACAGACCCCAACTCGGAGAGCAGGCTTTCTGCTGTAAC	780
Qy	1015	CTGAACATCTACGCTCCCGGTGACGAGCGTTTGGGATCTCAAGATGCGGACTTCCTT	1074
Db	781	CTGAACATCTACGCTCCCGGTGACGAGCGTTTGGGATCTCAAGATGCGGACTTCCTT	840
Qy	1075	GGGTACTCGTGAAGACGATCATGAGGCTGTCTTCTTCCAACTATGGGACTTTCTGCTGAT	1134
Db	841	GGGTACTCACTGAAGGGGATCATGAGGCTGTCTTCTCCGACGCTGGGACGTTTCTGCTGAC	900
Qy	1135	GACACGCCAGGAGTTTGGATTCGTTTGGAGTATCTCGGGCTCTACGAGCTGGGCCCA	1194
Db	901	GATACGCCAGGAGTTTGGATTCGTTTGGAGATATCTTGGGCTCTACGAGCGGGTCCA	960
Qy	1195	GAGGACCCCAACACCCACTGTAGCAGAGATCAGGAAGAGATCCCGACGAGTTCCCTT	1254
Db	961	GAGGACCCCAACACCCACTGTAGCAGAGATCAGGAAGAGATCCCGACGAGTTCCCTT	1020
Qy	1255	CGAAGCATCTTCGCGAACGGTAGCCATGACCAACCGGCTAAGATGGCCCTTCCAAATGTC	1314

Db	1021	AGAAGCATTTCTCCCGATGCTAGCCATGACCACCCCTGGAAGATGCCCTTCCAAATATC	1080
Qy	1315	ATCAATCAGATGTGTTGAAAAGGCTCCGAGTTTAAAGTTTGGCTGGAGACTGACGAA	1374
Db	1081	ATCAATCAGATGTGTTGAAAAGGCTCCAGAGTTTAAAGTTTGGCTGGAGACTGACGAA	1140
Qy	1375	GAGTTCCGAGAGAGACACTTTCAGGGGTGAACCCAGTAAATCATCAAACGCTCTGACGAG	1434
Db	1141	GAGTTTCGAGGAGAGCGTTTGCAGGCGTGAACCCAGTAAATCATCAAACGCTCTGACGAG	1200
Qy	1435	TTCCCCGTAAAGACCCCTGGACCCRANGGAGTACGAGAGACCAACAGCAAGATCACT	1494
Db	1201	TTCCCCGTAAAGTACCTTGGACCCAAAGTCAATACGAGAGCCTATACAGCAAGATCACT	1260
Qy	1495	GAAAGTCACTATCCGCGCATAAATGGGAGGCGTGTGGTGCAGAGCGCATCTGAGGAACAAG	1554
Db	1261	GAAAGTCACTATCCGCGCATAAATGGGAGGCGTGTGGTGCAGAGTGCATCTGAAGAAGAAC	1320
Qy	1555	AGGCTCTTATCTAGACCAACATGACCATTTTATGCGGTACCTTCGAGAGATCAACGAG	1614
Db	1321	AGGCTCTTATCTAGACCAACATGACCATTTTATGCGGTACCTTCACCAAGATCAACGAG	1380
Qy	1615	CTGAGGGGAACTTCTCATCTACGCGAGAGGACCTACTGTTCCTGAAAGGACGATGGGACG	1674
Db	1381	TTGAGGGGAACTTCTCATCTAGCGCAGAGGACCTACTGTTCCTGAAAGGACGATGGGAC	1440
Qy	1675	CTGAAGCCCTGGGCGATCGAGCTGTGCCCACTGACGGCGTGCAGGGCCAGCTGTGCGAC	1734
Db	1441	CTGAAGCCCTGGGCGTGTGAGCTGTGCCCACTGACGGCGTGCAGGGCCAGCTGTGCGAC	1500
Qy	1735	CTCAGCAAGGTGTACACCCCGGCTCACACCGGCTGCAGGGCCAGCTGTGCGACGCTGCC	1794
Db	1501	CTCAGCAAGGTGTACACCCCGGCTCACACCGGCTGCAGGGCCAGCTGTGCGACGCTGCC	1560
Qy	1795	AAGGCTTATGCTGCGTAAACGACTCTGCTGGGATCAGCTGATCAGCCACTGGGCTGAAC	1854
Db	1561	AAGGCTTATGCTGCGTAAACGACTCTGCTGGGATCAGCTGATCAGCCACTGGGCTGAAC	1620
Qy	1855	AGGACGGGCTGATCGAGCGGTGTGTAATCGGCAAAACCGGCGAGCTCAGGGTGGTGCAT	1914
Db	1621	AGGACGGGCTGATCGAGCGGTGTGTAATCGGCAAAACCGGCGAGCTCAGGGTGGTGCAT	1680
Qy	1915	CCCGTGCAAGAGCTGCTGAGCGCGCATCTACCGTGACACGCTGAAACATCAAGCCCTGGCA	1974
Db	1681	CCCGTGCAAGAGCTGCTGAGCGCGCATCTACCGTGACACGCTGAAACATCAAGCCCTGGCA	1740
Qy	1975	GGCCAGACATCATCAACCGCGGCGGTCTTTCGAGCGGCAACCGTTCCTCTGCAAGTAC	2034
Db	1741	GGCCAGAGCTCATCAACCGCGGCGGTCTTTCGAGCGGCAACCGTTCCTCTGCAAGTAC	1800
Qy	2035	GGCTGGGGATGTGGGAGAGCTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA	2094
Db	1801	GGCTGGGGATGTCTCCGACGTGTACAAGAGCTGGAATTTCAACGAGCAGGCTCTCCCA	1860
Qy	2095	GCAGATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCGATCAAGCCCATATGTTGTCGGA	2154
Db	1861	GCAGACCTCGTCAAGAGAGGTGTGGCTGTGCGGACCGATCAAGCCCATATGTTGTCGGA	1920
Qy	2155	CTGCTGATCAAGGACTACCTTATGCGGTGACGGGCTCGTCACTTGGTGGGCGATCGAG	2214
Db	1921	CTGCTGATCAAGGACTACCTTATGCGGTGACGGGCTCGTCACTTGGTGGGCGATCGAG	1980
Qy	2215	CGGTGGGTCAAGGAGTACCTGACATCTATCTACCTTAACGACGGGAGCTCCAGCGTGAC	2274
Db	1981	CGGTGGGTCAAGGAGTACCTGACATCTATCTACCTTAACGACGGGAGCTCCAGCGTGAC	2040
Qy	2275	GTGAGCTGCGAGGCGTGTGAAAGAGGTGCGTGAGAGGCGGACCGGCGACTCAAGAGAC	2334
Db	2041	GTGAGCTGCGAGGCGTGTGAAAGAGGTGCGTGAGAGGCGGACCGGCGACTCAAGAGAC	2100
Qy	2335	CGAGACTGCTGCCCGAGGATGACACCGTCCAGAGCTGGCTAGGGCTGCACGACCATC	2394
Db	2101	CGAGACTGCTGCCCGAGGATGACACCGTCCAGAGCTGGCTAGGGCTGCACGACCATC	2160

QY 2395 ATCTGGTGCATCCCGCGTGCACGGGTGTCAACTTTGGGCGAGTACCACATACGCCGG 2454
Db 2161 ATCTGGTGCATCCCGCGTGCACGGGTGTCAACTTTGGGCGAGTACCACATACGCCGG 2220
QY 2455 TACCTCCGAAACCGCGCGAGCGCGACCGCGGCCCGATGCCGAGCGAGCGAGCGACGAC 2514
Db 2221 TACCTCCGAAACCGCGCGAGCGCGACCGCGGCCCGATGCCGAGCGAGCGAGCGACGAC 2280
QY 2515 TACAAGAAGCTGGAGCGGGGCGAGAGGAGCGGACATGTTTCATCCGCGACCATCAC 2574
Db 2281 TACAAGAAGCTGGAGCGGGGCGAGAGGAGCGGACATGTTTCATCCGCGACCATCAC 2340
QY 2575 AGCCAGTTCAGACCATCTCTGGGCATCTCGCTCATCGAGATCTCTCCAGGACCTCTCC 2634
Db 2341 AGCCAGTTCAGACCATCTCTGGGCATCTCGCTCATCGAGATCTCTCCAGGACCTCTCC 2400
QY 2635 GAGGAGGTGTACTCTGGCCGCGGTGAGGAGCGCTGATCGCTGAGCGTGCAGCGCGAGCG 2694
Db 2401 GAGGAGGTGTACTCTGGCCGCGGTGAGGAGCGCTGATCGCTGAGCGTGCAGCGCGAGCG 2460
QY 2695 CTGATGCGCTTCAAAAGATTCCGGGAGCGCGCTGCTGCGAGATTCAGAAATCGGATCAAGACG 2754
Db 2461 CTGAGCGCTTCAAAAGATTCCGGGAGCGCGCTGCTGCGAGATTCAGAAATCGGATCAAGACG 2520
QY 2755 ATGAACGACAGTCCGAGCTTTGAAGAACCGGAGCGCGCTGCTGCGAGATTCAGAAATCGGATCAAGACG 2814
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QY 2815 CTGTACCCCAACACGCTCGGACGTTTACCGGCGAGAGCGCGAGCGCGCTTACTCCCATGGCG 2874
Db 2581 CTGTACCCCAACACGCTCGGACGTTTACCGGCGAGAGCGCGAGCGCGCTTACTCCCATGGCG 2640
QY 2875 ATTCACCAACAGCATCTCCATATGA 2898
Db 2641 ATTCACCAACAGCATCTCCATATGA 2664

RESULT 9

US-10-132-350-53
; Sequence 53, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Davick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(2086)
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: (1548)...(1555)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1864)...(2086)
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (28)...(31)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (86)...(89)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (345)...(348)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (414)...(417)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (733)...(736)
; OTHER INFORMATION: W box
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; NAME/KEY: misc_feature
; LOCATION: (928)...(931)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1022)...(1025)
; OTHER INFORMATION: W box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (260)...(266)
; OTHER INFORMATION: MRE-like element
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (167)...(172)
; OTHER INFORMATION: H box
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1446)...(1552)
; OTHER INFORMATION: C2H2 response element
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (6569)...(6767)
US-10-132-350-53

Query Match 54.2%; Score 1698.4; DB 14; Length 7492;
Best Local Similarity 79.4%; Pred No. 0;
Matches 2369; Conservative 0; Mismatches 11; Indels 604; Gaps 6;
QY 718 ATCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGCGGCTTGGTGCCTTAT 777
Db 3785 ATCTTCTTCTTCGCCAACGACACCTATCTGCCGAGCAAAATGCCGCGGCTTGGTGCCTTAT 3844
QY 778 GCGCAAGATGAGTCTCAGATTCTCCGTGGCGAGCAATATCTCGACCATACACGAGGAGCAT 837
Db 3845 GCGCAAGATGAGTCTCAGATTCTCCGTGGCGAGCAATATCTCGACCATACACGAGGAGCAT 3904
QY 838 GATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAGGCGCGAAGAG 897
Db 3905 GATCGCGTCTACCGTTACGACTACTACAATGACCTTGGTGATCCCGACAGGCGCGAAGAG 3964
QY 898 CACGCTCGCGCGATCTCCGTGGCGAGCAACACCGCTATCCCGTGCCTGCAGACT 957
Db 3965 CACGCTCGCGCGATCTCCGTGGCGAGCAACACCGCTATCCCGTGCCTGCAGACT 4024
QY 958 GCGCGGACCCCAACAAGAA----- 977
Db 4025 GCGCGGACCCCAACAAGAAAGGTACTAGCTCAGTCTAGTCTAGTCCATACATA 4084
QY 978 -----AGACCCAAA 986
Db 4085 CAGGATCCAGAAATTGGCTGAAATCTTGTCTGAGTTAACTTTTACGACAGCCAAA 4144
QY 987 TTCCGAGAGCAGGCTTTTCCTGCTGACCTGACATCTAGCTCCCGCTGCAGCAAGCTT 1046

Db 4145 TTCCGAGAGCAGGCTTTCTGCTGAACCTGAACATCTACGTCCCGGTGACGAACGCTT 4204
Qy 1047 TGGGCATCTCAAGATGTCGACATCTCTTGGTACTGCTGAACGATCATCGAGCCTGT 1106
Db 4205 TGGGCATCTCAAGATGTCGACATCTCTTGGTACTGCTGAACGATCATCGAGCCTGT 4264
Qy 1107 TCTTCCAACTGCGGACTTTCTGCTGATGACAGCCCAAGGAGTTCGATTCTGTTTGGGA 1166
Db 4265 TCTTCCAACTGCGGACTTTCTGCTGATGACAGCCCAAGGAGTTCGATTCTGTTTGGGA 4324
Qy 1167 TATCCTCGGCTCTACAGCTGGGCCCGCAGAGCCCAACCAACCCACTGATAGCAGAT 1226
Db 4325 TATCCTCGGCTCTACAGCTGGGCCCGCAGAGCCCAACCAACCCACTGATAGCAGAT 4384
Qy 1227 CAGGAAGAATCCCGAGCAGTTCCTTTCGAAGCATCTCTCCGAAACGCTAGCCATGACCA 1286
Db 4385 CAGGAAGAATCCCGAGCAGTTCCTTTCGAAGCATCTCTCCGAAACGCTAGCCATGACCA 4444
Qy 1287 CCGCTAAAGATGCCCTTCCAAATGTCATCAAT 1321
Db 4445 CCGCTAAAGATGCCCTTCCAAATGTCATCAATCAGGTAAACCCAAATTTCTTTTTT 4504
Qy 1322 ----- 1321
Db 4505 TTTGGAATCTTTCTATGTTTAAACGCGCGTGCCTGAACCTAGAAAAAATTTACCATGGCT 4564
Qy 1322 ----- CAGATGTTGTTGAAAAAGGCTCCGGAGTTTAAGT 1354
Db 4565 AAGSCTGAATCTTGGTTGGTATAAACACAGATGTTGTTGAAAAAGGCTCCGGAGTTTAAGT 4624
Qy 1355 TTGGCTGGAGACTGACGAAGAGTTTCGCGAGAGAGACACTTCGAGCGGTGAACCCAGTAA 1414
Db 4625 TTGGCTGGAGACTGACGAAGAGTTTCGCGAGAGAGACACTTCGAGCGGTGAACCCAGTAA 4684
Qy 1415 TCATCAAACTGTCGAC ----- 1430
Db 4685 TCATCAAACTGTCGACGGTTAGCGTTCTTGATCANTTTGGATCGGCMAAATAACACCTTG 4744
Qy 1431 ----- 1430
Db 4745 CCCCATATATTAAGTACTGAGTACAGAGCCTTAAAGCCCTTTTTTATATATATATTTCTGAT 4804
Qy 1431 ----- GGAAGTTCCCGCTTAAAGACACCTTGACCCCAAGGAGTACGAGACCCACACAGCA 1486
Db 4805 CTAGAGAGTTCCCGCTTAAAGACACCTTGACCCCAAGGAGTACGAGACCCACACAGCA 4864
Qy 1487 AGATCACTGAAGCTCAATCCGCGATACATGGAGGCGCTTGTGCTGCGAGAAC ----- 1539
Db 4865 AGATCACTGAAGCTCAATCCGCGATACATGGAGGCGCTTGTGCTGCGAGAACGATATGCT 4924
Qy 1540 ----- 1539
Db 4925 GGAATGATGAACGACGACGCTACAAACGAAAGCGCTTAAACCATCGACTGATCTGA 4984
Qy 1540 ----- GCACCTGAGGAACAAGAGCTCTTATCTCTAGACCA 1574
Db 4985 TTTCCGCGTAAACCACTGTGAGGACCTTGAGGAACAAGAGCTCTTATCTTAGACCA 5044
Qy 1575 CCATGAOCATTTATGCGCTACTCTGACGAGATCAACGAGCTGGAGGGAACCTTATCTTA 1634
Db 5045 CCATGAOCATTTATGCGCTACTCTGACGAGATCAACGAGCTGGAGGGAACCTTATCTTA 5104
Qy 1635 GGCAGCAGGACCTACTGTTCTGAGGACGATGGCAGCCTGAAGCCCTGGCCATCGA 1694
Db 5105 GGCAGCAGGACCTACTGTTCTTGAAGGACGATGGCAGCCTGAAGCCCTGGCCATCGA 5164
Qy 1695 GCTGAGCTGCCCCACCTGACGCGCCACGAGCGCGCGCTCAGCAAGGTGTACACCCC 1754
Db 5165 GCTGAGCTGCCCCACCTGACGCGCCACGAGCGCGCGCTCAGCAAGGTGTACACCCC 5224
Qy 1755 GGTCAACCGCGCTCGAGGGCCACGTTCTGGAGCTCGCCAGGCTTATGCTTGGCTGATAA 1814
Db 5225 GGTCAACCGCGCTCGAGGGCCACGTTCTGGAGCTCGCCAGGCTTATGCTTGGCTGATAA 5284

Qy 1815 CGACTCTGCTCGCATCAGCTGATCAGCCACT ----- 1846
Db 5285 CGACTCTGCTCGCATCAGCTGATCAGCCACTGGTATAGAAATGTTTCTGGTGCCTTTT 5344
Qy 1847 ----- 1846
Db 5345 TCTCTTTTTTTTTTCTTTAATTAATGATACATAGATAAATGAAGCACTAATCTTAA 5404
Qy 1847 ----- GGCTGACACGACGCGGTGATCGAGCGTTCGTAA 1882
Db 5405 TTGTGTGCTTGCATGCAATTCAGGGCTGAACACGACGCGGTGATCGAGCGTTCGTAA 5464
Qy 1883 TCGGACAAAAACCGGAGCTCAGCGTGTGCTATCCCGTGCAAAAGCTGCTGAGCCCGCACT 1942
Db 5465 TCGGACAAAAACCGGAGCTCAGCGTGTGCTATCCCGTGCAAAAGCTGCTGAGCCCGCACT 5524
Qy 1943 ACCGTGACACGCTGAACATCAACGCGCTGGACGCGAGACACTCATCAACGCGCGCGCG 2002
Db 5525 ACCGTGACACGCTGAACATCAACGCGCTGGACGCGAGACACTCATCAACGCGCGCGCG 5584
Qy 2003 TCTTCGAGCGCACGCTGTTCCCTGCAAAAGTACGCGTGGGATGTCGGCAGACGCTGACA 2062
Db 5585 TCTTCGAGCGCACGCTGTTCCCTGCAAAAGTACGCGTGGGATGTCGGCAGACGCTGACA 5644
Qy 2063 AGAGTGGAAATTTCAAAGAGCAGCTCTCCAGCAGATCTCGTCAAG ----- 2109
Db 5645 AGAGTGGAAATTTCAAAGAGCAGCTCTCCAGCAGATCTCGTCAAGAGGTACGTAGACA 5704
Qy 2110 ----- 2109
Db 5705 ATACACTGAGGTGAGCAGCACTAAACGCTATAGAAAATCTTTCGTTCTTTGACGTGGT 5764
Qy 2110 ----- AGAGGTGTGGCTGTGCGGACAGCTCAAGCCCATATGTTGTCG 2153
Db 5765 GTGGTGGCTGCGTTCAGAGGTGTGCTGTGCGGACAGCTCAAGCCCATATGTTGTCG 5824
Qy 2154 ACTGCTGATCAAGGATACCCCTATGCGTTGAGCGGCTCGTCACTCTGTTGGTGGCGATCGA 2213
Db 5825 ACTGCTGATCAAGGATACCCCTATGCGTTGAGCGGCTCGTCACTCTGTTGGTGGCGATCGA 5884
Qy 2214 GCGTGGGTCAAGGATACCTTGGACATCTACTACCTAAACGCGCGAGCTCCAGCGTGA 2273
Db 5885 GCGTGGGTCAAGGATACCTTGGACATCTACTACCTAAACGCGCGAGCTCCAGCGTGA 5944
Qy 2274 CGTGAGCTGACGCGTGTGTTGGAAGGAGTGTGCTGAGAGGCGCAAGCGCACTCAAGGA 2333
Db 5945 CGTGAGCTGACGCGTGTGTTGGAAGGAGTGTGCTGAGAGGCGCAAGCGCACTCAAGGA 6004
Qy 2334 CCGAGACTGTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGGTGACGACCAT 2393
Db 6005 CCGAGACTGTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGGGTGACGACCAT 6064
Qy 2394 CATCTGGTGGCATCCGCGCTGACGCGGTGTCAACTTTTGGGAGTACCCATACGCGG 2453
Db 6065 CATCTGGTGGCATCCGCGCTGACGCGGTGTCAACTTTTGGGAGTACCCATACGCGG 6124
Qy 2454 GTAACCTCCGAAACCGCGCAGCGCCAGCGCGCGCGATGCCGAGCCAGCAGCAGCA 2513
Db 6125 GTAACCTCCGAAACCGCGCAGCGCCAGCGCGCGCGATGCCGAGCCAGCAGCAGCA 6184
Qy 2514 CTACAAGAGCTGGAGCGGGCAGAGGAGCGGACATGTTGTTCACTCCGACCATCAC 2573
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Qy 2574 CAGCCAGTTCCAGACCATCTTGGGATCTCTGCTCATCGAGATCTCTTCCAAAGCATCTCTC 2633
Db 6245 CAGCCAGTTCCAGACCATCTTGGGATCTCTGCTCATCGAGATCTCTTCCAAAGCATCTCTC 6304
Qy 2634 CGAGAGGTGTACCTCGGCGCAGCGTGTGAGCGCTGATCGCTGAGCAGCGCAAGGC 2693
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QY 2694 GCTGATGCGTTCAAAAGATTCCGGAGCCGGCTGGTGACAGATTGAGAAATCGGATCAAGAC 2753
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QY 2934 GCTGCCCGCTGGCATGTTTCTTCAATGCTTTTGTGTCATCTCAGGTCAGGCTAGGGGATGGAGA 2993
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QY 2994 TCATACCATGATCTTTGTAGGGTTGAGAGGAGTCCACGCTTGAATATTTGTGTATGT 3053
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Db 6665 TCATACCATGATCTTTGTAGGGTTGAGAGGAGTCCACGCTTGAATATTTGTGTATGT 6724
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QY 3054 ATGTAATTTCTGTTAATATAAAGTTCGTCAGTTCAATTTCTTA 3097
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RESULT 10

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US-10-132-350-56
; Sequence 56, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navazro
; APPLICANT: Duviok, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 4483
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(211)
; OTHER INFORMATION: LOX5
; FEATURE:
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; NAME/KEY: exon
; LOCATION: (916)...(1205)
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; LOCATION: (1206)...(1716)
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; NAME/KEY: intron
; LOCATION: (1961)...(2051)
; FEATURE:
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US-10-132-350-56
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Query Match 47.8%; Score 1499.4; DB 14; Length 4483;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 2170; Conservative 0; Mismatches 11; Indels 604; Gaps 6;

QY 718 ATCTTCTTCGCCAACGACCTATCTCCGAGCAAAATCCGGGGCGGTGGTGCCTTAT 777
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QY 778 CGCAAGATGAGCTCAAGATTCTCCGTGGCGAGATAATCTCGACCAATACCAAGAGCAT 837
Db 1759 CGCAAGATGAGCTCAAGATTCTCCGTGGCGAGATAATCTCGACCAATACCAAGAGCAT 1818
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|
QY 838 GATCGCTTACCGTTACGACTACTACATGACTTGGTGATCCCGACGAGCGGAGAG 897
Db 1819 GATCGCTTACCGTTACGACTACTACATGACTTGGTGATCCCGACGAGCGGAGAG 1878
|
|
|
QY 898 CAGCTCGCGGATCTCTCGGTGGCAGCAAGAACACCCGTATCCCGTCCGTCGAGAACT 957
Db 1879 CAGCTCGCGGATCTCTCGGTGGCAGCAAGAACACCCGTATCCCGTCCGTCGAGAACT 1938
|
|
|
QY 958 GGCGGCACCCCAACAAAGAA----- 977
Db 1939 GGCGGCACCCCAACAAAGAAAGGTACTAGTCAAGTCAGTAGTGTAGTCCATACATA 1998
|
|
|
QY 978 ----- 986
Db 1999 CAGGATGCCAGAAATTTGGCTGAAATCCCTTGTGAGTTAACTTTTACGACACCCAAA 2058
|
|
|
QY 987 TTCGAGAGCAGGCTTTTCTGCTGAACCTGAACATCTAGTCCCGGTGACAGCGCTT 1046
Db 2059 TTCGAGAGCAGGCTTTTCTGCTGAACCTGAACATCTAGTCCCGGTGACAGCGCTT 2118
|
|
|
QY 1047 TGGCATCTCAAGATGTCGAGCTTCTTGGGTACTCGTGAAGACCATCATCGAGCTGT 1106
Db 2119 TGGCATCTCAAGATGTCGAGCTTCTTGGGTACTCGTGAAGACCATCATCGAGCTGT 2178
|
|
|
QY 1107 TCTTCCAACTCGGGACTTTTCGTGATGACAGCCCAAGAGTTCGATTCTGTTTGAGA 1166
Db 2179 TCTTCCAACTCGGGACTTTTCGTGATGACAGCCCAAGAGTTCGATTCTGTTTGAGA 2238
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Db 4399 GCTGTACCCCAACACAGCTCGGAGTTCACCGCGAGAGCCGAGGGCTTACTGCCATGGG 4458
QY 2874 CATTCCTCAACAGCATCTCCATATGA 2898
Db 4459 CATTCCTCAACAGCATCTCCATATGA 4483

RESULT 11
US-10-132-350-9
; Sequence 9, Application US/10123350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: Of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (65)...(2659)
; OTHER INFORMATION: LOX2b
US-10-132-350-9
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Query Match 42.4%; Score 1327.6; DB 14; Length 3007;
Best Local Similarity 71.7%; Pred. No. 0;
Matches 1907; Conservative 0; Mismatches 679; Indels 72; Gaps 10;

QY 246 CGGGTTCGGGACCGGCTGACGGGAAAGAAACAAAGAGCGGTGGAGCGAGGCGCAAGATCCG 305
Db 73 CGGGATCATCGACGGGCTGACGGGGGGAACAAAGCATGCGGGCTCAAG----- 121
QY 306 CGGCAAGGTGAGGCTGGTCAAGAGAGGTGTGTGACGTGCGGCGACTTCAACGGCTCGCT 365
Db 122 -GGCACGGTGGTGTCTATGCGCAAGAACGTGTGGACCTCAACGACTTTCGGCGCCACGT 180
QY 366 CTTGACCGGCTTCACAGATCTCTGGGTGGAGACGACGGCTGCGCTTCCAGCTCGTCAG 425
Db 181 CGTTGACAGCATCAGCGAGTTCCTCGGCA-----AGGGGTTCACCTGCCAGCTCATCAG 234
QY 426 CGCCACCGCGGCGGACCCCGACGACGAGGGGCGGTGGAGGTGGGAGGCGGCGCACCT 485
Db 235 CTTCCACCTTCGTCGACGCGCAACACGCGGCGGTTCGGGCGAGGCGAACCT 294
QY 486 GGAGAGGCGGTGGTGTGCTCAAGTCCAGCGCGGACGCGGAGACCGGTGTACCGGGTGA 545
Db 295 GGAGCAGTGGCTGACGAGCTGCGCTGACGACCGGCGGAGTCAAGTTCGGCGTCA 354
QY 546 CTTTCAGTGGGA---CGAGTGCAGGGATCTCCGCGCGCGCTCTGTTCAAGACCTTGA 602
Db 355 GTTTCAGTGGGAGTGGAGAGTGGAGTGGCGGGGCGCTGTGTTCAAGAAACACCA 414
QY 603 GCACCGGAGTTCCTTCCTCAAGACGCTCACCTCGAGGGCGTCCGAGGCAAGGCAACCGT 662
Db 415 CGCCCGCGAGTTCCTTCCTCAAGACCAATCACCTCGACGACGTGCGCGCGCGCGGT 474
QY 663 GGTCTTCGCGCAACTGTTGGGTACCGCGACAGCTCTACTCTCCAGGACCATCTT 722
Db 475 CACCTTCGTGCGCAACTCTGCGGTCTACCCCGCGGGCAAGTACCGCTACAAACCGGTCTT 534
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QY 723 CTTCCGCAACGACACCATCTCTCCGAGCAAAATGCGGGGGGCTTGGTGCCTTATCGGCA 782
Db 535 CTTCTTCAACGATACCTACCTGCAAGCCAGATGCGGGGGGCTGAAGCCGTACCGCA 594
QY 783 AGATGAGCTCAAGATTCCTCGTGGCGACGATATCTTGACCATATACGAGGAGCATATCG 842
Db 595 CGAGAGCTCCGCAACTCTCGCGGCGACGACGAGGAGGCCCCCTACGAGGACGACCG 654
QY 843 CTTCTACCTTACGATCTACATGACCTTGGTGTATCCGCAACAGGGGCAAGAGCAGC 902
Db 655 CGTGTACCGCTACGACGCTTACAAACGACCTCGCGAGCGCCGACGGCGC-----AACCC 708
QY 903 TCGGCGGATCTCTCGTGGCGAGCCAAACACACCGGTATCCCGTCTGCTGAGAACTGGCCG 962
Db 709 GCGCCCATCTCTCGGGGCTTCGCCGACACACCGGTACCGCGCGCTGCGACGCGGCG 768
QY 963 GCACCCAAACAAAGAGACCCAAATTCGGAGAGAGGCTTTCTCTCTGAACTGAACAT 1022
Db 769 CAAGCCCAACCAACCGACCCCAACTCGATAGCCGACTGTGCTGTTGA---GCAGAT 825
QY 1023 CTACGTCCTCGGTGACGAGCGCTTTGGGATCTCAAGATGTCGAGCTTCTTGGGTACTC 1082
Db 826 CTACGTCCTCGGAGCAGCGCTTTGCGCACCTCAAGATGTCGAGCTTCTTGGGCTACTC 885
QY 1083 GCTGAAGACGATCATCGAGGCTTTCTTCCAAACACTGGGGGACTTTCTGTCGATGACGCG 1142
Db 886 CATCAAGGCCATCAGCAGGGCATCATCCGCGGTGCGACGCTACGTGGACACCAACCC 945
QY 1143 CAAGGAGTTCGATCTCTTGGAGATATCTCGGCTCTACGAGCTGGGCGCCAGAGCACC 1202
Db 946 GGGCGAGTTCGACTCTCTCCAGGACATCATCAACCTGTAGAGGGCGGATCAAGTGGC 1005
QY 1203 CAACAAACCCACTGATAGCAGATCAGGAAGAGATCCCGAGCGAGTTCCTTCGAAGCAT 1262
Db 1006 CAGATCCAGGCGCTCGAGACATGCGCAAGCTTTCGCGCTCCAGCTGTCAAGGACCT 1065
QY 1263 TCTGCGAAGCGGTAGCATGACCCGCTAAGATGCGCCCTTCCAAATGTATCAAAATC 1322
Db 1066 CTTCCC---CGCGCGGGGACTACCTGCTCAAGCTCCCATCCACAGATCATCAA--- 1120
QY 1323 AGATGTGTTGMAAAGGCTCCGAGTTTAAAGTTTGGCTGGAGACTGACGAAGAGTTTCG 1382
Db 1121 -----GAGACAAGAACGCTGGAGGACCGAGCAGGAGTTTCG 1158
QY 1383 GAGAGACACTTTCAGGCGTGAACCCAGTATCATCAACCTCTGACGAGTTCCCGC 1442
Db 1159 GCGGAGGTGCTCGCGCGGTCAACCGATGCTGATCACGCGCTCACGAGTTCCCGC 1218
QY 1443 TAAAGCACCTTGGACCCAGGCGTACGAGACACACACGAGAGATCACTGAGCTCA 1502
Db 1219 CAAGACAAGTGGACCCAGCAGTACGCGCACCAACACGACGATCACGGCGAGCA 1278
QY 1503 CATCCGCGCATACATGGAGGCTCTGCTGTCAGAACGCACTGAGGAAACAAGAGGCTCTT 1562
Db 1279 CATCGAGAAGAACCTCGAGGCGCTCACGCTGAGCGGCTGGACGGCAACAGGCTCTA 1338
QY 1563 CATCTAGACACCATGACCATTTATGCGCTACTCGACGAGATCAACGAGCTGAGG 1622
Db 1339 CATCTGGACACCAACGACCGCTTATGCGGTTCTCTATCGACGTCAACAACTGAGG 1398
QY 1623 GAATTCATCTACGCGCAGGACCTACTCTTCTGAAGGACGATGGCACTGAGGCT 1682
Db 1399 TAACTTCATCTAGCAACGAGACCTCTTCTTCTGCGCGGCGAGGAGGCTCGCGC 1458
QY 1683 CTTGGCCATTCGAGCTGAGCTGCCCAACCTCAACGCGCAGCAGCGCGCGCTGAGCA 1742
Db 1459 CTTGCTATTCGAGCTCAGCGAGCGCTATCATCGAGGGACCTTACCGTGGCGCAAGGCA 1518
QY 1743 GGTGTACACCGCGCTCACACCGGCTGAGGGCCACCTCTGTCGAGCTCGCCAGGCTTA 1802
Db 1519 GGTCTACACGCGCGGCTTCAGCGCGTTCAGGCGCTGGGTGTGGCAGCTCGCCAGGCTTA 1578
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1803 TGCCTGGTAAACGACTCTGCTGGCATCAGCTGATCAGCCACTGGCTGAACACGACGC 1862
1579 TGTCCCGCTCAACGACTCTGGCTGGCACTGCTGAGCCACTGGCTGAACACGACGC 1638
1863 GGTGATCAGCCGTTGTAATCGCGACAAACCGGACGCTCAGCGTGGTGCATCCCGTGCA 1922
1639 GGTGATCAGCCGTTGTAATCGCGACAAACCGGACGCTCAGCGTGGTGCATCCCGTGCA 1698
1923 CAGCTCTGAGCCGCTACCTACCTGACGACGCTGACGCTGACGCTGACGCTGACGCTGAC 1982
1699 CAGCTCTGAGCTGACCTACCTGACGACGCTGACGCTGACGCTGACGCTGACGCTGAC 1758
1983 ACTCATCAAGCCGCGCGCTCTTCGAGCGCACCGTGTTCCTGCAAAAGTACCGCTGGG 2042
1759 GCTCATCAAGCCGCGCGCTCTTCGAGATGACGCTCTCCCGGCAAGTACGCGTGGG 1818
2043 GATGTCGGCAGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 2102
1819 CATGCTCTGCTGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 1878
2103 CGTCAAGAGAGGCTGCTGCTGCGGACGCTGACGCTGACGCTGACGCTGACGCTGACG 2162
1879 CGTCAAGAGAGGCTGCTGCTGCGGACGCTGACGCTGACGCTGACGCTGACGCTGACG 1938
2163 CAAGGACTACCCCTATCCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 2222
1939 CGAGGACTACCCCTATCCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 1998
2223 CAAGGACTACCCCTATCCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 2282
1999 GGGCGAGTACCTGCGCATCTACTACCTGACGCTGACGCTGACGCTGACGCTGACGCT 2058
2283 GCAGGCGTGTGGAAGAGGCTGCTGAGGAGGCGGACGCGGACCTCAAGGACCGGAGCTG 2342
2059 GCAGGCGTGTGGAAGAGGCTGCTGAGGAGGCGGACGCGGACCTCAAGGACCGGAGCT 2118
2343 GTGCCCCAGGATGACACCTGCTGACGCTGCTGCTGAGGCGGTGACGACGCTGCTGCTG 2402
2119 GTGCCCCAGGATGACGCTGCTGAGGCTGCTGAGGCGGTGACGACGCTGCTGCTGCTG 2178
2403 GGCATCCGCGCTGACGCGGCTGCTCAACTTTGGGAGTACCTATCCGCGGCTACCTCC 2462
2179 CGCTGCGGCTGACGCGGCTGCTCAACTTTGGGAGTACCTATCCGCGGCTACCTCC 2238
2463 GAACCGCGCAGCGGCTGACGCGGCTGCTCAACTTTGGGAGTACCTATCCGCGGCTACCTCC 2522
2239 GAACCGCGCAGCGGCTGACGCGGCTGCTCAACTTTGGGAGTACCTATCCGCGGCTACCTCC 2298
2523 GCTGGAGCGGGGACGAGGAGGCGGACATGCTGTTTCATCGGACCATCACGACGAGTT 2582
2299 GCTGG-----AGCGCGACCGGAGCGCGGCTTCCATCCACCATCACGAGCCAGAT 2349
2583 CCAGACCATCTGGGCACTCTGCTCATCGAGATCTCTTCCAGCATCTCTCCGACGAGGT 2642
2350 CCAGACCATCTGGGCACTCTGCTCATCGAGATCTCTTCCAGCATCTCTCCGACGAGGT 2409
2643 GTACTCTGGCAGCGTGAAGCGCTGATCGCTGAGACGCTGAGACGCGGCTGATGC 2702
2410 GTACTCTGGCAGCGTGAAGCGCTGATCGCTGAGACGCTGAGACGCGGCTGATGC 2466
2703 GTTCAAAAGATTGGGAGCGGCTGCTGAGATGAGATCGGATCAAGACGATGAACGA 2762
2467 GTTCAAAAGATTGGGAGCGGCTGCTGAGATGAGATCGGAGCGGATGGTGGGCGAGAACCG 2526
2763 CAGTCCGAGCTTGAAGAACCGGAGGCGCTGTGGAATGCCGTATGCTGTGTACCC 2822
2527 CGACCGCAGCTGAGGAGAACGAGGAGCGGCGGCGGAGTTCCTTCCATGCTGTCTACCC 2586
2823 CAACGCTCGACGTTTACCGGAGAGCGGAGGCGGCTTACTGCGCATGGGCAATCCCA 2882
2587 CAACGCTCTGACCAAGTGGCG-----CCGCGCGAGGCGCTCACTGCGCAAGGCGCATCCCA 2643
2883 CAGCATCTCCATATGAGC 2900

Db 2644 CAGCATCTCCATCTGAGC 2661
RESULT 12
US-10-132-350-11
; Sequence 11, Application US/10132350
; Publication No. US2003016685A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxxygenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2595)
US-10-132-350-11
Query Match 42.3%; Score 1325.6; DB 14; Length 2595;
Best Local Similarity 71.7%; Pred. No. 0;
Matches 1905; Conservative 0; Mismatches 679; Indels 72; Gaps 10;
QY 246 CGGGTTCGCGACCGCTGACGCGGAGAAAGAAACAAGAGCGCTGGAGCGGCAAGTCCG 305
Db 9 CGGGATCATCGACGGGCTGACGGGCGGCGAACAAGCATGCGCGGCTCAAG-----57
QY 306 CGGCACCGTGGAGTGGTCAAGAAAGGAGGTGCTGACGCTCGGCGACTTCAACGCTCCCT 365
Db 58 -GGACAGTGGTGTCTCATGCGCAAGACGCTGCTGACCTCAACGCTTCGCGGCGCACCGT 116
QY 366 CTTGACGCGCTGCTCAAGATCTCTGGCTGGGACGAGCGCTCGCTTCAGCTGCTGAG 425
Db 117 CTTGACAGCATCAGCGAGTTCCTCGGCA-----AGGGGCTCACCTGCCAGCTCATCAG 170
QY 426 CGCACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 485
Db 171 CTTCAACCTCTGCTGACGCGCAACAAGCGGCAACCGGCGGCGGCTCGGGCGGCGGCGG 230
QY 486 GGAGAGCGGCTGGTGTGCTCAAGTCCACGCGCGGACGCGGAGACCGGTGTACCGGCTGAG 545
Db 231 GGAGAGTGGCTGACGAGCTGCGCTGCTGACGCGGCGGCTCAAGTTCGCGCTCAC 290
QY 546 CTTGAGTGGGA---GAGTGGAGGATCCCGGCGGCGGCTCTGCTGAGAACCTGCA 602
Db 291 GTTCACTGGGAGTGGAGAGCTGGGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 350
QY 603 GCACGCGGCTGCTTCTTCTCAAGAGCTCACCTCGAGGCGGCTCCAGGAGGCGGCGGCGG 662
Db 351 GCGCGCGGCTTCTTCTTCAAGACATCACTCTGACGAGCTGCGGCGGCGGCGGCGGCGG 410
QY 663 CTTCTGCTGCGCAACTCTGCTGGGTCTACCCGCAACAAGCTCTATCCCAAGAACGCACTTT 722
Db 411 CACCTTCTGCGCAACTCTGCTGGGTCTACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCT 470
QY 723 CTTGCGCAACGACGCTTCTGCGGAGCAAAATGCGGCGGCGGCTTGGTCCCTTATCGGCA 782
Db 471 CTTTCCAAACATAGTACCTACCTGCGCAAGCCAGATGCGCGGCGGCGGCTGAAGCGGCTACC 530

Qy 783 AGATGAGCTCAAGATTCCTCGTGGCGACGATAATCTCTGGACCATACACAGAGCATGATCG 842
Db 531 CGAGAGCTCGCAACCTCCGCGCGACGACACGAGGCGCCCTTACAGAGACACGACCG 590
Qy 843 CGTCTACGGTTACGACTTACTACATGACCTTGGTGTATCCCGACAAAGGCGAAGAGACCG 902
Db 591 CGTGTACCGCTACGACCTTACTACAGACCTTCGCGAGCGCCGCGCGC-----AACCC 644
Qy 903 TCGGCCGATCCTCGGTGGCGACCAAGAACACCCGATATCCCGCTCGCTGCAGAACTGGCGG 962
Db 645 GCGCCCATCTCGCGCGCTCGCGGACCAACCCGATACCCGCGCGCTGCGGACACGCGCG 704
Qy 963 GCACCGACAAAGAACACCCAAATTCGGAGACGAGCTTCTCTGCTGACCTGACAT 1022
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Qy 1383 GAGAGAGACATTTCAGCGGTGAACCCAGTAATCATCAACGCTGACGAGGTTCCCGCG 1442
Db 1095 GCGGAGGTGCTCGCGCGCTCAACCGATGGTGTATCAGCGCTCACGAGTTCCGCGC 1154
Qy 1443 TAAAGCACCTTGACCAAGGCAAGTACGGAGACCAACAGCAAGATCACTGAAGTCA 1502
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Db 1215 CATCGAAGAACCTCGAGGCGCTTACGGTGCAGCGCGCTGACCGCAACAGGCTCTA 1274
Qy 1563 CATCTAGACCAACCATGACCAATTTTATGCGGTACTCTGACGAGATCAACGAGCTGAGGG 1622
Db 1275 CATCTGAGCACCAACGACCGCTTATGCGGTCTCTCATCGAGCTCAACAACTGGAGGG 1334
Qy 1623 GAATTCATCTACGCGACGAGGCTGTCGTTGCGAGACGCACTGAGGAACAAGAGGCTCTT 1562
Db 1335 TAACTTCACTACGCGCAACGAGACCTCTTCTTCTCGCGGGGACGCGAGGCTCGCGC 1394
Qy 1683 CTTGGCCATCGAGTGAAGCTGCGCCACCTCTGACGCGCAGCAGCGCGCGGTTCAGCAA 1742
Db 1395 CTTGCTATCGAGCTACGAGCGCTGATATCGAGCGGACCTTACCGTGGSCCAAGAGCAA 1454
Qy 1743 GGTGTACACCCCGGCTCACCGCGCTGAGGGGCACTGTGGAGCTCGCCAAAGGCTTA 1802
Db 1455 GGTCTACACCGCGCGCTCGAGCGCTCGAGGGCTGGGTGGAGCTCGCCAAAGGCTTA 1514
Qy 1803 TGCCTGCTAAACGACTTCTGCTGGCATCAGCTGATCAGCACTTGGCTGAACACGACGCG 1862
Db 1515 TGTGCGCGTCAACGACTTGTGCTGGACCACTCGTCAGCCACTGCTGAGCACTGAGCAAGC 1574
Qy 1863 GGTGATCGAGCGCTTGTGTAATCGCGCAAAACCGGACGCTCAGCGTGGTGCATCCCGTGCA 1922

RESULT 13

Db 1575 GGTGATGAGCGGTTTGTGATCGCGAGAACCGGACGCTGAGCGCTGACGACCCGCTGCA 1634
Qy 1923 CAAGCTGTGAGCGCGACACTACCGTGCACGCTCAACATCAACCGCTTGGCACCCAGAC 1982
Db 1635 CAAGCTCTGAGCTGCACTTCCGCGACACATGACCATCAACGCGTGGCGCGGAGAC 1694
Qy 1983 ACTCATAAACCGCGCGCGCTTTCGAGCGCACCGTGTTCCTCTCAAGTACGCGCTGG 2042
Db 1695 GCTCATCAACCGCGCGCGCATCTTCGAGATGACCGTCTTCCCGGCAAGTACGCGCTGG 1754
Qy 2043 GATGTCGGCACAGTGTACAGAGCTGGAATTTCAACGAGCAGGCTCTCCCGACAGATCT 2102
Db 1755 CATGTCCTCGTGTGTATCAAGAGCTGGAATTTCAACGAGCAGGCGCTTCCCGCGACCT 1814
Qy 2103 CGTCAAGAGAGGTGTGCTGTGCGGACCAAGTCAAGCCCATATGCTGTGCGATGCTGAT 2162
Db 1815 CGTCAAGAGGCGCTGCGGTGGCGGACCCCTCCAGCGCTGTACAAAGTGGCGCTGCTGAT 1874
Qy 2163 CAAGGACTACCCCTATGCTGTTGACGGGCTCGTCTCATCTGTGTGGCGGATCGAGCGGTGG 2222
Db 1875 CGAGGACTTACCCGTACCGGACGAGCGGCTGGCCATCTTGGACGCGCATCGAGCAGTGGT 1934
Qy 2223 CAAGGAGTACCTGGACATCTACTACCTTAACGACGCGGAGCTCCAGCGTGCAGTGGAGCT 2282
Db 1935 GGGCGAGTACTCTGGCCATCTACTACCCGACGACGCGCGCTGCGGGCGACGAGGAGCT 1994
Qy 2283 GCAGCGTGTGGAGAGGCTCGTGGAGGCGCACGCGGACCTCAAGGACCCGAGACTG 2342
Db 1995 GAGGCGTGTGGAGAGGCTCGCGAGGTCGGGACGCGGACCAAGGACGCGCCCTG 2054
Qy 2343 GTGGGCCAGGATGGAACCCGTCACGAGCTGGCTAGGGCGTGCACGACCATCATCTGGGT 2402
Db 2055 GTGGGCCAAGATGAGGCGGCTGTGCGAGCTGCGCAGCGCTGCACACCATCATCTGGAT 2114
Qy 2403 GGCATCGCGCTGCACGCGGCTGTCAACTTTGGGAGTACCCATACGCGCGGTACTCCC 2462
Db 2115 CGCTGCGCGCTGCACGCGCGCTCAACTTCGCGCAGTACCCGTACGCGGGGTACTCCC 2174
Qy 2463 GAAACCGCGCGCGCGACGCGCGCGCGATGCGCGGAGCGAGCGACCAAGTACAGAA 2522
Db 2175 GAAACGCGCGCGCGAGCTGAGCGCGCGCGATGCGCGGAGCGCGAGCAAGGAGTACGAG 2234
Qy 2523 GCTGGAGCGGGGAGAGGAGGCGGACATGCTGTTTATCCGACCATCACCAGCGAGTT 2582
Db 2235 GCTGG-----AGCGGACCGCGGCGGCTTATCCACCATCATCAGCGCGAGAT 2285
Qy 2583 CCAGACCATCTGGGCACTCTCGCTCATCGAGATCTCTTCAAGCACTCTCTCCGACGAGGT 2642
Db 2286 CCAGACCATCATCGGCACTCTCGCTCATCGAGATCTCTTCAAGCACTCTCTCCGACGAGGT 2345
Qy 2643 GTACTCGCGCGAGCGTGCAGCGCTGATCGCTGGAAGTGCAGCGCAAGGCGCTGATGC 2702
Db 2346 GTACTCGCGCGAGCGGACACCCCGA---GTGGACCTCGGACCGCGCGGCTGCGCGC 2402
Qy 2703 GTTCAAAAGATTTCGGAGCGCGCTGGTGCAGATTGAGATTCGATCAAGACGATGAACGA 2762
Db 2403 GTTCAAGAGTTTCAGGACGCGCTGGTCAAGATCGAGGCAAGGTGGTGGCGGAGAACCG 2462
Qy 2763 CAGTCCGCACTTGAAGAACCGGAGGCGCTGTGGAAATGCGGTAATGCTGCTGTATCCC 2822
Db 2463 CGACCGCGAGCTGAGGAACAGGAACCGCGCGCGAGTTCCCTTACATGCTGTCTATCCC 2522
Qy 2823 CAACAGCTCGGACGTTTACCGCGGAGAGGCGCGGCGGCTTACTGCGATGGGCAATCCCCA 2882
Db 2523 CAACACCTTGTACCAACAGTGGCG---CGCGCGAGGCTGCTGCGCAAGGCAATCCCCA 2579
Qy 2883 CAGCATCTCCATATGA 2898
Db 2580 CAGCATCTCCATCTGA 2595

Qy	935	CGTATCCCCGTGCGTGAGAACTTGGCCGGGACCCAAACAAGAAAGACCCAAATTCGGAGA	994
Db	778	CCTACCCGCGCGCTGCGCACCGCGGGAAGCCCAAGAGCGACCCCAAACAGCGAGA	837
Qy	995	GCAGGCTTTTCTCTGCTGAACCTCAACATCTACGTCGCGGTGACGAACGCTTTGGGCATC	1054
Db	838	GCAGGCTCAGCTTGCTGACGGCGAAGTCTACGTGCGCGGACGACGCTTCGGCCACA	897
Qy	1055	TCAAGATGTCGGACTTCTTTGGGTATCTGCTGAAGACGATCATCGAGGCTGTGTTCTCCAA	1114
Db	898	TCAAGAAGTCGGACTTCTACGGCTAGCGCCATCAAGGCGTGTGTGAACGCGCTCATCCCG	957
Qy	1115	CACCTGGGACTTTCTGTCGATGACACGCCCAAGAGTTCGATTCTGTTTGAGGATATCCTCG	1174
Db	958	CAATCCGCACCTACGTCGACTCTGCGCCGGCGAGTTCGATCTCTCAAGGACATCATGA	1017
Qy	1175	GGCTCTACGAGCTGGGCCAGAGGCCACCAACAACCCACTGATAGCAGAGATCAGGAAGA	1234
Db	1018	AGCTGTACGAGGCGGGATCCAGCTGCCCAAAATACAGCCCTCGAGGACCTTCGGGAAGC	1077
Qy	1235	AGATCCCCAGCGAGTTCCITTCGAAGCATTTCTGCCGAACGCTAGCCATGACCAACCCCTAA	1294
Db	1078	AGTTCCCATCTCGAGCTCGTCGAAGATGTCTCTCCGCTGCGCGGC---GACTACTCTCTCA	1134
Qy	1295	AGATGCCCTTCCAAATGTTCATCAAAATCAGATGTGTGAAAAGGCTCCGGAGTTTAAAGT	1354
Db	1135	AGCTCCCATCGCGCAGATCATCAAA-----GAGGACAAGA	1170
Qy	1355	TTGGCTGAGGACTGAGGAAGTTCGAGAGAGACACTTCGAGCGGTGAACCCAGTAA	1414
Db	1171	CAGGTTGGATGACAGATGAGGATTTTGGACGGGAGATTTCTGCGCGCGTGAACCCCATGC	1230
Qy	1415	TCATCAAACTGTGACGGAGTTCCTCCGCTTAAAGACCTCGACCCCAAGGACGACTACGGAG	1474
Db	1231	TCGCTAAGCTCTCACGGAGTTCCTTCGAGGAGCAGTCTTGACCCGACGACGATCGGG	1290
Qy	1475	ACCACACAGCAAGATCACTGAAGCTCAATCCGGCATAACTATGGAGGCGCTTCGGTGC	1534
Db	1291	ACCACACAGCAATCAGGAGCGGACCTCGAGAAACAGCTCGAGGCGCTTCAACGCTGC	1350
Qy	1535	AGAACCACTGAGGAACAGAGGCTCTTCATCTCTAGACCAACATGACCATTCATGCCGT	1594
Db	1351	AGCAGCGCTGCACGGCAACCGGCTCTACATCTCGACCAACACGAACTTCATGCGCT	1410
Qy	1595	ACCTCAGCAGATCAACGAGCTGAGGGGAATTCTACTACGCCAGCAGGACCTACTGT	1654
Db	1411	TCCTGCTCAGGTGAACAGCCTGGAGGGAACCTTCATCTACGCCACGAGACCGTCTGT	1470
Qy	1655	TCCTGAAGACGATGCGACGCTGAGCCCTTGGCCATCGAGCTGAGCTGCCCCACCTTG	1714
Db	1471	TCCTGCGCGCAGCGACGCTGTGCTCGGTCGCCATCGAGCTGAGCTGCGCGAGCTCC	1530
Qy	1715	ACGGCCAGACGCGCGCGGTTCAGCAAGGTGTACACCCC---GGCTCACACCGGCGTCTG	1771
Db	1531	GGGACGGCTTGACACCGGCCAGAGCACCGTGTACAGCCCCAAGTCGACACCGGCGGG	1590
Qy	1772	AGGGCCAGCTGTGGCAGCTGCGCAAGGCTTATGCTCTGGTAAACGACTCTGCTGCGCATC	1831
Db	1591	AGGCGTGGGTGTGGCACTTGGCCAAAGCCCTAGCCAAACGTGAACGACTACTGCTGGCAC	1650
Qy	1832	AGCTGATCAGCCACTGGCTGAACACAGCCCGGTGATCGAGCGCTTCGTAATCGGACAA	1891
Db	1651	AGCTCATCAGCCACTGGCTCAACCCACGCGTGTATGAGCGGTCTGTGATCGCACCA	1710
Qy	1892	ACCGGAGCTCAGCGTGTGTGCTATCCGCTGCAACAAGCTGTGAGCCGCGACTACCGTGACA	1951
Db	1711	ACCGGAGCTCAGCGTGAAGCGCACCCCGTGCACAAAGCTCCTCTCGCGCGCATACCGTGACA	1770
Qy	1952	CGCTGAACATCAACGCCCTGGGACGCGCACACTCATCAACGCGCGCGCGCTTCGAGC	2011
Db	1771	CCATGAACATCAACTCAACGCGCGCCAGTGTGTCTGTCAAACGCGCGCGCATCTTCGAGA	1830
Qy	2012	GCACCGTGTTCCTGCAAAGTACGCGCTCGGGATGTGCGCAGACGCTGTACAAGAGCTGGA	2071

1831 Db CCACCGTCTTCCCGCGCAGTACGCGTTCGAGATGCTCTCCGTCATCTCAAGGACTGGA 1890
2072 Qy ATTTCACGAGAGGCTTCCGAGCAGATCTCTGTCAGAGAGGTGGTGTGCGCGACC 2131
1891 Db ACTTCACAGAGAGGCTTCCCTGACACCTAATCAAGAGAGGCAATGGCGGTGCGAGACC 1950
2132 Qy AGTCAAGCCCATATGTTGTCGCGACTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGC 2191
1951 Db CGTCGAGCCCGTCAAGGTACGCGTCTGCTGAGGACTACCGGTACGCGTTCGAGCGGC 2010
2192 Qy TCGTCATCTGTTGGCGGATCGAGCGGTGGGTCAAGAGTACCTTGGACATCTACTACCTTA 2251
2011 Db TGGCCATCTGCGACGCGCATCGAGAGTGGGTGAGGAGTACCTTCGCGCTTACTACCCCA 2070
2252 Qy ACGACGCGGAGCTCCAGCGTGAAGTGTGAGAGTGGTGGTGAAGAGGAGTGGTGGAG 2311
2071 Db ACGACGCGGTGCTGCGCGGAGAGTGGAGCTGAGCGGTGGTGAAGAGGAGCGCGAGG 2130
2312 Qy AGCGGACGCGGAGCTCAAGAGCGGAGACTGTTGGTGGCGGAGGATGGACACCTGCCAGC 2371
2131 Db TCGGGACGCGGAGCTCAAGGAGCGCGCTTGGTGGCGGAGGATGGAGAGCGGTGGCGAGC 2190
2372 Qy TGGGTAGGCGGTGACGACCATCATCTGGGTGGCATCTCGCGCTGACGCGGCTGTCAACT 2431
2191 Db TGGTCAAGGCTTGACACCATCATCTGGATCGGTGGGCTTCCAGCGGCGCTCAACT 2250
2432 Qy TTGGCGATACCATAGCCGGGTACTCTCCGAACCGCGCGAGCGCGGCGCGCGCCGA 2491
2251 Db TCGGGCAGTACCGGTAGCGCGGTACTCTCCGAACCGCGCGCTCGCTCAGCGCGGAGCGGA 2310
2492 Qy TGGCGGAGCAGGACGACGACTACAAAGCTGGGAGCGGGGCAAGAGGAGCGGACA 2551
2311 Db TGGCGGCGCGGAGCGGAGAGTACGCGGAGCTGG-----AGCGCAAGCGGAGA 2361
2552 Qy TGGTGTTCATCCGACCATCACGAGGATTCAGACCATCTCTGGGCACTCTCGCTCATG 2611
2362 Db AGGTGTTCGTGCGCACCATCACGAGCAGTTCAGGCGCTCTCGTGGCATCTCGCTGCTGG 2421
2612 Qy AGATCTCTCCAGCACTCTCCGAGAGTGATCTCGGCGAGTACCTCGGCGAGCGTGCATGATC 2671
2422 Db AGATCTCTCCAGCACTCTCCGAGAGTGATCTCGGCGAGTACCTCGGCGAGCG-----CGACACAGG 2478
2672 Qy GTGGAGCTCAGACGCGGAGGCTGATGCGTTCMAAGATTCGGGAGCGCGCTGGTGC 2731
2479 Db AGTGGAGCTCGGAGCGCGGAGGCGGCTTCAAGCGGTTCGGCGCGGCTGACCG 2538
2732 Qy AGATTGAGATCGGATCAAGACGATGAACGAGTCCGAGCTTGAAGACCGGAGGGGC 2791
2539 Db AGATCGAAGAACGCTGCTCACCATGAACGCGGACCTCTCGCTCAAGAACCGCAACGCGC 2598
2792 Qy CTGTGGAATGCGGTATCTGCTGTACCCCAACAGTTCGAGCGTTACCGGCGAGAGG 2851
2599 Db CGGCGAGTTCCTTACAGCTGCTCTACCCCAACACCTCCGACACAGAGGCGG--ACG 2655
2852 Qy CCGAGGGCTTACTGCGATGGGCAATTCACACAGCATCTCCATATGAGCTTGGGAGATT 2911
2656 Db CCGCGGCAATCACCGGCAAGGGCATTCACAAAGCATCTCCATTTGAGTCTGTCTGTCT 2715
2912 Qy GTG 2914
2716 Db GAG 2718

RESULT 14
US-10-425-114-17199
; Sequence 17199, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yifua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53513)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17199
; LENGTH: 2874
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-041-P8_FLI
US-10-425-114-17199

Query Match 40.5%; Score 1268.8; DB 12; Length 2874;
Best Local Similarity 71.0%; Pred. No. 0;
Matches 1831; Conservative 0; Mismatches 687; Indels 60; Gaps 9;
Qy 338 TGGACGTGCGGAGATTCAACGCTTCGCTTCGACGCGGTCCACAGATCTCTCGCTGGG 397
Db 166 TGGACGTGCGGAGATTCAACGCTTCGCTTCGACGCGGTCCCTCGACGCGATCGGCGAGTTCCTCGGCG-- 223
Qy 398 ACGACGCGTTCGCTTCAGCTGTCAGCGCCACCGCGCGGCGGCGGCGGCGGCGG 457
Db 224 ----CGGCGTCACTGCGAGCTTATCAGCTCCACCGCTCGACCTTAAACGCGAACC 279
Qy 458 GTGCAAGGTGGGAAGCGCGGCGACCTGAGAGGCGGTGGTGTCTCAAGTCCACGG 517
Db 280 GCGGGAAGTTGGGCGCGGAGCGGAGCTTGAGAGTGGCTGCTGAACCGCGCGCGCTTC 339
Qy 518 CGGACGCGGAGACCGGTACCGGGTGGCTTCGAGTGGGA---CGAGTCCGAGGATCC 574
Db 340 TGTCAAGGAGAACCGATTCCGGGTCACTTCGACTGGAGGTGGAGAACGAGGATCC 399
Qy 575 CGGCGCGCTCTGCTGTCAGGAACCTGACGACCGCGAGTTCTTCTCAAGACGCTCACCC 634
Db 400 CGGCGCGCATCATCTCAAGAACAAACCGCGCTCCGAGTTCTTCTCAAGACCATCACCC 459
Qy 635 TCGAGGCGCTCCAGGAGGAGCGGCGCTGCTCTGCTGCGGCGGCGGCGGCGGCGG 694
Db 460 TCAAGACGCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519
Qy 695 ACAAGCTCTACTCCAGGAACGATCTTCTTCGCAACGACGACGCTATCTCCGAGCAAAA 754
Db 520 AGTCCAGTACCGGTACACCGCGTCTTCTTCTTCCAGGACGCTACCTCCCGGCGAGA 579
Qy 755 TCGCGGCGGCTTGGTGGCTTATCGGCAAGATGAGTCAAGATCTCCGTCGCGGAGATA 814
Db 580 TCGCGGCGGCGCTGAAGCCCTACCGGACGACGAGCTCCGGAACCTGAGGGGCGGAGCC 639
Qy 815 ATCTGGAACCATACGAGGAGCATGATCGCGTCTACCGTTACGACTACTACAATGAGCTTG 874
Db 640 AGCAGGCGCGGTACGAGGAGCAGCGCGTCTTACCGCTACGAGCTTACAACGAGCTGG 699
Qy 875 GTGATCCCGCAGAGGCGGAAGAGACGCTCGGCGGATCTCTCGGTGGAGCAAGACACC 934
Db 700 GCCTGCTGACAGCGG-----GAACCGCGCGCGCTCTCGGCGGCGGCGGAGGCTCC 753
Qy 935 CGTATCCCGCTCGCTGAGAACTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 994
Db 754 CTTACCGCGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
Qy 995 GCAGGCTTTCTGCTGAACCTGAAACATCTACGTCGCGGTGAGCAAGCGGTTTGGGATC 1054
Db 814 GCAGGCTCAGCTGGTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 873
Qy 1055 TCAGATGTCGAGCTTCTTTGGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTCCAA 1114
Db 874 TCAAGAACTCGGACTTCTACGGCTACGCCATCAAGGCGGTGGTGAACCGGCTCATCCCG 933
Qy 1115 CACTGGGAGCTTTCTGTCGATGACACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1174

Db 934 CAATCCGACCTACGTGACCTGTCGCGCGCGAGTTCGACTCTCTCAAGGACATCATGA 993
QY 1175 GGCTCTACGAGCTGGCGCCAGAGGACCCAAACAAACCACTGATAGACAGATCAGGAAGA 1234
Db 994 AGCTGTACGAGCGCGGATCCAGCTGCTCCCAAAATACACGCCCTCGAGACCTCGGAGC 1053
QY 1235 AGATCCCGAGGAGTTCCTTCGAAGCATTCGCGCGAAGCGTAGCCATGACACCCGGTAA 1294
Db 1054 AGTTCACACTCGAGCTCGTCAAGGATGTCTCTCCCGGTGCGCGGC--GACTACCTCTCTCA 1110
QY 1295 AGATGCCCTTCCAAATGTCTCAATCAATCAGATGTGTTGMAAAAGGCTCCGGAGTTAAGT 1354
Db 1111 AGCTCCCATGCGCAGATCATCAA-----GAGACAGAGA 1146
QY 1355 TTGCTGAGAGCATGACGAGAGTTGCGGAGAGAGACACTTTCAGAGCGGTGAACCCAGTAA 1414
Db 1147 CAGGTTGATGACAGATGAGGAGTTTGACGGGAGATTCTCGCGCGGTGAACCCCATGC 1206
QY 1415 TCATCAAAAGCTCTGACGAGTTCCTCCGCTAAAGCACCTTGGACCCCAAGCAGTACGGAG 1474
Db 1207 TCCTCAAGCTCTCAGCGAGTTCCTCGAGGAGCATCTTGACCCGAGCAAGTACGGCG 1266
QY 1475 ACCACACAGCAAGATCACTGAAGCTCACTTCGCGCATACATGGGAGGCTGTGCGGTGC 1534
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Db 1327 AGCAGGCTCTCAGCGCAACCGGCTCTACATCTCGGACCAACCATGACCACTTCATGCCGT 1386
QY 1595 ACCTCGACGAGATCAACGAGCTGAGGAGGAACTTCATCTACGCGCAGCAGGACCTTACTGT 1654
Db 1387 TCCTGGTCAGGCTCAACAGCTCGAGGAGCACTTCATCTACGCCACACGAGCACTGTGT 1446
QY 1655 TCCTGAAGGAGCATGAGCAGCTGAAGCCCTGGCCATCAGCTGAGGCTGCCACCGCTG 1714
Db 1447 TCCTGCGCGGCGGACGCTGTGTGCGGTGCGCATCGAGCTGAGCTGCCGAGTCC 1506
QY 1715 ACGGCCAGCAGCGCGGCGGTGACCAAGGTGTACACCC--GGCTCACACGCGGCTG 1771
Db 1507 GGGACGCTGACACACCGCAGAGACCCGTGTACACGCCCAAGTCGACCAACCGCGCGG 1566
QY 1772 AGGCCAGCTGTGACAGCTGCGAAGGCTTATGCTGCTGCTAAAGCATCTGCTTGGCATC 1831
Db 1567 AGGCGTGGGTGCGCACTGCGCAAGGCTTACGCCAAAGCTGAGTGTGCTGCGCAC 1626
QY 1832 AGCTGATCAGCCTGCTGAAACGACGACGCGGTGATCGAGCGCTTCGTAATCGCAGCA 1891
Db 1627 AGCTCATCAGCCACTGAGTCAACACCGCCGCTGATGAGAGCGCTTCGTAATCGCACCA 1686
QY 1892 ACCGCGAGCTCAGCGTGTGATCCCGTGAACAGCTGCTGAGCCGCACTACCGTGACA 1951
Db 1687 ACCGCGAGCTCAGCGTGACGACACCCCGTGCAAGCTCTCTCTGCGCGCACTACCGTGACA 1746
QY 1952 CGCTGAACATCAACGCTGCGACGCGCAGACACTCATCAACGCGCGGCGCTTCGAGC 2011
Db 1747 CCATGAACATCACTCAACGCGCGCAGATGCTCTGTCAGCGCGCGGCGATCTTCGAGA 1806
QY 2012 GCACCGGTTCCTGCAAAAGTACGCTGCGGATGTCGGCAGACGCTGTACAAGAGCTGGA 2071
Db 1807 CCACCGCTCTCCCGCGCAGTACGCTTCGAGATGCTCTCCGTCATCTACAAGGACTGGA 1866
QY 2072 ATTTCAAGGAGCGGCTCTCCAGAGATCTCTGCAAGAGAGTGTGGTGTCCCGACC 2131
Db 1867 ACTTCAAGAGCGGCTCTCCCTGACGACCTATCAAGAGGAGTGTGGCGTTCGAGACC 1926
QY 2132 AGTCAAGCCCATATGTTGTCGAGTGTGATCAAGGACTACCCCTATGCGGTTGAGCGGC 2191
Db 1927 CGTCGAGCCGTCACAAGTACGGCTGTGTGTGAGGACTACCCGTACGCTCGGACGGGC 1986
QY 2192 TCCTCATCTGTTGGGCGCATCGAGGCTGGGTCAAGGAGTACCTGAGCATCTACTACCTTA 2251

Db 1987 TGGCCATCTGGCAGCGCCATCGAGCAGTGGGTGACGGAGTACCTCGCCCTCTACTACCCCA 2046
QY 2252 AGCAGCGGAGCTCCAGCGTGAAGTGGAGCTGAGAGTGGTGAAGGAGGTGCGTGAAG 2311
Db 2047 ACGAGCGGTGTGTCGGCGGAGACGTGGAGCTGCAAGCTGTGGTGAAGGAGCGCGGAG 2106
QY 2312 AGCGCAGCGGCACTCAAGGACCGAGACTGTGGTGGCCAGAGATGACACCGTTCAGAGC 2371
Db 2107 TCGGCGAGCGCCAGCTCAAGGACGCGCCCTGTGGTGGCCCAAGATGACAGCGGTGGCGGAGC 2166
QY 2372 TGGCTAGGCGGTGACGACCATCATCTGGTGGCATCGCGCTGACCGCGGTGTCAACT 2431
Db 2167 TGGTCAAGGCTGACACCATCATCTGGATCGCGCTCCAGCGGCGCTCACT 2226
QY 2432 TTGGGAGTACCCATACGCGCGGTACCTCCGAAACCGCGCAGCGCCAGCGCGCCCGA 2491
Db 2227 TCGGCGAGTACCGGTACGCGCGGTACCTCCGAAACCGCGCGCTCCGTCAGCGCGGAAGCGA 2286
QY 2492 TCGGCGAGCGGACGACGACGACGACGAGTGGAGCGGGGAGAGGAGGCGGAGCA 2551
Db 2287 TCGCGCGCGGCGAGCGACGAGTACGCGGAGCTGG-----AGCGCAGCGCGAGA 2337
QY 2552 TGGTGTTCATCGCAGCATCAACAGCCAGTTCAGACCATCTCGGCGATCTGCTTCATCG 2611
Db 2338 AGGTGTTCGTGGCAGCATCAACAGCCAGTTCAGGCGCTCGTCCGATCTCGTGTGG 2397
QY 2612 AGATCCTCTCAAGCACTCTCCGAGAGGTGTACTCGGCGCGGTGACGAGCTGATC 2671
Db 2398 AGATCCTGTCCAGCCACTCTCCGAGAGGTGTACTCGGCGAGCG-----CGACACAAAG 2454
QY 2672 GTTGACGCTCAGACGCCAAGCGCTGGATGCGTTCAAAAGATTCGGGAGCGCGGTGTC 2731
Db 2455 AGTGACGCTCGACGCCAAGCGCGAGGAGCGTTCAAGCGGTTGCGCGCGGCTGACCG 2514
QY 2732 AGATTGAGATCGGATCAAGAGCATGAACGACGATCCGAGCTTGAGAGACCGGAAGGCG 2791
Db 2515 AGATCGAAGACGCTGCTCACCATGAACGCGGACCTCGGCTCAAGAACCGCAACGCGC 2574
QY 2792 CTGTGGAATGCGGTACATGCTGTACTACCCCAACACGTCGAGACGTTACCGCGGAGAGG 2851
Db 2575 CGGCGGAGTTCCTTACGCTGTCTACCCCAACACCTCCGACACGAGGCG--ACG 2631
QY 2852 CGAGGCGGTACTGCGCATGGCATCCCAAGCATCTCCATATGAGCCTGGGCGAGA 2909
Db 2632 CGCGCGCATCACCGCCCAAGGCGCATTCACAAACAGCATCTCCATTTGAGTTCTGTCTGA 2689

RESULT 15
US-10-132-350-3
; Sequence 3, Application US/10132350
; Publication NO. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duveck, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS

LOCATION: (1)...(2622)				Db			
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Query Match				QY			
Best Local Similarity 40.4%; Score 1267.4; DB 14; Length 2622;				1355 TTGCTGGAGACTGACGAAGAGTTTCGAGAGAGACACTTGCAGGCGTGAACCCAGTAA 1414			
Matches 1826; Conservative 71.1%; Pred. No. 0; Mismatches 681; Indels 60; Gaps 9;				Db			
338 TGGACGTCGGGACTCAACGCTCGCTCTGACGCGTCCACAGAGTCTTCGCTGGG 397				1091 CAGGTTGATGACAGATGAGGAGTTTGCACGGGAGATTCTCGCGGGGTGAACCCCATGC 1150			
110 TGGACGTCACAGATCGCGGCTCCCTCTCGACGGCATCGCGAGTTCTTCGGCGC-- 167				QY			
398 ACAGCGGCTCGGCTTCAGCTCGTCAGCGCCACCGCGCGACCCACGAAACGGGGCC 457				1415 TCATCAACGCTCTGACGGAGTTCCCGCTAAAGCAACCTTGAAGCCCAAGGAGTACCGAG 1474			
168 ----CGGCGTCACTGCGAGCTTATCAGCTCCACCGCTGTCGACCCCTAAACACGGCAAC 223				Db			
458 GTGCAAGGTGGGAGGCGGCGCACCTGAGAGAGCGGTGGTGTGCTCAAGTCCACGG 517				1151 TCGTCAAGCGTCTCACGGAGTTCCCTCCGAGGAGCATTTTGACCCGAGCATGACGGCG 1210			
224 GCGGGAAGTTGGGCGGAGCGAGCGCTGGAGCAGTGGCTGTGAACCCGCGCGCTTC 283				QY			
518 CGGACGGGAGACCGGTGTACCGGCTGAGCTTCAGTGGGA---CGAGTCGAGGGCATCC 574				1475 ACCACACAGCAAGATCACTGAAGCTCACATCCGGCATATACTGGGAGGCGCTTCGCTGC 1534			
284 TGTCCAGCGAAGAACAGTTCCGCGTCACTTCGACTGGGAGTGGAGAACGAGGCGATCC 343				Db			
575 CGGCGCGCTCTGCTGTCAGAACTGAGCAACCGCGAGTTCTCTCAAGAGCTCACCC 634				1535 AGAAGCACTGAGGAAACAGAGCTCTTCACTAGACCAACCATGACATTTATGCGCT 1594			
344 CGGCGCGCATCATCGTCAAGAACACACCGCTCCGAGTTCTTCCTCAAGACCATCACCC 403				1271 AGCAGGCGCTGCAACGCAACCGGCTCTACATCTCGACCAACACGACACTTATGCGCT 1330			
635 TCGAGGCGCTCCAGGCAAGGCGACCGTCTGCTTCGTCGCAACTCGTGGGTCTACCCGC 694				QY			
404 TCACGAGCTCCCGCGCCACGGACCATCGTCTTCGTCGCAACTCATGGAATCTACCCGC 463				1595 ACCTCGACGAGATCAACGAGCTGGAGGGAACTTTCATCTACGCGCAGCAGGACCTACTGT 1654			
695 ACAAGCTCTACTCCAGGAAACGATCTTCTGCGCAACGACACCTATCTGCGGAGCAAAA 754				Db			
464 AGTCCAGTACCCTACACCGGCTCTTCTTCTCAACGACACGTACTCTCCCGAGCCAGA 523				1331 TCCTGGTCAAGGTGAACAGCTGGAGGGCACTTTCATCTACGCCACAGGACCGTGTGT 1390			
755 TGC CGGCGGCTTGGTGCCTTATCGGCAAGATGAGCTCAAGATTCTCGTGGCGAGATA 814				QY			
524 TGC CGGCGGCTTGAAGCCCTACCGGACGACGAGCTCCGAACTCCGAACTGAGGCGGAGCACC 583				1655 TCCTGAAGGAGGATGGGACGCTGAGCCCTGGCCATCGAGCTGAGCTGCGCCACCGCTG 1714			
815 ATCTGGAACATACAGGAGCATGATCGGCTTACCGTTACCGTTACGACTACTCAATGACCTTG 874				1391 TCCTGCGCGGCGAGCGGACGCTGGTCCGGTGGCCATCGAGCTGAGCTTCCCGAGTCC 1450			
584 AGCAGGCGCGCTACAGGAGCAGCGCGGCTTACCGCTACGACGCTTCAACGACCTCG 643				QY			
875 GTGATCCGACAGGCGGAGACGCTCGCGCGGATCTCGTGGCAGCGAGACACC 934				1715 ACGCCACGACGCGCGCGCTCAGCAAGGTGTACACCCC---GGTCAACACCGCGCTCG 1771			
644 GCCTGCTGACGCG-----GAACCGCGCGCGCTCTCGCGGACCAAGGAGCTCC 697				1451 GGGACGCGCTGACCAACCGCCAGAGCACCGGTGTACACGCCCAAGTCGACCAACCGCGCG 1510			
935 CGTATCCCGCTCGTGCAGAACTGGCGCGCACCCAAACAAAGAAAGACCCAAATTCGGAGA 994				QY			
698 CTTACCGCGCGCTGCGGACCGCGGGAAGCCACCAAGAGCGACCCCAACAGCGAGA 757				1772 AGGCGCAGCTGTCGACGCTGCGCAAGGCTTATGCTCGGTAAAGACTCTGCTTGGCATC 1831			
995 GCAGGCTTTCTGCTGTAACCTGAACTCTAGCTCCGCGGTGACGACGCTTGGGCATC 1054				Db			
758 GCAGGCTCAGCTGGTTCGAGCGGAGCTCTAGCTGCGCGGACGAGCGCTTTCGGCCACA 817				1511 AGGCGTGGGTGTGACCTGCGCCAGGCTTACGCCAACGCTGTAAGGACTTCTGCTGGCACC 1570			
1055 TCAAGATGTCGAGCTTCTTGGTACTCGCTGAAGACGATCATCGAGGCTGTCTTTCCAA 1114				QY			
818 TCAAGAGTCGAGCTTCTACGGCTACGCGCATCAAGCGCTGGTGAACGCGCTCATCCCG 877				1832 AGCTGATCAGCCACTGCTGCTGAACACGACGCGGTGATCGAGCGGTTCTGTAATCGCGACA 1891			
1115 CACTGGGACTTTCTGCTGATGACACCGCCAGAGTTCCATTTGTTTGAAGTATCTCTCG 1174				1571 AGCTCATCAGCCACTGGCTCAACACCGCGGTGATGAGCGGTTCTGCTGATCGCCACCA 1630			
878 CAATCCGCACTACGTCGACCTTCGCGCGGAGTTTCGACTCTTCAAGGACATCATGA 937				1892 ACCGCGAGCTCAGCGTGGTGTGATCCCGTGCAACAGTGTCTGAGCGCGCACTACCGTGACA 1951			
1175 GGCCTACGAGCTGGGCGGAGGACCCAAACACCACTGATAGCAGAGATCAGGAAGA 1234				Db			
938 AGCTGTACGAGGCGGAGTCCAGCTGCGCAAAATACAGCCCTCGAGGACCTCGGAGC 997				1631 ACCGCGAGCTCAGCGTGACGACCCCGTGCAAGCTCTCTCTGCGCGCACTACCGTGACA 1690			
1235 AGATCCCGCAGGAGTTCTCTGAGGATCTGCGGCAACGCTGAGCATGACACCGCTGAA 1294				QY			
998 AGTTCACACTCGAGCTCGTCAAGGATGTCTCCCGGTGCGCGC---GACTACCTCTCA 1054				1952 CGCTGAACATCAACGCGCTGGCGCGCACGACACTCATCAACGCGCGGCGGTCTTCGAGC 2011			
1295 AGATGCGCCCTTCCAAATGTCATCAATCAGATGTGTGAAAGGCTCCGAGGTTTAAGT 1354				1691 CCATGAACATCACTCAACGCGCGCAGATGCTCTGTCACGCGCGCGGCGATCTTCGAGA 1750			
				2012 GCACCGTGTTCCTTGCAAAAGTACGCGTGGGATGTGGGAGATGCGGACAGCTGTACAAGTGTGA 2071			
				1751 CCACCGTCTTCCCGCGCCAGTACGCGTTCGAGATGTCTCCGTCACTCAAGGACTGGA 1810			
				2072 ATTTCAAGGAGCAGGCTCTCCGCGAGATCTCTGTCAGAGAGGTGCGGCTGCGCGACC 2131			
				1811 ACTTCAAGAGAGGCTCTCCCTGACGACCTATCAAGAGAGCATGCGGCTGCGAGACC 1870			
				2132 AGTCAAGCCCATATGGTGTCCGACTGCTGATCAAGGACTACCCCTATGCGGTTGACGGGC 2191			
				1871 CGTCAAGCCGCTCAAGGTACGGTCTGCTGGTGGAGGACTACCCGTCACGCTCGAGCGGC 1930			
				2192 TCGTCACTCGTGGCGCATCGAGGCTGGGTCAAGGATACCTGGAATCTACTTACCCCTA 2251			
				1931 TGGCCATCTGGCACGCGCATCGAGAGTGGGTGACGAGTACCTTCGCGCTCTACTACCCCA 1990			
				2252 ACAGCGCGAGCTCCACGCTGAGCTGAGCTGAGCGCTGGTGAAGGAGGTGCGTGAGG 2311			
				1991 ACAGCGCGTCTGCGGGCGGACGTTGGAGCTGCAAGGCGTGGTGAAGGAGCGCGCGAG 2050			
				2312 AGGCGCACGGGAGCTCAAGGACGAGACTGGTGGCCAGGATGGAACCGTCCAGCAGC 2371			
				2051 TCGGGACGCGCGCTCAAGGACGCGCCCTGGTGGGCCAAGATGCAAGCGGTGGCGGAGC 2110			
				2372 TGGCTAGGGGTGCACGACCATCATCTGGGTGGCATCCGCGCTGCAACCGCGCTGTCAACT 2431			
				2111 TGGTCAAGGGCTGCACCAACCATCATCTGATCGGTCGGGCTCCAGCGGCGCGTCAACT 2170			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 21:59:41 ; Search time 7580 Seconds

(without alignments)
12346.712 Million cell updates/sec

Title: US-10-059-909-15

Perfect score: 3134

Sequence: 1 ccacgcctccggccgagcg.....aaaaaaaaaaaaaaaaaaag 3134

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107.8	99.2	3135	11	AV103567
2	805	25.7	805	29	CG626033
3	715	22.8	944	29	CG157905
4	698.8	22.3	992	29	CG238091

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
5	660.8	21.1	848	14	CB669925											
6	647	20.6	1158	14	CK161284											
7	639.4	20.4	758	13	CA139868											
8	637	20.3	886	14	CF636987											
9	622.6	19.9	709	13	CA145829											
10	617.6	19.7	772	14	CA279071											
11	603.4	19.3	892	29	CG325032											
12	594.2	19.0	679	14	CA298585											
13	592.6	18.9	707	13	CA135806											
14	591.2	18.9	674	14	CA164910											
15	590	18.8	715	14	CA487017											
16	588.6	18.8	715	14	CA484330											
17	587.8	18.8	696	14	CA165248											
18	577.6	18.4	800	14	CB652144											
19	572.6	18.3	649	14	CA285554											
20	565.6	18.0	715	14	CA172152											
21	565.4	18.0	639	14	CA191428											
22	545.8	17.4	658	14	CA485119											
23	545.8	17.4	664	13	CA113357											
24	544.6	17.4	849	28	BZ794401											
25	542.2	17.3	821	29	CG127849											
26	536.6	17.1	650	14	CA299776											
27	533.4	17.0	642	13	CA107183											
28	530.4	16.9	558	9	AI738271											
29	520.6	16.6	901	14	CA177530											
30	520	16.6	654	13	CA069001											
31	518.2	16.5	608	14	CA259761											
32	512	16.3	604	13	CA139158											
33	511.8	16.3	804	13	CA117590											
34	509.2	16.2	826	14	CB628822											
35	508.2	16.2	1081	13	CA150941											
36	502.8	16.0	968	29	CG204365											
37	497.4	15.9	723	12	BZ258623											
38	493.2	15.7	722	14	CD861927											
39	493.2	15.7	1015	12	BG837969											
40	493	15.7	551	14	CA248559											
41	491.6	15.7	564	14	CA272189											
42	491.2	15.7	516	12	BG267942											
43	489.2	15.6	837	29	CG381850											
44	488.8	15.6	854	29	CG346711											
45	488.8	15.6	916	29	CG381488											

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
5	660.8	21.1	848	14	CB669925											
6	647	20.6	1158	14	CK161284											
7	639.4	20.4	758	13	CA139868											
8	637	20.3	886	14	CF636987											
9	622.6	19.9	709	13	CA145829											
10	617.6	19.7	772	14	CA279071											
11	603.4	19.3	892	29	CG325032											
12	594.2	19.0	679	14	CA298585											
13	592.6	18.9	707	13	CA135806											
14	591.2	18.9	674	14	CA164910											
15	590	18.8	715	14	CA487017											
16	588.6	18.8	715	14	CA484330											
17	587.8	18.8	696	14	CA165248											
18	577.6	18.4	800	14	CB652144											
19	572.6	18.3	649	14	CA285554											
20	565.6	18.0	715	14	CA172152											
21	565.4	18.0	639	14	CA191428											
22	545.8	17.4	658	14	CA485119											
23	545.8	17.4	664	13	CA113357											
24	544.6	17.4	849	28	BZ794401											
25	542.2	17.3	821	29	CG127849											
26	536.6	17.1	650	14	CA299776											
27	533.4	17.0	642	13	CA107183											
28	530.4	16.9	558	9	AI738271											
29	520.6	16.6	901	14	CA177530											
30	520	16.6	654	13	CA069001											
31	518.2	16.5	608	14	CA259761											
32	512	16.3	604	13	CA139158											
33	511.8	16.3	804	13	CA117590											
34	509.2	16.2	826	14	CB628822											
35	508.2	16.2	1081	13	CA150941											
36	502.8	16.0	968	29	CG204365											
37	497.4	15.9	723	12	BZ258623											
38	493.2	15.7	722	14	CD861927											
39	493.2	15.7	1015	12	BG837969											
40	493	15.7	551	14	CA248559											
41	491.6	15.7	564	14	CA272189											
42	491.2	15.7	516	12	BG267942											
43	489.2	15.6	837	29	CG381850											
44	488.8	15.6	854	29	CG346711											
45	488.8	15.6	916	29	CG381488											

AV103567 Zea mays
LOCUS AV103567 3135 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays P00116252 mRNA sequence.
ACCESSION AV103567
VERSION AV103567.1 GI:21206645
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission

Submitted (25-APR-2002)

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,

these are publicly available from ZmDB and may be found by BLAST

searching at MSL.maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from 2mDb:

FEATURES

source
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/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:636769"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 99.2%; Score 3107.8; DB 11; Length 3135;
Best Local Similarity 99.9%; Pred. No. 2.5e-304;
Matches 3131; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy	61	GGAGTTCCACATTCCTCATACAGCGCTGCTTGCCTTCCCTTCCCTTGCCTTGCCTTGC	120
Db	61	GGAGTTCCACATTCCTCATACAGCGCTGCTTGCCTTCCCTTCCCTTGCCTTGCCTTGC	120
Qy	121	TTATTGCGGCACATCATCTCGGCGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG	180
Db	121	TTATTGCGGCACATCATCTCGGCGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG	180
Qy	181	CAGCCAGCCACCGGTTCTTGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG	240
Db	181	CAGCCAGCCACCGGTTCTTGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG	240
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Db	241	TGGCAGCGGCTCGCGGACCGCTGACCGGGAAGAAAGAGGAGCGAGCGAGCGAGCG	300
Qy	301	ATCCGCGGCGAGTGGTCAAGAGGAGTGTGAGAGCGAGCGAGCGAGCGAGCGAGCG	360
Db	301	ATCCGCGGCGAGTGGTCAAGAGGAGTGTGAGAGCGAGCGAGCGAGCGAGCGAGCG	360
Qy	361	TGCTCTCTCGACGCGTCCACAGATCTCGGCTGGGACGACGCGCTTCCAGCTTC	420
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Qy	421	GTACGCGCCACCGCGGCGAGCCCGAGCAACGCGGCGCGTGGCAAGGTGGGAGGCGG	480
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Qy	481	CACCTGGAGGAGCGGTTGCTCAAGTCCACGCGGACGCGGAGCGGAGCGGTTACCG	540
Db	481	CACCTGGAGGAGCGGTTGCTCAAGTCCACGCGGACGCGGAGCGGAGCGGTTACCG	540
Qy	541	GTGAGCTTCGAGTGGGACGAGTGGGAGCGATCCCGGCGCGCTTCTGCTCAGGAACCT	600
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Qy	601	CAGCAGCCAGTTCCTTCAGACGCTCACCTCGAGGGCGTCCAGGCAAGGCGACC	660
Db	601	CAGCAGCCAGTTCCTTCAGACGCTCACCTCGAGGGCGTCCAGGCAAGGCGACC	660
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Qy	721	TTCTTCGCCAAGCAGACATCTGCGGAGCAAAATGCGCGCGCGTGTGCTTATCGG	780
Db	721	TTCTTCGCCAAGCAGACATCTGCGGAGCAAAATGCGCGCGCGTGTGCTTATCGG	780

Db	721	TTCTTCGCCAAGCAGACACCTATCTCCGAGCAAAATGCGCGCGCGTGTGCTTATCGG	780
Qy	781	CAAGATGAGCTCAAGATTCTCGTGGGAGCATATCTCTGAGCATTACCGAGCATGAT	840
Db	781	CAAGATGAGCTCAAGATTCTCGTGGGAGCATATCTCTGAGCATTACCGAGCATGAT	840
Qy	841	CGCGTCTACCGTTACGACTACTACAATGACCTTGGTATCCCGACAAGGGCGAAGAGC	900
Db	841	CGCGTCTACCGTTACGACTACTACAATGACCTTGGTATCCCGACAAGGGCGAAGAGC	900
Qy	901	GCTCGCGCATCTCGTGGGAGCAAGCAACCCGCTATCCCGCTCGCTGCGAGACTGGC	960
Db	901	GCTCGCGCATCTCGTGGGAGCAAGCAACCCGCTATCCCGCTCGCTGCGAGACTGGC	960
Qy	961	CGGCAACCAACAAAGAAAGACCCAAATTCGAGAGCAGGCTTTCTCTGCTGAACCTGA	1020
Db	961	CGGCAACCAACAAAGAAAGACCCAAATTCGAGAGCAGGCTTTCTCTGCTGAACCTGA	1020
Qy	1021	ATCTACGTCGCGCTGAGCAAGCGCTTTGGGATCTCAAGATGTCGAGCTTCCTTGGGTAC	1080
Db	1021	ATCTACGTCGCGCTGAGCAAGCGCTTTGGGATCTCAAGATGTCGAGCTTCCTTGGGTAC	1080
Qy	1081	TCGCTGAAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGGACTTTCTGCTGATG	1140
Db	1081	TCGCTGAAAGACGATCATCGAGGCTGTTCTTCCAAACACTGGGGACTTTCTGCTGATG	1140
Qy	1141	CCCAAGGATTCGATTGTTGAGGATATCTCTGGGCTCTACGAGCTGGGCGGAGAGCA	1200
Db	1141	CCCAAGGATTCGATTGTTGAGGATATCTCTGGGCTCTACGAGCTGGGCGGAGAGCA	1200
Qy	1201	CCCAACCAACCACTGATAGCAGAGATCAGGAAGAGATCCCGAGGAGTTCCTTCGAAGC	1260
Db	1201	CCCAACCAACCACTGATAGCAGAGATCAGGAAGAGATCCCGAGGAGTTCCTTCGAAGC	1260
Qy	1261	ATTCTGCGAAGCGGTAGCATGACCCCGTAAAGATGCCCCCTTCCAAATGTCTATCAA	1320
Db	1261	ATTCTGCGAAGCGGTAGCATGACCCCGTAAAGATGCCCCCTTCCAAATGTCTATCAA	1320
Qy	1321	TCAGATGTTTGAAGAAAGGCTCC--GGAGTTTAAAGTTTGGCTGGAGGACTGACGAAG	1379
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Qy	1380	CGGAGAGAGACATTCGAGCGGTGAACCCAGTAAATCATCAAGCTCTGACGAGTTCCC	1439
Db	1381	CGGAGAGAGACATTCGAGCGGTGAACCCAGTAAATCATCAAGCTCTGAGGAGTTCCC	1440
Qy	1440	CGCTAAAGACCCCTGAGCCCAAGCAGTAGACGAGACACACAGCAAGATCACTGAAGC	1499
Db	1441	CGCTAAAGACCCCTGAGCCCAAGCAGTAGACGAGACACACAGCAAGATCACTGAAGC	1500
Qy	1500	TCACATCCGGCATAAATGGGAGGCTGTGCTGTCAGAAACGCACTGAGGAACAGAGCT	1559
Db	1501	TCACATCCGGCATAAATGGGAGGCTGTGCTGTCAGAAACGCACTGAGGAACAGAGCT	1560
Qy	1560	CTTCATCTAGACACCATGACATTTTCATGCGCTACCTCGAGAGATCAACGAGCTGGA	1619
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Qy	1620	GGGGAATTCATCTACGCCAGCAGGACCTTACTGTTCTTGAAGGACGATGGCAGCTGAA	1679
Db	1621	GGGGAATTCATCTACGCCAGCAGGACCTTACTGTTCTTGAAGGACGATGGCAGCTGAA	1680
Qy	1680	GCCCTCGCATCAGCTGAGCTGCCCACTTCGAGCGGACGAGCGCGCGGCTCAG	1739
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Qy	1740	CAAGTGTATACCCCGGCTCACACCGGCTCGAGGGCCAGCTGTGGAGCTTCGCCAAGGC	1799
Db	1741	CAAGTGTATACCCCGGCTCACACCGGCTCGAGGGCCAGCTGTGGAGCTTCGCCAAGGC	1800
Qy	1800	TTATGCTGCGTAAACGACTCTGCTGCTCAGTATCAGGCTGAGCTGCTGCTGACGCA	1859
Db	1801	TTATGCTGCGTAAACGACTCTGCTGCTCAGTATCAGGCTGAGCTGCTGCTGACGCA	1860

QY	1860	CGCGTGATCGAGCGGTTTCGTAATCGCGACAAAACGGCGAGCTCAGCGTGTGATGCCGT	1919
DB	1861	CGCGGTGATCGAGCGGTTTCGTAATCGCGACAAAACGGCGAGCTCAGCGTGTGATGCCGT	1920
QY	1920	GCACAGTGTGTGAGCCGGCACTACCGTGAACCGCTGAAATCAACACGCCCT- GGCACGCC	1978
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QY	1979	AGACACTCATCAAACGCCCGCGCGCTTCGAGCGCACCGTGTTCCTGTCAAAAGTAGTACGCGC	2038
DB	1981	AGACACTCATCAAACGCCCGCGCGCTTCGAGCGCACCGTGTTCCTGTCAAAAGTAGTACGCGC	2040
QY	2039	TGGGGATGTCCGCGACAGCTGTATCAAGAGCTGGAAATTTCAACGAGCAGGCTCTCCACAGCAG	2098
DB	2041	TGGGGATGTCCGCGACAGCTGTATCAAGAGCTGGAAATTTCAACGAGCAGGCTCTCCACAGCAG	2100
QY	2099	ATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAGTCAAGGCCNATATGGTGTCCGACTGC	2158
DB	2101	ATCTCGTCAAGAGAGGTGTGGCTGTGCGGACCAAGTCAAGGCCNATATGGTGTCCGACTGC	2160
QY	2159	TGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGCTCATCTGGTGGGCGATCGAGCGGT	2218
DB	2161	TGATCAAGGACTACCCCTATGCCGTTGACGGGCTCGCTCATCTGGTGGGCGATCGAGCGGT	2220
QY	2219	GGGTCAAGGAGTACTCTGGACATCTACTACCTTAACGACGCGAGCTCCAGCGTGAAGTGG	2278
DB	2221	GGGTCAAGGAGTACTCTGGACATCTACTACCTTAACGACGCGAGCTCCAGCGTGAAGTGG	2280
QY	2279	AGCTCGAGCGGTGTGAAAGAGAGTGGTGTGAGAGGCGCACGGGACCTCAAGACCGAG	2338
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QY	2339	ACTGGTGGCCAGGATGGACACCGTCCAGAGCTGGCTAGGGGGTGCACAGACCATCATCT	2398
DB	2341	ACTGGTGGCCAGGATGGACACCGTCCAGAGCTGGCTAGGGGGTGCACAGACCATCATCT	2400
QY	2399	GGGTGGCATCCGCGCTGCACGCGCTGTCAACTTTGGGCAATACCATAGCGCGGTACC	2458
DB	2401	GGGTGGCATCCGCGCTGCACGCGCTGTCAACTTTGGGCAATACCATAGCGCGGTACC	2460
QY	2459	TCCCGAACCCGCGCACGCGCCAGCGCGCCGATGCCGAGCACGAGCAGCCACGACTACA	2518
DB	2461	TCCCGAACCCGCGCACGCGCCAGCGCGCCGATGCCGAGCACGAGCAGCCACGACTACA	2520
QY	2519	AGAGCTGGGAGCGGGCGAGAGGCGGACATGTTGTTTCATCCGACCATCACAGGCC	2578
DB	2521	AGAGCTGGGAGCGGGCGAGAGGCGGACATGTTGTTTCATCCGACCATCACAGGCC	2580
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QY	2639	AGGTGTACCTCGGCCAGCGGTGACGAGCTGATCGCTGGAGCTCAGAGCGCAAGGCGCTGG	2698
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QY	2699	ATCGGTTCAAAAGATTCCGGAGCGCGGTGGTGCAGATTGAGAAATCGGAATCAAGACATGA	2758
DB	2701	ATCGGTTCAAAAGATTCCGGAGCGCGGTGGTGCAGATTGAGAAATCGGAATCAAGACATGA	2760
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Qy	2399	GCCTGCGCATGCTGTTTCTTCATTGGTTTCTCAGTCTCAGGCTAGGGATGGAGATCATCA	2399			
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Qy	2999	CCATGATCTTTTAGGGTTGAGAGAGAGTCCACGCTTGAATATTTGTCTGATGATGTA	3058			
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Qy	3059	ATTCCTGGTTAAATAAATAAGTTCGTCAGTTTCATTTCTTAAAAAAAACAAAAA	3118			
Db	3061	ATTCCTGGTTAAATAAATAAGTTCGTCAGTTTCATTTCTTAAAAAAAACAAAAA	3120			
Qy	3119	AAAAAAAAAAAAA	3133			
Db	3121	AAAAAAAAAAAAA	3135			
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CC626033/c						
LOCUS	CC626033	805 bp	DNA linear GSS 19-JUN-2003			
DEFINITION	CGWH42TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0582G12, genomic survey sequence.					
ACCESSION	CC626033					
VERSION	CC626033.1					
KEYWORDS	GSS.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	1 (bases 1 to 805) Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Reeseck,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.					
TITLE	Consortium for Maize Genomics					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Cathy Whitelaw					
TIGR						
9712 Medical Center Drive, Rockville, MD 20850, USA						
Tel: 301-838-5843						
Fax: 301-838-0208						
Email: whitelaw@tigr.org						
Seq primer: TR						
Class: sheared ends.						
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Best Local Similarity 100.0%; Pred. No. 3.1e-72;						
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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Qy	2276	TGAGCTGCAGGCGTGGTGGAAAGGAGGTGCGTGAGGAGCGCA CGCGCACCTTCAAGGACC	2335			
Db	745	TGAGCTGCAGGCGTGGTGGAAAGGAGGTGCGTGAGGAGCGCA CGCGCACCTTCAAGGACC	686			
Qy	2336	GAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGGTGCACGACATCA	2395			
Db	685	GAGACTGGTGGCCAGGATGGACACCGTCCAGCAGCTGGCTAGGCGGTGCACGACATCA	626			
Qy	2396	TCTGGGTGCATCCGCGCTGCACGCGGGTGTCAACTTTGGGCGAGTACCATACGCCGGGT	2455			

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Db      625  TCTGGTGCATCCGCGTGCACGCGGTGTCACATTGGGAGTACCCATACGCCGGT 566
QY      2456  ACCTCCGAAACGGCCGAGCGCGCGCCGATGCCGAGGCCAGGCCAGCCAGCT 2515
Db      565  ACCTCCGAAACGGCCGAGCGCGCGCCGATGCCGAGGCCAGGCCAGCCAGCT 506
QY      2516  ACAAGAGCTGGAGCGGGGAGAGAGGCGGACATGCTGTTTCATCCGACCATCACCA 2575
Db      505  ACNAGAAGCTGGAGCGGGGAGAGAGGCGGACATGCTGTTTCATCCGACCATCACCA 446
QY      2576  GCCAGTTCAGACCATCTCGGCGATCTCGCTCATCGAGATCCTCTCAAGCATCTCCG 2635
Db      445  GCCAGTTCAGACCATCTCGGCGATCTCGCTCATCGAGATCCTCTCAAGCATCTCCG 386
QY      2636  ACGAGGTGTACTCTCGGCGAGCGTGACGAGCGCTGATCGCTGACGCTCAGACGCCAAGCGC 2695
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QY      2696  TGGATGCGTTCAAGAGATTCGGGAGCGCGGCTGGTGAGATTCGATTCGATTCGATTCG 2755
Db      325  TGGATGCGTTCAAGAGATTCGGGAGCGCGGCTGGTGAGATTCGATTCGATTCGATTCG 266
QY      2756  TGAAGCAGTCGGGATTCGAGACCGGAGAGCGGCTGGTGAGATTCGATTCGATTCGATTCG 2815
Db      265  TGAAGCAGTCGGGATTCGAGACCGGAGAGCGGCTGGTGAGATTCGATTCGATTCGATTCG 206
QY      2816  TGTACCCCAACGCTCGACGCTTACCGCGAGAGAGCGGCGCTTACTGCCATGGGCA 2875
Db      205  TGTACCCCAACGCTCGACGCTTACCGCGAGAGAGCGGCGCTTACTGCCATGGGCA 146
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QY      2936  TCGCGCGTGCATGTTTCTTCATTTGTTGTCAGTCTCAGGTTAGGCGATCGAGATC 2995
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QY      2996  ATACCATGATCTTTGTAGGTTGAG 3020
Db      25  ATACCATGATCTTTGTAGGTTGAG 1

RESULT 3
CG157905
LOCUS      944 bp      DNA      linear      GSS 21-AUG-2003
DEFINITION  FUFQD69TS ZM.0.6_1.0_KB Zea mays genomic clone ZMBrta0707L18,
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ACCESSION  CG157905
VERSION    CG157905.1 GI:34048706
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 944)
            Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
            Maize Genomics Consortium
            Unpublished (2003)
            Other GSSs: FUFQD69TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
            Location/Qualifiers

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ORIGIN

Query Match      22.8%; Score 715; DB 29; Length 944;
Best Local Similarity 88.8%; Pred. No. 3.4e-63;
Matches 788; Conservative 0; Mismatches 90; Indels 9; Gaps 1;

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QY      2170  TACCCTATGTCGCTTACGCGGCTCGTCTATCTGTCGTCGTCGATCGAGCGTGGTCAAGGAG 2229
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QY      2230  TACCTGGACATCTACTACCTTAACGACGCGGAGCTCGAGCGTGGTCAAGGAG 2289
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QY      2290  TGGTGAAGAGGTGCTGAGGAGCGCAACGCGACCTCAAGGACCGGAGACTGTGGGCC 2349
Db      238  TGGTGAAGAGGTGCGCGAGGAGCGCAACGCGACCTCAAGGACCGGAGACTGTGGGCC 297
QY      2350  AGATGGACACCGTCAGCAGCTGGTGGGAGTCGACGACCATCATCTGGTGGTCATCC 2409
Db      298  AGATGGAGCGCTCAGCGGCTGGCGAGGCGTCGACGCGTCACTGTGGTAGCGTCC 357
QY      2410  GCGCTGCACGCGGCTGTCAACTTTTGGGAGTACCCATACGCGGCTACTCCCAACCGG 2469
Db      358  GCGCTGCACGCGGCTGTCAACTTTGCGGAGTACCCGTACGCGGCTACTTCGCAACCGG 417
QY      2470  CCGAGCGCACCGCGCGCGGATGCGGAGCGCAGCAGCAGCTACAAAGAGCTGGGA 2529
Db      418  CCGAGCGTGAAGCGCGCGGATGCGGAGCGCGGAGCGCAGCAGCTACAAAGAGCTGGAG 477
QY      2530  GCGGGGCGAAGGAGGCGGACATGCTTTCATCCGACCATCACGAGCAGTTCAGACCC 2589
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QY      2830  TCGGACGTTACCGGAGAGCGCGGCTTACTGTCATGGGCAATTCCTCAAGAGCATC 2889
Db      778  TCGGATGTCACCGGCGAGAGCGGCGGCTACTGTCATGGGCAATTCCTCAAGAGCATC 837
QY      2890  TCCATATGAGCTGGCGAGATTTG-----GTCGCTAGTAGTAATTTGTTGCTGCTGGC 2940
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Genomic survey sequence.
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CG238091.1 GI:34137977
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 992)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGRHX42TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
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FEATURES
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Query Match 22.3%; Score 698.8; DB 29; Length 992;
Best Local Similarity 89.8%; Pred. No. 1.4e-61;
Matches 799; Conservative 0; Mismatches 2; Indels 89; Gaps 1;

QY 1845 CTGGCTGAACACGACGCGGTGATCGAGCGCTTCTGTAATCGCGACAAACCGGACGCTCAG 1904
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QY 1905 CTGGTGTATCCCGTGCACAAAGCTGCTGAGCGCCGCACTACCGTGACACGCTGAACATCAA 1964
Db 163 CTGGTGTATCCCGTGCACAAAGCTGCTGAGCGCCGCACTACCGTGACACGCTGAACATCAA 222
QY 1965 CGCCCTGGCAGCGACGACCTATCAACGCGCGGGGTCTTCGAGCGCACCGGTGTTCCC 2024
Db 223 CGCCCTGGCAGCGACGACCTATCAACGCGCGGGGTCTTCGAGCGCACCGGTGTTCCC 282
QY 2025 TGCAAAGTACGCGTGGGGATGTCCGCGACAGCTGTACAAGAGCTGGAATTTCAACGAGCA 2084
Db 283 TGCAAAGTACGCGTGGGGATGTCCGCGACAGCTGTACAAGAGCTGGAATTTCAACGAGCA 342
QY 2085 GGCTCTCCACAGATCTCGTCAAG-----AGAGGT 2109
Db 343 GGCTCTCCACAGATCTCGTCAAGAGGTACGTAGACAATACATGAGGTGAGCGCACT 402
QY 2110 -----AGAGGT 2115
Db 403 AAACGCTATAGAAACTGTTCCGTTCTTGACGTGTTGTTGTTGCGTTCAGAGGT 462
QY 2116 GTGGCTGTGCGGACCACTGAGCCCATATGGTGTCCGACTGCTGATCAAGACTACCCC 2175

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Db      463 GTGGCTGTCCCGACCAAGTCAAGCCCATATGTTGTCGACTCTGATCAAGACTACCCC 522
QY 2176 TATGCCGTTTGAAGCGGCTCGTCTATCTGTTGGGCGATCGAGCGGTGGGTCAAGAGTACCTG 2235
Db 523 TATGCCGTTTGAAGCGGCTCGTCTATCTGTTGGGCGATCGAGCGGTGGGTCAAGAGTACCTG 582
QY 2236 GACATCTACTACCTTAACGACGCGAGCTCCAGCGTGCAGCTGAGCTGAGCTGAGCGGTGGTGG 2295
Db 583 GACATCTACTACCTTAACGACGCGAGCTCCAGCGTGCAGCTGAGCTGAGCGGTGGTGG 642
QY 2296 AAGGAGGTGCTGAGGAGGCGACGCGGACCTCAAGACCCGAGACTGTGTGGGCCAGGATG 2355
Db 643 AAGGAGGTGCTGAGGAGGCGACGCGGACCTCAAGACCCGAGACTGTGTGGGCCAGGATG 702
QY 2356 GACACCGTCCAGAGCTGCTAGGCGTGCACAGCACTATCTGCGTGCATCCGCGCTG 2415
Db 703 GACACCGTCCAGAGCTGCTAGGCGTGCACAGCACTATCTGCGTGCATCCGCGCTG 762
QY 2416 CACGCGGCTGTCAACTTTGGGCACTACCATACGCGGCTACTCTCCGAACCGCGGACG 2475
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QY 2476 GGCAGCGCGGCCGATGCCGAGCGACGACGACGACGACGACGACGACGACGACGACG 2535
Db 823 GGCAGCGCGGCCGATGCCGAGCGACGACGACGACGACGACGACGACGACGACGACG 882
QY 2536 CAGAGGAGGCGGACATGTTGTTTCATCCGACCATCACCAGCAGTCCAGACCATCCTG 2595
Db 883 CAGAGGAGGCGGACATGTTGTTTCATCCGACCATCACCAGCAGTCCAGACCATCCTG 942
QY 2596 GGCATCTGCTCATCGAGACTCTCTCAAGCACTCTCCGACGAGGTGTA 2645
Db 943 GGCATCTGCTCATCGAGACTCTCTCAAGCACTCTCCGACGAGGTGTA 992

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clone OSJNE0122 5', mRNA sequence.
CB669925
CB669925.1 GI:29673650
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 848)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
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/mol_type="mRNA"
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FEATURES
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ORIGIN
Query Match 21.1%; Score 660.8; DB 14; Length 848;
Best Local Similarity 86.2%; Pred. No. 1e-57;
Matches 731; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

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Db 1 GACAAGATCAACAAGTTCCTTGTGTAACCTCATATATCGGAGGAGCAATTCCTGCTCCTG 60
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Qy 1720 CAGCAGCGCGCGCGGTGACGAGGTGACACCCCGGCTCACCCGCGTFCGAGGCGCAC 1779
Db 121 CAGCAGCAGCGCGCGGTGACGAGGTGACACCCCGGCTFCGAGGCGCAC 180
Qy 1780 GTCTGGCAGCTCGCAGAGCTTATGCTGCTGTAACGACTCTGCTGCGATCAGCTGATC 1839
Db 181 ATCTGGCAGCTCGCAGAGTTCAGCTCTCGTCAACGACTCTGCTGCGACGAGCTGATC 240
Qy 1840 AGCCACTGGTGAACACGACGCGGTGATCGAGCGGTTCGTGTAATCGCGCAAAACCGGCGAG 1899
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Qy 1900 CTCAGCGTGTGATTCGCTGACAGCTGCTGAGCGCGCACTACCGTGCAGCGCTGAC 1959
Db 301 CTCAGCGTGTGATTCGCTGACAGCTGCTGAGCGCGCACTACCGTGCAGCGCTGAC 360
Qy 1960 ATCAACGCGCTGCGACGCGAGACTCATCAACGCGCGCGCTTCCTGAGCGCACCGCTG 2019
Db 361 ATCAACGCGCTGCGACGCGAGACTCATCAACGCGCGCTTCCTGAGCGCACCGCTG 420
Qy 2020 TTCCCTGCAAGTACGCGTGGGATGTCGCGAGACGTGTACAGAGCTGGATTTCAAC 2079
Db 421 TTCCCGAGCAAGTACGCGTGGGATGTCGCGAGACGTGTACAGAGCTGGATTTCAAC 480
Qy 2080 GAGCAGGCTCTCCCGAGAGATCTCTGCAAGAGAGGTGCTGTCGCGGACCAAGTCAAGC 2139
Db 481 GAGCAGGCTCTCCCGAGAGATCTCTGCAAGAGAGGTGCTGTCGCGGACCAAGTCAAGC 540
Qy 2140 CCATATGCTGCTGCTGATCAAGGACTACCCCTATGCGGTGACGCGGCTGCTGATC 2199
Db 541 CCGTACAACTGCTGCTGATCAAGGACTACCCCTATGCGGTGACGCGGCTGCTGATC 600
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Qy 2320 GCGACCTCAAGGACCGAGAGTGGTGGCGAGAGTGGACCGCTCCAGAGCTGGCTAGG 2379
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Qy 2380 GCGTGCAGCAATCATCTGGTGGCATCCGCGCTGCAACGCGCTGTCAATTTGGGCGAG 2439
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Qy 2440 TACCCATA 2447
Db 841 TACCCGTA 848
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RESULT 6
CK161284
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CK161284
FGAS033850 Triticum aestivum FGAS: Library 4 Gate 8 Triticum
aestivum cDNA, mRNA sequence.
CK161284
CK161284.1 GI:38989328
EST.

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE

1 (bases 1 to 1158)

AUTHORS

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033

Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [58,840].

Plate: L4B001 row: E column: 21.

FEATURES

source

Location/Qualifiers

1..1158

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/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial

parts (Crown and leaf) of wheat cultivar Norstar during

dehydration stress. 8 mRNA populations were combined

before constructing the library. The first four come from

removing plants from vermiculite (7 day old plants) and

incubating them at 20C on the bench without water for 1,

2, 3 and 4 days. The last four come from plants grown in

soil in a growth chamber after watering is terminated

Four samplings were taken in a two week period; the first

after wilting was observed and the last, two weeks later,

consisted of live crown and stem tissue (leaf tissue was

yellow and dead). First strand synthesis in this library

was done in the presence of methylated dCTP thereby

protecting from internal cleavage with NotI."

ORIGIN

Query Match

Best Local Similarity

Matches 756; Conservative

0; Mismatches 160; Indels

6; Gaps

1;

Qy 1555 AGGCTCTTCATCTAGACCATGACCATTTTCATGCGTACCTCGACGAGATCAACGAG 1614

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Qy 1615 CTGAGGAGGAACTTCATCTAGCGCAGAGGACCTTCTGCTTCGAGGAGGAGTGGCAG 1674

Db 65 CTGAGGAGGAACTTCATCTAGCGCAGAGGACCTTCTGCTTCGAGGAGGAGTGGCAG 124

Qy 1675 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1734

Db 125 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 184

QY 1735 GTCACGAGGTGTACACCCGGC-----TCACACCGGCTCGAGGCGACGCTGGCAG 1788
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 Db 305 CTGAACACACGCGGTGATCGACCGCTTCGTGATTCGACGAACCGGCAACTCAGGTG 364
 QY 1909 GTGCATCCCGTGCACAAAGCTCTGAGCCGCGACCTACCGTGACACGCTGAACATCAACGCC 1968
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 EST 24-SEP-2003
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 ORGANISM Saccharum officinarum
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Saccharum.
 1 (bases 1 to 758);
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 017 row: B column: 11
 Seq primer: F7 Promoter Primer.
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 /clone_lib="RP2"
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 Vector: pSPori1; Site 1: SalI; Site 2: NotI; An
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 from polyA+ mRNA using SuperScript Plasmid System Kit
 (Invitrogen). The double-strand cDNAs were fractionated
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 between 0.8 and 1.5 Kb were directionally cloned into the
 vector. Details of each source of RNA and library
 construction can be obtained at
 http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 20.4%; Score 639.4; DB 13; Length 758;
 Best Local Similarity 90.2%; Pred. No. 1.5e-55;
 Matches 682; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
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 Db 121 AGCCGTTGTCATCGCAACTAACCGGAGCTCAGCGTGTGTCATCCCGTGCAATAGCTGC 180
 QY 1931 TGAGCCGCGACTACCGTGACAGCTGAAACATCAACGCGCTCGCAGCGCAGACACTATCA 1990
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 Db 361 GAGGTGTGCTGTACAGACCAATCAAGCCATATGTTGCGACTGTGATCAAGGACT 420
 QY 2171 ACCCTATGCGGTTGACCGGCTGTGTCATCTGTTGGCGCATCGAGCGTGGTTCAGGAGT 2230
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 QY 2231 ACTTGACATCTACTACCTAACGCGGAGCTCCAGCGTCAAGCTGAGCTGCAAGGCGT 2290
 Db 481 ACTTGAGCTCTACTACTCTTAACGAGCGTGAAGCTCCAGCGTATGTTGAGCTGCAAGAT 540
 QY 2291 GGTGGAAGAGGTGCGTGAAGGCGGCGACGCTCAAGACCGGAGACTGTGTGCGCCA 2350
 Db 541 GGTGGAAGAGGTGCGTGAAGGCGGCGACGCTTTAAGGATCGAGACTGTTGGGCCA 600

2582 TCCAGACCATCTGGGCTCTCGCTCATCGAGATCTCTCAAGACATCTCTCCGACGAGG 2641
Db TCCAGACCATCTCTGGGCTCTCGCTCATCGAGATCTCTCAAGACATCTCTCCGACGAGG 468
2642 TGTACTCTGGCCAGCGTGCAGCGCTGATCGCTGACGCTGACGACCCAGCGCTGGATG 2701
Db TGTACTCTGGCCAGCGCGACGAGCTGAGCGCTGACGCTGACGACCCAGCGCTGGACG 408
2702 CTTTCAAAAGATTCCGGAGCGCGCTGTCAGATTGAGATCGGATCGGATCGGATCGG 2761
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2762 ACAGTCCCGACTTGAAGAACCGAAGGGGCTGTGGAATCCGCTACATGCTGCTGACC 2821
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2882 ACAGCATCTCCATATGAGCGCTGGGCGAGATTGT-----GTCTCGTAGTAAATTTGT 2932
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2933 TGCTCGCGCTGCGATGTTTCTTCATGTTTGTGATGCTCAGGCTAGGCGATGAG 2992
Db TGCTCGCTGATGATGTTTCTTCATGTTTGTGATGCTCAGGCTAGGCGATGAG 108
2993 ATCATACCATGATC-----TTTGTAGGCTTCAGAGAGGAGTCCACGCT--TGAATATTGT 3045
Db ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48
3046 TGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3092
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RESULT 9
CA145829
LOCUS
DEFINITION
SCVPR2073G08.9 RT2 Saccharum officinarum cDNA clone SCVPR2073G08
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CA145829.1 GI:35044262
Saccharum officinarum
Saccharum officinarum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 709)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 073 row: G column: 08
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..709
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPR2073G08"
/lab_host="DH10B"

FEATURES
source
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/organism="Saccharum officinarum"
/mol_type="mRNA"
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/clone="SCVPR2073G08"
/lab_host="DH10B"

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/notes="Organ: Root tips (0.3cm-long) from adult plants;
vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Root
tips (0.3cm-long) from adult plants]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a separose CL-2B 40cm-column and fragments sizing
between 0.8 and 1.5 kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 19 %; Score 622.6; DB 13; Length 709;
Best Local Similarity 94.8%; Pred. No. 7, 7e-54;
Matches 643; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
2240 TCTACTACCTTAACGACGCGAGCTCCAGCTGACGTGAGCTGCGAGCGTGTGGAAG 2299
Db 2 TCTACTACTTAACGACGCGTGTGCTCCAGCTGATGTGAGCTGCGAGGATGTTGGAAG 61
2300 AGGTGCTGAGGAGGCGCACGCGGACCTCAAGACCGAGACTGTGCGCCAGATGGACA 2359
Db 62 AGGTGCTGAGGAGGCGCACGCGGACCTTAAGAGATCGAGACTGGTGGCCAGATGAACA 121
2360 CGTCCAGCAGCTGGCTAGGCGGTGTCACGACCATCATCTGGGTGGCATCCGCGCTGCAG 2419
Db 122 CGTCCAGCAGCTGGCTAGGCGGTGTCACGACCATCATCTGGGTGGCATCTGGCTGCAG 181
2420 CGGCTGTCACTTTGGGCGAGTACCCATAGCGCGGTGACCTCCGAAACCGCGCGACGCA 2479
Db 182 CAGCTGTCACTTTGGGCGAGTATCCATAGCGCGGTGACCTCCGAAACCGCGCGACGCA 241
2480 GCGGCGCGCGGATGCGGAGCGCAGCAGCTACAGAGAGCTGCGAGCGGCGGACG 2539
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2600 TCTCGCTCATCAGATCTCTCCAGGACCTCTCCAGGAGGTGACCTCCGCGGAGCGTG 2659
Db 362 TCTCGCTCATCAGATCTCTCCAGGACCTCTCCAGGAGGTGACCTCCGCGGAGCGTG 421
2660 ACAGCGCTGATCGCTGAGAGCTCAGACGCGCAGCGCTGATGCTGCTCAAAAGATTTCGG 2719
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2720 GCGGCTGCTGAGATTTGAGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 2779
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2840 CCGGCGAGAGCGCGGAGGCTTACTGCGATGCGGATTCCTCCACAGCATCTCCATATGAG 2899
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2900 CTTGGCGAGATTGTGTCT 2917
Db 662 CTTGGCGAGATTGTGTCT 679

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DEFINITION
SCBPR3094B01.9 RT3 Saccharum officinarum cDNA clone SCBPR3094B01
5', mRNA sequence.
ACCESSION
CA279071

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VERSION CA279071.1 GI:36004162
SOURCE EST.
ORGANISM Saccharum officinarum
          Saccharum officinarum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 772)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.I. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
          Centro de Biologia Molecular e Engenhariaia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bccccenter.fcav.unesp.br
          Plate: 094 row: B column: 01
          Seq primer: T7 Promoter Primer.
          Location/Qualifiers
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              /clone_lib="RR3"
              /note="Organ: Root apex from adult plants; Vector:
              pSport1; Site 1: SalI; Site 2: NotI; An unidirectional
              cDNA library generated from [Root apex from adult
              plants]. cDNA was prepared from polyA+ mRNA using
              Superscript Plasmid System Kit (Invitrogen). The
              double-strand cDNAs were fractionated in a sepharose
              CL-2B 40cm-columns and fragments sizing between 0.8 and
              1.5 kb were directionally cloned into the vector. Details
              of each source of RNA and library construction can be
              obtained at http://sucet.lad.ic.unicamp.br/public"

FEATURES
  source
    1948 GACACGCTGAACATCAACGCCCTGGCACGCCAGACACTCATCAACGCCGCGCTTC 2007
    3 GACACATTGACCATCATGTCCTGACACGCCAGACACTCATCAACGCCGCTGGCATCTTC 62
    2008 GAGCGCACCGTGTTCCTCGCAAGTAGCGCGCTGGGATGTCGCCAGACGTGTACAGAGC 2067
    63 GAGCGCACTGTGTTCCTCGCAAGTAGCGCGCTGGGATGTCCTCCGACGTGTACAGAGC 122
    2068 TGGAAATTCACAGCAGGCTCTCCAGCAGACTCGTCAAGAGAGGTGCTGGCGG 2127
    123 TGGAAATTCACAGCAGGCTCTCCCGCAGACTCTCGTCAAGAGAGGTGCTGGCGG 182
    2128 GACAGTCACAGCCCATATGTTGTCGCACTGCTGATCAAGGACTACCCCTATGCGGTGAC 2187
    183 GACCAATCAAGCCCATATGTTGTCGCACTGCTGATCAAGGACTACCCATATGCGGTGAT 242
    2188 GGGCTCGTATCTGTTGGGCGATCGAGCGGTGGTCAAGGACTACCTGGACATCTACTAC 2247
    243 GGGCTCGTATCTGTTGGGCGATGAGCAGTGGGTCAAGGACTACCTGGACATCTACTAC 302
    2248 CCTAACGACGGCGAGCTCCAGCGTGCAGCTGGAGCTGCAGGCGTGGTGGAGAGGTGGCT 2307
    303 TCTAACGACGGTGCAGCTCCAGCGTGTGAGCTGCAGGCTGAGTGGTGGAGAGGTGGCT 362
    2308 GAGGAGCGCACGGGACCTCAAGGACCGAGACTGTTGGCCCAAGGTGACACCGTCCAG 2367
  
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Db 363 GAGGAGCGGCACGCGGACGCTTAAGGATCGAGACTGGTGGCCCGAGATGAACACCGTCCAG 422
Qy 2368 CAGCTGGCTAGGCGGTGACGACCATCATCTGGGTGGCATCGCGCTGCACGCGGCTGTC 2427
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Qy 2428 AACTTTGGGCGAGTACCCATACGCGGGTACCTCCGAAACCGCGCGACGCGCGCGGC 2487
Db 483 AACTTTGGGCGAGTATCCATACGCGGGTACCTCCGAAACCGCGCGACGCGTGAAGCGGCGG 542
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Qy 2668 GATCGCTCGAGCTCAGACGCCAAGCGGTGATCGCTTCAAAAGATTGGGA 2719
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DEFINITION Genomic survey sequence.
ACCESSION CG325032
VERSION CG325032.1 GI:34242298
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 892)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
          Resnick,A., Fraser,C.M., Sudiman,M.A., Bedell,J.A., Rohlfing,T.,
          Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
          Consortium for Maize Genomics
          Unpublished (2002)
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TF
          Class: sheared ends.
FEATURES
  source
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  Matches 703; Conservative 0; Mismatches 1; Indels 89; Gaps 1;
  Qy 1845 CTGGCTGAACACGACCGCGGTGATCGAGCGCTTCGTAATCGGACAAACCGGAGCTCAG 1904
  Db 100 CAGGCTGAACACGACCGCGGTGATCGAGCGCTTCGTAATCGGACAAACCGGAGCTCAG 159

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1905 CTTGTTGTCATCCGTCGACCAAGTCTGTGAGCCCGCACTACCGTGTGACAGCTGACATCAA 1964
 160 CTTGTTGTCATCCGTCGACCAAGTCTGTGAGCCCGCACTACCGTGTGACAGCTGACATCAA 219
 1965 CGCCCTGGCAGCCGACGACTCATCAAGCCCGCGGCTTTCGAGCGCAGCGTTCCTCC 2024
 220 CGCCCTGGCAGCCGACGACTCATCAAGCCCGCGGCTTTCGAGCGCAGCGTTCCTCC 279
 2025 TGCAAGTACGCGCTGGGATGTGCGCAGACGCTGTACAAGAGCTGGAATTTCAACAGACA 2084
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 2085 GCGTCTCCAGCAGATCTCGTCAAG----- 2109
 340 GCGTCTCCAGCAGATCTCGTCAAGAGGTATGTACAGACATACACTGAGGTGAGCAGCACT 399
 2110 -----AGAGGT 2115
 400 AAACGCTTATAGAAACTTTCGGTTCTTGACGTGGTGTGCTGCGTGGCTTACAGGT 459
 2116 GTGGCTGTCCGAGCAGTCAAGCCCATATGTTGTCGAGTCTGTGATCAAGGACTTACCCC 2175
 460 GTGGCTGTCCGAGCAGTCAAGCCCATATGTTGTCGAGTCTGTGATCAAGGACTTACCCC 519
 2176 TATGCGTTGACGGCTGTCTATCTGTGGGCGATCGAGCGGTGGTCAAGAGTACCTG 2235
 520 TATGCGTTGACGGCTGTCTATCTGTGGGCGATCGAGCGGTGGTCAAGAGTACCTG 579
 2236 GACATCTACTACCTTAAGCAGCGGAGCTCCAGCGTGTGACGTGTGAGCTGTGAGCGTGGTG 2295
 580 GACATCTACTACCTTAAGCAGCGGAGCTCCAGCGTGTGACGTGTGAGCTGTGAGCGTGGTG 639
 2296 AAGGAGTGTGAGAGCGCAGCGGACCTCAAGGACCGAGTGTGGTGGCCAGGATG 2355
 640 AAGGAGTGTGAGAGCGCAGCGGACCTCAAGGACCGAGTGTGGTGGCCAGGATG 699
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 2476 GCCAGCGCGCGCGATGCGGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2535
 820 GCCAGCGCGCGCGATGCGGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 879
 2536 CAGAAGGAGCGGG 2548
 880 CAGAAGGAGCGGG 892

RESULT 12
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 5', mRNA sequence.
 ACCESSION CA298585
 VERSION CA298585
 KEYWORDS EST, GI:36069249
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum.
 1 (bases 1 to 679)
 Vettore, A.L., da Silva, P.R., Kemper, E.L. and Arruda, P.
 The libraries that made SUCST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bccc.net.br

Plate: 044 row: A column: 07

Seq primer: T7 Promoter Primer.

Location/Qualifiers

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/clone="SCSPFL8044A07"

/lab_host="DH10B"

/clone_lib="FL8"

/notes="Organ: Developing inflorescence and rachis

(10cm-long); Vector: pSPORT1; Site 1: SalI; Site 2: NotI;

An unidirectional cDNA library generated from [Developing

inflorescence and rachis (10cm-long)]. cDNA was prepared

from polyA+ mRNA using SuperScript Plasmid System Kit

(Invitrogen). The double-strand cDNAs were fractionated

in a Sepharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library

construction can be obtained at

http://sucst.lad.ic.unicamp.br/public"

ORIGIN

Query Match 19.0%; Score 594.2; DB 14; Length 679;
 Best Local Similarity 92.2%; Pred. No. 5.6e-51;
 Matches 626; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy 1790 TCGCCAAAGGTTATGCTGCTGCTAAAGCACTTCGCTTGGCATCAGCTGATCAGCACTGCG 1849
 Db 121 TTGCAAGGCTTACGCTCGGTAAAGCACTTCGCTTGGCATCAGCTGATCAGCACTGCT 180

Qy 1850 TGAACACGACGCGGTGTATCGAGCGCTTCGTAAATCGCGCAAAACCGGCGAGCTGAGCGG 1909
 Db 181 TGAACACGACGCGGTGTATCGAGCGCTTCGTAAATCGCGCAAAACCGGCGAGCTGAGCGG 240

Qy 1910 TGCATCCGTCGACAAAGCTGTGAGCCCGCACTTACCGTGACACGCTGAACATCAACGCC 1969
 Db 241 TGCATCCGTCGACAAAGCTGTGAGCCCGCACTTACCGTGACACGCTGAACATCAACGCC 300

Qy 1970 TGCACGCGCAGACACTCATCAACGCGCGCGGCTTTCGAGCGCACCGGTGTTCCCTGCAA 2029
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Qy 2030 AGTACGCGTGGGATGTGCGCAGAGCTGTACAAGAGCTGGAAATTCACAGCAGCGGCTC 2089
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Qy 2090 TCCAGCAGACTCTCGTCAAGAGAGGTGTGGCTGTGCGCGGACCGAGTCAAGGCCATATGGTG 2149
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Qy 2150 TCGGACTGTGTATCAAGGACTACCCCTATGCGGTGTGAGCGGCTTCATCTGTGGGCGGA 2209
 Db 481 TCGGACTGTGTATCAAGGACTACCCCTATGCGGTGTGAGCGGCTTCATCTGTGGGCGGA 540

Qy 2210 TCGAGCGGTGGGTCAAGGAGTACCTTGGACATCTACTACCTTAACGCGCGAGCTCCAGC 2269

Db 541 TTGAGCAGTGGGTCAAGAGTACTTTGGAGCTTACTACTCTAACAAGCGGTGAGCTCCAGC 600
 QY 2270 GTGACGTGAGCTCAGCGCTGTGCGAAGAGGTGCGTGAAGGCGCAGCGGCACTCA 2329
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 Db 661 AGGATCGAGACTGTGGCC 679

RESULT 13

CA135806 707 bp mRNA linear EST 24-SEP-2003
 LOCUS SCJLRT1021H02.9 RT1 Saccharum officinarum cDNA clone SCJLRT1021H02
 DEFINITION 5', mRNA sequence.
 ACCESSION CA135806
 VERSION CA135806.1 GI:35024177
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum.
 1 (bases 1 to 707)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 021 row: H column: 02
 Seq primer: 17 Promoter Primer.
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 /mol_type="mRNA"
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 /note="Organ: Root tips (0.3cm-long) from adult plants;
 Vector: pSport1; Site 1: SalI; Site 2: NotI; An
 unidirectional cDNA library generated from [Root tips
 (0.3cm-long) from adult plants]. cDNA was prepared from
 polyA+ mRNA using SuperScript Plasmid System Kit
 (Invitrogen). The double-strand cDNAs were fractionated
 in a sepharose CL-2B 40cm-columns and fragments sizing
 between 0.8 and 1.5 Kb were directionally cloned into the
 vector. Details of each source of RNA and library
 construction can be obtained at
 http://sucest.lad.ic.unicamp.br/public"

FEATURES

source

Query Match 18.9%; Score 592.6; DB 13; Length 707;
 Best Local Similarity 90.7%; Pred. No. 8e-51;
 Matches 631; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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 QY 1672 ACGCTGAAGCCCTGGCCATCGAGCTGAGCCTGCCCAACCTCAGCCGAGCGCGGC 1731
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ORIGIN

Query Match 18.9%; Score 592.6; DB 13; Length 707;
 Best Local Similarity 90.7%; Pred. No. 8e-51;
 Matches 631; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
 QY 1612 GAGCTGAGGGGAATTCATCTAGCCAGGAGGACCTACTGTTCCTGAAGGACGATGGC 1671
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 QY 1672 ACGCTGAAGCCCTGGCCATCGAGCTGAGCCTGCCCAACCTCAGCCGAGCGCGGC 1731
 Db 71 ACCCTGAAGCCCTGGCCATCGAGCTGAGCCTGCCCAACCTCAGCCGAGCGCGGC 130

QY 1732 GCGGTCAAGAGTGTACACCCCGCTCACACGGCGTCGAGGGCCAGCTCTGGCAGCTC 1791
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 QY 1792 GCCAAGGCTTATGCTTGGGTAAACGACTTCTGCTTGGCATCAGCTGATCAGCCACTGGGTG 1851
 Db 191 GCCAAGGCTTATGCTTGGGTAAACGACTTCTGCTTGGCATCAGCTGATCAGCCACTGGGTG 250
 QY 1852 AACACGACGCGGTGATCGAGCGCTTCTGTAATCGGACAAACCGGACGCTCAGCGTGGTG 1911
 Db 251 AACACGACGCGGTGATCGAGCGCTTCTGTAATCGGACAAACCGGACGCTCAGCGTGGTG 310
 QY 1912 CATCCGCTCACAAAGTGTGCTGAGCCCGCAGCTACCTGTCAGCTGAAATCAACCCCTG 1971
 Db 311 CATCCGCTCACAAAGTGTGCTGAGCCCGCAGCTACCTGTCAGCTGAAATCAACCCCTG 370
 QY 1972 GCACGCCAGACACTCATCAACCGCGGCGCTTTCGAGCGCACCGTGTTCCTCCAAAG 2031
 Db 371 GCACGCCAGACACTCATCAACCGCTGTGGCATCTTCGAGCGCACCTGTGTTCCTCGAAA 430
 QY 2032 TAGCGCTGGGATGTTCGCGACAGCTGTACAGAGCTGGAATTTCAACGAGCAGGCTCTC 2091
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 Db 551 CGACTGTCTGATCAAGAGCTTACCCCTATGCTGCGGTGAGCGGCTCGTCACTCTGGTGGCGATC 610
 QY 2212 GAGCGTGGGTCAAGAGTGTCTGACATCTACTACTACCTTAACGAGCGGAGGCTCAGGCT 2271
 Db 611 GAGCAGTGGGTCAAGAGTGTCTGACATCTACTACTACTACTTAACGAGCGGAGGCTCAGGCT 670
 QY 2272 GAGCTGGAGCTCAGCGCTGGTGGAGGAGGTCGT 2307
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RESULT 14

CA164910 674 bp mRNA linear EST 24-SEP-2003
 LOCUS SC5BR23124H05.9 R23 Saccharum officinarum cDNA clone SC5BR23124H05
 DEFINITION 5', mRNA sequence.
 ACCESSION CA164910 GI:35082793
 VERSION CA164910
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum.
 1 (bases 1 to 674)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 124 row: H column: 05
 Seq primer: 17 Promoter Primer.
 Location/Qualifiers
 1..674
 /organism="Saccharum officinarum"

FEATURES

source

1..674
 /organism="Saccharum officinarum"

```

/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSRZ3124H05"
/lab_host="DH10B"
/clone_lib="RZ3"
/note="Organ: Shoot-root transition zone from adult
plants; Vector: pSPORT1; Site_1: SalI; Site_2: NotI; An
unidirectional cDNA library generated from (shoot-root
transition zone from adult plants). cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucet.fad.ic.unicamp.br/public"

ORIGIN
Query Match 18.9%; Score 591.2; DB 14; Length 674;
Best Local Similarity 93.8%; Pred. No. 1.1e-50;
Matches 625; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

QY 2110 AGAGGTGGCTGTCGGGACCAAGTCAAGCCCATATGTTGTCGGACTCTCTGATCAAGGAC 2169
DB |||||
2 AGAGTGTGGCTGTACCAAGCAATCAAGCCCATATGTTGTCGGACTCTCTGATCAAGGAC 61
QY 2170 TACCCCTATGCCGTTGACGGGCTCGTCTATCTGGTGGCGATCGAGCGTGGTCAAGGAG 2229
DB |||||
62 TACCCATATGCCGTTGATGGGCTCGTATCTGGTGGCGATGACGATGGTCAAGGAG 121
QY 2230 TACCTGGACATCTATACCTTAACGACGGGAGTCTCAGCGTGAAGTCAAGGCTCGAGCG 2289
DB |||||
122 TACTTGGAGCTTACTACTTAACGACGGTGAAGTCCAGCGTGAAGTGGAGCTCGAGGCA 181
QY 2290 TGGTGGAGGAGTGGTGGAGGCGGACGCGGACCTCAAGGACCGAGCTGGTGGCC 2349
DB |||||
182 TGGTGGAGAGTGGTGGAGGCGGACGCGGACCTTAAGATCGAGATGGTGGCC 241
QY 2350 AGATGGACACCGTCCAGCAGTGGCTAGGCGGTGCAGACCATCATCTGGTGGCATCC 2409
DB |||||
242 AGGATGAACACCGTCCAGCAGTGGCTAGGACGTGCAGACCATCATCTGGTGGCATCT 301
QY 2410 GCGTGCACGGGCTGTCACTTTGGGCGAGTACCATCGCGGGTACTCTCCGACCGG 2469
DB |||||
302 GCGTGCACGGGCTGTCACTTTGGGCGAGTATCCATACGCGGGTACTCTCCGACCGG 361
QY 2470 CCGACGGCCAGCGCGGCGCCGATGCGGAGCGAGCCAGCAGCTCAAGAGCTGGGA 2529
DB |||||
362 CCGACGGTGAAGCGCGCGCGATGCGGAGCGCGGCGAGTACTCAAGAGTGGAA 421
QY 2530 GCGGGGCGAGAGGAGCGGACATGTTGTTATCCGACCATCACAGCGATTCAGACC 2589
DB |||||
422 GCGNGCGAGAGGAAGCGGACATGTTGTTATCCGACCATCACAGCGATTCAGACC 481
QY 2590 ATCTTGGGCACTCTCGCTCATCGAGATCTCTCCAGCACTCTCCGAGAGGTGTACTC 2649
DB |||||
482 ATCTTGGCACTCTCGCTCATCGAGATCTCTCCAGCACTCTCTCGAGAGGTGTACTC 541
QY 2650 GCGCAGCGTGAAGACCTGATGCTGGACGTCAGACGCGAGCGCTGGATGCGTTCAAA 2709
DB |||||
542 GCGCAGCGTGAAGACCTGAGCGCTGGACGTCAGACGCGAGCGCTGGATGCGTTCAAA 601
QY 2710 AGATTTCGGGA-GCCGGCTGGTGCAGATGAGATCGGATCAAGACGATGACGACATCC 2768
DB |||||
602 AGATTTCGGANCGCGGCTGGTGGAGATTGAGATCGGATCAAGACGATGACGACATCC 661
QY 2769 GCACTT 2774
DB |||||
662 CGACTT 667

RESULT 15
CA487017

```

LOCUS CA487017 715 bp mRNA linear EST 14-NOV-2002
DEFINITION WHE4339_F08_L15ZS Wheat meiotic anther cDNA library Triticum aestivum cDNA clone WHE4339_F08_L15, mRNA sequence.
ACCESSION CA487017
VERSION CA487017.1 GI:24981221
KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1 (Bases 1 to 715)
AUTHORS Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.
TITLE The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595773
Fax: 510595818
Email: candersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer.
FEATURES
Location/Qualifiers
1..715
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4339_F08_L15"
/tissue_type="Anther"
/dev_stage="Meiotic stages pre-meiosis-metaphase I"
/lab_host="E. coli DH10B"
/clone_lib="Wheat meiotic anther cDNA library"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plants were grown in a glasshouse. Anther meiotic stage was determined by removing anthers from individual primary flowers. One anther was sacrificed for microscopic staging, and if determined to be between (and including) meiotic stages pre-meiosis and metaphase I, the remaining two anthers were collected and pooled for library construction. The tissue, total RNA, and poly(A) RNA were prepared, cDNA synthesised, and directionally ligated into pSPORT1 by Tim Sutton in the P Langridge Lab at the Department of Plant Science, University of Adelaide, Waite Campus, Australia. Average insert size 1.5Kb. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Query Match 18.8%; Score 590; DB 14; Length 715;
Best Local Similarity 89.8%; Pred. No. 1.5e-50;
Matches 645; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

QY 783 AGATGAGCTCAAGATTCCTCGTGGGACGATTAATCTGGACCATACCGAGGACATGATCG 842
DB |||||
1 AGATGAATCAAGATTCCTCGTGGTGAATGATGATCTCTGGACCATACAGGAGCATGATCG 60
QY 843 CGTCTACCGTTCAGCTACTACATGACCTTGGTGTATCCGACAGGGCGAGAGACGCG 902
DB |||||
61 CGTCTACCGTTCAGCTACTACATGACCTTGGTGTATCCGACAGGGGTGAAGACATGCG 120
QY 903 TCGGCGGATCTCGGTGGCAGCAAGAACACCCGATATCCCGTCTGCTGAGAACTGGCGG 962
DB |||||
121 TCGGCGGATCTCGGTGGCAGCC---AACACCATATCCCGTCTGCTGAGAACTGGTCTG 177
QY 963 GCACCCCAACAGAAAGACCCAAATTCGGAGAGCGAGGCTTTTCTGCTGAACCTGAACAT 1022
DB |||||
178 GCACCCCAACAGAAAGACCCAAATTCGAGAGAGCGGCTTTTCTGCTGAACCTGAACAT 237

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 03:44:22 ; Search time 85 Seconds
(without alignments)
2948.466 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFHWGVADRLTGKKEAWSE.....VTGKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4723	100.0	887	6	AAO27494 Corn (Zea
2	3478	73.6	837	6	Ada48504 Rice prot
3	2987.5	63.3	863	7	Adc53139 9'-specif
4	2936.5	62.2	862	5	Aau9691 Barley w
5	2931.5	62.2	862	5	Abg30566 Wild type
6	2929.5	62.0	862	5	Aau99693 Barley w
7	2929.5	62.0	862	5	Aau99692 Barley w
8	2929.5	62.0	862	5	Abg30567 Mutant ty
9	2860	60.6	864	5	Abg30571 Barley lo
10	2829.5	59.9	865	2	Aar23797 Rice lipo
11	2829.5	59.9	865	2	Aar2670 Lipoxysen
12	2795.5	59.3	859	6	Abc19443 Wine grap
13	2777.5	58.8	862	6	Abc19442 Wine grap
14	2724.5	57.7	862	6	Abp70404 Amino aci
15	2630.5	55.7	857	4	Aab46803 Potato LO
16	2491.5	52.8	857	5	Abg30570 Glycine m
17	2486	52.6	865	5	Abg30569 Glycine m
18	2476	52.4	880	6	AAO27492
19	2423.5	51.3	878	4	AAE11500 C. sativu
20	2423.5	51.3	878	4	AAE11500 C. sativu
21	2375	50.3	853	4	AAE86036 Cucumber
22	2369.5	50.2	864	2	AAR50220 Soybean l
23	2355.5	49.9	839	5	AAR24042 Lipoxysen
24	1760.5	37.3	491	7	Abg30568 Glycine m
25	1634	34.6	924	6	AAE39891 Human lip
					AAE38266 Rice dise

ALIGNMENTS

RESULT 1

AAO27494

ID AAO27494 standard; protein; 887 AA.

XX AAO27494;

AC AAO27494;

DT 06-NOV-2003 (first entry)

XX 06-NOV-2003 (first entry)

DE Corn (Zea mays) lipoxigenase isozyme 4 amino acid sequence.

XX Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;

XX fatty acid metabolite synthesis; signal molecule; growth regulation;

XX development regulation; plant development; wound response;

XX genetic mapping; hyperoxidation catalysis; Corn; enzyme.

XX Zea mays.

OS Zea mays.

PN US2003074693-A1.

XX 17-APR-2003.

XX 29-JAN-2002; 2002US-00059909.

XX 10-FEB-1999; 99US-0119597P.

XX 09-FEB-2000; 2000US-00501422.

XX (CAHO/) CAHOON E B.

XX (KINN/) KINNEY A J.

XX (KLEI/) KLEIN T M.

XX (LEEJ/) LEE J.

XX (PEAR/) PEARLSTEIN R W.

XX (RAPA/) RAFALSKI J A.

XX (SHEN/) SHEN J B.

XX (THOR/) THORPE C J.

XX (TING/) TINGEY S V.

XX (WENG/) WENG Z.

XX Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;

XX Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;

XX WPI; 2003-567325/53.

XX N-PSDB; AAL57714.

XX New isolated polynucleotides encoding plant lipoxigenases, useful in

XX genetic mapping, particularly in catalyzing hyperoxidation of

XX polyunsaturated fatty acids.

XX Claim 19; Page 29-31; 36pp; English.

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XX CC This invention relates to novel nucleotide sequences which encode
CC proteins which have lipoxigenase activity. Lipoxigenases are membrane
CC bound ubiquitous enzymes which catalyze the hydroperoxidation of
CC polyunsaturated fatty acids in the first step of fatty acid metabolism
CC synthesis. Products of this pathway are found as signal molecules
CC involved in growth and development regulation. A knowledge of the amino
CC acid sequence of lipoxigenases may allow the understanding of plant
CC development and wound response. The polynucleotides, polypeptides and
CC lipoxigenases of the invention may therefore be useful in genetic mapping
CC and particularly for catalysing hydroperoxidation of polyunsaturated
CC fatty acids. The present sequence is the amino acid sequence of the Corn
CC (Zea mays) lipoxigenase protein 4 of the invention
XX CC
SQ Query Match 100.0%; Score 4723; DB 6; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHGVADRLTGKKEAWSEKIRGTVRLVKKEVLDVGDENASLLDGVHRLGWDGQVAF 60
DB 1 MFHGVADRLTGKKEAWSEKIRGTVRLVKKEVLDVGDENASLLDGVHRLGWDGQVAF 60

QY 61 QLVSATADPNSGGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESGQIPGAVLVR 120
DB 61 QLVSATADPNSGGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESGQIPGAVLVR 120

QY 121 NLQAEFFLKTLLTEGVPGKTVVFNANSWVYVPHKLYSQERIFPANDTYLPSKMPALVP 180
DB 121 NLQAEFFLKTLLTEGVPGKTVVFNANSWVYVPHKLYSQERIFPANDTYLPSKMPALVP 180

QY 181 YRQDELKILRGDDNPGYQEHDRVYRYDYNLDGDPDKGEEHARPLIGSQEHPPRRCR 240
DB 181 YRQDELKILRGDDNPGYQEHDRVYRYDYNLDGDPDKGEEHARPLIGSQEHPPRRCR 240

QY 241 TGRHPTKOPNSERLFLANLNIYVPRDERFGLHAKMSDFLGYSKLTIEAVLTGTFVD 300
DB 241 TGRHPTKOPNSERLFLANLNIYVPRDERFGLHAKMSDFLGYSKLTIEAVLTGTFVD 300

QY 301 DTPKEFDSFEDILGYELGPEAPNPLIAIRKIPSEFLRSILPNSGSHDHPKMLPNV 360
DB 301 DTPKEFDSFEDILGYELGPEAPNPLIAIRKIPSEFLRSILPNSGSHDHPKMLPNV 360

QY 361 IKSVDLKAPEFKGWTDEEFARETAGVNPVLIKRLTEFPKASTLDPRQYGDHTSKIT 420
DB 361 IKSVDLKAPEFKGWTDEEFARETAGVNPVLIKRLTEFPKASTLDPRQYGDHTSKIT 420

QY 421 EAHIRHNMGSLVQNALRNKELFLDHDHFMFYPYLDINELEGNFYASRTLLFLKDDGT 480
DB 421 EAHIRHNMGSLVQNALRNKELFLDHDHFMFYPYLDINELEGNFYASRTLLFLKDDGT 480

QY 481 LKPLAIELSLPHDPGQORGAVSKYVTPAHTGVEGVHVLAKAYACVNDSSAWHQLISHWLN 540
DB 481 LKPLAIELSLPHDPGQORGAVSKYVTPAHTGVEGVHVLAKAYACVNDSSAWHQLISHWLN 540

QY 541 THAVIEPVIATNQLSVVHVKLLSPHYRDTLINALAROTLINAGGVFEFTVPAPY 600
DB 541 THAVIEPVIATNQLSVVHVKLLSPHYRDTLINALAROTLINAGGVFEFTVPAPY 600

QY 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVWMAIE 660
DB 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLIKDYPYAVDGLVWMAIE 660

QY 661 RWKXEYLDIYYPNDGELQORDVLAQWKEVREAHGDLKDRDWPMDTVQOLARACTTI 720
DB 661 RWKXEYLDIYYPNDGELQORDVLAQWKEVREAHGDLKDRDWPMDTVQOLARACTTI 720

QY 721 IWASALHAAVNFQYVAGYLPNRPPTASRRPPEPGSHDYKKLGAQKEADWVFRTIT 780
DB 721 IWASALHAAVNFQYVAGYLPNRPPTASRRPPEPGSHDYKKLGAQKEADWVFRTIT 780

QY 781 SQFTILGISLIEILSKHSSDEVILGQDEPDRTWSAKALDAFKRFGSLVQIENRIKT 840

DB 781 SQFTILGISLIEILSKHSSDEVILGQDEPDRTWSAKALDAFKRFGSLVQIENRIKT 840

QY 841 MNDSPDLKNRKGPEVMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

DB 841 MNDSPDLKNRKGPEVMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887

RESULT 2
ADA48504
ID ADA48504 standard; protein; 837 AA.
AC ADA48504;
XX DT 20-NOV-2003 (first entry)
XX DE Rice protein conferring disease resistance in plants.
XX KW disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX OS Oryza sativa.
XX FN WC2003000906-A2.
XX PD 03-JAN-2003.
XX PF 21-JUN-2002; 2002WO-IB002453.
XX PR 22-JUN-2001; 2001US-0300112P.
XX PR 26-SEP-2001; 2001US-0352277P.
XX PR 22-MAR-2002; 2002JUS-0366535P.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
XX PI Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPI; 2003-184052/18.
XX DR N-PSDB; ADA48503.
XX PT New polynucleotide comprising a plant nucleotide sequence having an open
XX PT reading frame that encodes a polypeptide associated with disease
XX PT resistance, useful for conferring resistance or tolerance to a plant
XX PT pathogen.
XX PS Claim 10; SEQ ID NO 574; 299pp; English.
XX CC The invention relates to a novel isolated polynucleotide comprising a
XX CC plant nucleotide sequence having an open reading frame that encodes a
XX CC polypeptide associated with disease resistance or its fragment having
XX CC substantially the same activity as the full-length polypeptide. The
XX CC polynucleotide of the invention is useful for conferring resistance or
XX CC tolerance to a plant pathogen. The present sequence represents a protein
XX CC conferring disease resistance used in the invention.
SQ Sequence 837 AA;

Query Match 73.6%; Score 3478; DB 6; Length 837;
Best Local Similarity 75.3%; Pred. No. 2.3e-314;
Matches 666; Conservative 68; Mismatches 98; Indels 52; Gaps 8;

QY 5 GVADRLTGKKEAWSEKIRGTVRLVKKEVLDVGDENASLLDGVHRLGWDGQVAFQVLS 64
DB 5 GFFDLTGKKEAWSEKIRGTAVLVKVDVGLGLGDFHSLLDGVH----- 49

QY 65 ATAADPSNGGKVGKAAHLEEAVALSKSTADGETVYRVSEFDESGQIPGAVLVRNLOH 124
DB 50 -----NGRGKLGKPAHLEELVVTMKSTAAGSVFRVAFWEDESQIPGAVVVTNSR 102

QY 125 AEFFLKTLLTEGVPGKTVVFNANSWVYVPHKLYSQERIFPANDTYLPSKMPALVPYRQD 184
DB 103 SEFFLKTLLTEGVPGKTVVFNANSWVYVPHKLYSQERIFPANDTYLPSKMPALVPYRQD 160

QY 185 ELKILRGDDNPGPYQEHDRVRYDYNDLGDPPDKGEEHARPILOGSQEHYPARCRTGRH 244
 Db 161 ELNLRGDKGKPGYKEHDDRIYDYNDLQDPDKGSLVRPVLGSGQSELPYPRGRGTGRA 220
 QY 245 PTK-KDPNSESRLFLNLNINIVPRDERFGLKMSDFLGYSLKTTIEAVLPTLGTFFVDDTP 303
 Db 221 PTKSDPNTESSLPLDLNINIVPRDERFGLKMSDFLGYSLKALVEGVLPIRTYVDTTP 280
 QY 304 KEFDSFEDILGYELGPEAPNPLIAEIRKIPSEFLRSILPNSGSHDHPKMLPNVKS 363
 Db 281 KEFDSFQDIMEYLGGLKLVANASALAEIKKVPFELIKSLPLVAG-QDVILKLPVHYKE 339
 QY 364 DVLKAPBEKFGWTDSEFARETLAGVNPVLIKLTFFPAKSTLDRPOYGDHSTKITEAH 423
 Db 340 -----KFAWTDSEFAREMLAGVNPVWIKELT-----SILDPNVDGHTSKITEAH 395
 QY 424 IHNMGGLSVQNALRNKRLFLDHDHMPVLDDEINELGNFIYASRTLLFLKDDGTLKP 483
 Db 386 IHNMEGLTVQNALKGNRLFLDHDHMPFLDKINKLDGNFIYASRTLLFLKDDGTLKP 445
 QY 484 LAIELSLPHDPGQORGAVSKVYTPAHTGVGHVWQAKAVACVNDSSAWHQLISHWLNTHA 543
 Db 446 LAIELSLPHDPGQORGAVSKVYTPANTGVESQIWLQAKAVASVNDSSAWHQLISHWLNTHA 505
 QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYLG 603
 Db 506 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYLE 565
 QY 604 MSADVYKSNFNEQALPADLVKRGVAVDPDSSPYGVRELLIKDYPYAVDGLVWATERWV 663
 Db 566 MSVVYKSNKTEQALPVDLVKRGVAVDPDTPSPYNVRLIKDYPYAVDGLVWATERWV 625
 QY 664 KEYLDIYYPNDGELQRDVELQAWKVEEAEAGHGLDKDRDWMFRMDTVQQLARACTIITW 723
 Db 626 GEYLAIYVPNDGVLGRDEELQAWKVEEVGHGLDKQDWMFKMDTVQELTRACTIITWI 685
 QY 724 ASALHAAVNFQGYAGVYLPNRPASRPMPBPESHYKKGAGQKEADWVFTITTSQF 783
 Db 686 ASALHAAVNFQGYAGVYLPNRPVSRPMPBPETEYAKLERGGDEADLVFTITTSQF 745
 QY 784 QTLIGISLIELSKHSSDEVVLGQDPRDWTSDAKALDAFKPGSLVQIENRIKTMND 843
 Db 746 QTLIGISLIELSKHSSDEVVLGQDTPPE-WTSDAKALDAFKPGSLVDIENRIKDMNG 804
 QY 844 SPDLKRNKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
 Db 805 NSALKNRNGPYKMPYMLLYP-----GLTAMGIPNSISI 837

RESULT 3
 ADC53139
 ID ADC53139 standard; protein; 863 AA.
 AC ADC53139;
 XX
 DT 18-DEC-2003 (first entry)
 DE 9'-specific lipoxigenase gene derived protein.
 XX
 KW 9-specific lipoxigenase; 9'-specific lipoxigenase activity; microbe;
 KW animal; plant.
 XX
 OS Unidentified.
 XX
 PN JP2002325577-A.
 XX
 PD 12-NOV-2002.
 XX
 PF 27-APR-2001; 2001JP-00133611.
 XX
 PR 27-APR-2001; 2001JP-00133611.
 XX
 PA (SHIS) SHISEIDO CO LTD.

XX WPI; 2003-460714/44.
 DR N-PSDB; ADC53127.
 XX
 PT A new rice-derived 9-specific lipoxigenase gene useful for production of
 PT 9-specific lipoxigenase.
 XX
 PS Disclosure; Page 7-10; 17pp; Japanese.
 XX
 CC The invention relates to a novel 9-specific lipoxigenase comprising a
 CC fully defined sequence of 863 amino acid residues, as given in the
 CC specification and a derivative having 9'-specific lipoxigenase activity.
 CC The 9-specific lipoxigenase gene is useful for production of the 9-
 CC specific lipoxigenase in microbes, animal or plant cells. This sequence
 CC represents the protein from the 9'-specific lipoxigenase gene of the
 CC invention.
 XX
 SQ Sequence 863 AA;
 Query Match 63.3%; Score 2987.5; DB 7; Length 863;
 Best Local Similarity 64.4%; Pred No. 1.3e-268;
 Matches 569; Conservative 111; Mismatches 179; Indels 25; Gaps 10;
 QY 5 GVADRLTGKKEAWSEGKIRGTVRLVKKEVLVDGDFNASLLDGVHRILGWDGVAFLVLS 64
 Db 4 GLKDKLTGKN-----GNKIKGLAVLMSRKLLDPRDFTASLLCNVHEVFG--NSITCQLVS 56
 QY 65 ATAADPSGGRGKGVKAAHLEAVVLSKSTADGETVYEVSPEDW-ESOGIPQAVLVRNLQ 123
 Db 57 ATVAQONNEGRTIVGEANLEQGLTDLPSVQGESKLTVRFNWMDKHGVPGLIINKNH 116
 QY 124 HAEFLKTLTLEGVPGKGTVPFVANSWYVPHKLSQERIFFANDTYLESKMPAALVPYRQ 183
 Db 117 STKFFLKTLTLDHVGCDTIVFVANSWYVPGKHYNRIFFANISYPPSQMPEALRPYRE 176
 QY 184 DELKILRGDDNPGPYQEHDRVRYDYNDLGDPPDKGEEHARPILOGSQEHYPARCRTGR 243
 Db 177 DELYLRGDEDRGQYQEHDRVRYDYNDLGEPRD--DNPRPVLGSGSQKHYPARRGTGR 234
 QY 244 HPTKDPNSESRLFLNLNINIVPRDERFGLKMSDFLGYSLKTTIEAVLPTLGTFFVDDTP 303
 Db 235 IFTKDPNSESRLSLE-QIVPDSERFAHLKMSDFAGYSIKAIVQGLPAIRTYVDTLP 293
 QY 304 KEFDSFEDILGYELGPEAPNPLIAEIRKIPSEFLRSILPNSGSHDHPKMLPNVKS 363
 Db 294 GEFDSFEDILKLYRGGLKLPISALPEELKSPVQLIKDLPLVGG-SYLLKFPKPIIK- 351
 QY 364 DVLKAPBEKFGWTDSEFARETLAGVNPVLIKLTFFPAKSTLDRPOYGDHSTKITEAH 423
 Db 352 -----ENEVAVRTDEFARELLAGLNPVIRLTFEPFKSTLDPKVGQDTTITPAH 404
 QY 424 IHNMGGLSVQNALRNKRLFLDHDHMPVLDDEINELGNFIYASRTLLFLKDDGTLKP 483
 Db 405 IEKNTLEGLSVQALDSNRLYLDDHDHMPFLDINSLDGIFTVATRTLLFLRDDDTLKP 464
 QY 484 LAIELSLPHDPGQORGAVSKVYTPAHTGVGHVWQAKAVACVNDSSAWHQLISHWLNTHA 543
 Db 465 LAIELSLPHIEGULTSAKSVHTTPASSGIESWVWQAKAVAVVNDSSGRLISHWLNTHA 524
 QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKAYLG 603
 Db 525 VMKPFVIATNRQLSVTHPVYKLLQPHYRDTMTINALARQTLINGGGIPEQTVFPGKHALA 584
 QY 604 MSADVYKSNFNEQALPADLVKRGVAVDPDSSPYGVRELLIKDYPYAVDGLVWATERWV 663
 Db 585 MSSAVYKSNFNEQALPADLVKRGVAVDPDSSPYGVRELLIKDYPYAVDGLVWATERWV 644
 QY 664 KEYLDIYYPNDGELQRDVELQAWKVEEAEAGHGLDKDRDWMFRMDTVQQLARACTIITW 723
 Db 645 TEYCAIYYPNDGVLQGDVALQAWKVEEVGHGLDKDADWVFKQSLPELTKACTIITWI 704
 QY 724 ASALHAAVNFQGYAGVYLPNRPASRPMPBPESHYKKGAGQKEADWVFTITTSQF 783

Db 705 ASALHAAVNFQGYVAGYLPNRTISRPMPEPGSKVETEL---DENPEKFFRTITTSQF 761
 QY 784 QTILGISLIETLSKSSDEVYLGORDPDRKTSADKALDAPKPGSLVIOENRIKTMND 843
 Db 762 QTILGVSLIELLSKSSADEIYLGORDTPE-WTSPDKALEAPKPSROLVIESKVLNMNK 820
 QY 844 SPDLKNRKGPVEMPYMLLYPNTSDVTGKAGLTAMGIPNSISI 887
 Db 821 DPLLKRVGFANFFYTLFMFNTSDNKG-AAEGITARGIPNSISI 863

RESULT 4

AAU99691
 ID AAU99691 standard; protein; 862 AA.

AC AAU99691;

XX 07-OCT-2002 (first entry)

XX Barley wild-type lipoxigenase 1, LOX-1.

XX Barley; plant; enzyme; lipoxigenase-1; LOX-1; transgenic; beer; beverage;
 KW malt; organoleptic property; brewing; trans-2-nonenal; T2N;
 KW elevated storage temperature; flavour stability; shelf-life.

XX Hordeum vulgare.

XX WO200253720-A1.

XX 11-JUL-2002.

XX 29-DEC-2000; 2000WO-IB002045.

XX 29-DEC-2000; 2000WO-IB002045.

XX (CARL-) CARLSBERG RES LAB.

PA (HBTB-) HEINEKEN TECH SERVICES BV.
 PA (BRAS-) BRASSERIES KRONENBOURG SA.

PI Douma AC, Doderer A, Camaron-Mills V, Skadhauge B, Bech LM;
 PI Schmitt N, Heistek JC, Van Mechelen JR;

DR WPI; 2002-557741/59.

DR N-PSDB; ABK98441.

XX Novel barley cultivar having reduced lipoxigenase 1 activity and which
 PT expresses mutant lipoxigenase protein, useful in brewing processes to
 PT reduce formation of off-flavors in brewed products e.g. beer during
 PT storage.

PS Example 3; Page 86-89; 112pp; English.

XX The invention relates to a barley plant or portion comprising a mutant
 CC lipoxigenase-1 (LOX-1) protein, characterised by a reduction or absence
 CC of LOX activity as compared to a non-mutated control, or comprising a
 CC heterologous nucleic acid sequence expressing an antisense sequence to a
 CC portion of a transcribed region of barley lox-1 gene, operably linked to a
 CC promoter and a transcription terminator sequence. Also included are
 CC grain or plant progeny produced from the barley plant or its portion, a
 CC plant product produced from the barley plant or its portion or progeny,
 CC and a beverage e.g. beer, manufactured using the plant product, plant or
 CC its portion or progeny. The mutated barley plant, portions, progeny and
 CC products are useful in the manufacture of a beverage, preferably malt or
 CC beer, for stabilising organoleptic properties of a brewed product over a
 CC measured period of time for the manufacture of a brewed product having
 CC reduced levels of free trans-2-nonenal (T2N) over a measured period of
 CC time or under conditions of elevated storage temperature and for the
 CC preparation of beverage presenting organoleptic qualities that remain
 CC stable over a measured period of time or at elevated storage
 CC temperatures. Beer with significantly enhanced flavour stability, both
 CC during storage and on exposure to elevated storage temperatures is
 CC obtained. These properties enhance the quality of beer and are useful to
 CC extend its shelf-life and reduce the need to cool beer during transport

CC and storage. The present sequence is the wild-type LOX-1 protein

XX Sequence 862 AA;

QY Query Match 62.2%; Score 2936.5; DB 5; Length 862;

XX Best Local Similarity 63.1%; Pred. No. 7.6e-264;

XX Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY 1 MFHGVADRLTGKNEAMSEGIKRGTVLKVKEVLVDGDNASLLDGVHRLTGWDGVAF 60

Db 1 MLGLGLIDTLTGANKSA---RLKGTVVMKRNVLNDLNDFOATIIDGGEFLG--KGVC 54

QY 61 QLVSAATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSPFWD--ESQGPAGVAV 119

Db 55 QLISSSTAVDQNGGRGKVGAEAELEQWVTSLSPTLTGSGEGLTFEDVEVEKLVGPAIV 114

QY 120 ENLQHAETFLKTLLEGVPGK-GTVVFVANSWVPHKLYSQERIFFEANDTVLPSPKMPAAL 178

Db 115 NNYHSSEFLKTLITLHDVFGSGNLTFVANSWIYPAANYRYSRVFFPANDTVLPSPKMPAAL 174

QY 179 VPYRQDELKILRGDNPQGYQEHDRVRYDYNDLGDPKGEHARFILGSGQEHYPYPR 238

Db 175 KPYRDELRLNRGDDQGPYQEHDRIVRYDYNDLGE-----GRPLGGNSDHPYPR 227

QY 239 CRTGSHPTKDPNSESRLFLNLNLYVPRDERFGHLKMSDPLGYSLSLTIIEAVLPTLGT 298

Db 228 GRTERKPNASDPSLESLSLLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRY 286

QY 239 VDDTPKPEFDFEDILGLYELGFEAPNPNFLIAEIKKIPSEFLRSILFNGSHDHLKMLP 358

Db 287 VDDTPGEBFDSQDIINLYEGGILKPKVAALBELRKQFPQLIKDLLPVGG--DSLKLVP 345

QY 359 NVIKSDVLKKAPEKFGNRTDEEPARETLAGVNPVILKLTETFEPAKTLTPROVGDHTSK 418

Db 346 HIIQ-----ENKQAWRTDEEPAREVLAGVNPVIMITRLTEFPFKPSLSPKSGDHTST 397

QY 419 ITEAHIRHMGGLSVQNALRNKRLFIIDHDFHFPYLDINELEGNITYASRTLLFLKDD 478

Db 398 ITAEHIEKNLGLTVQQALESNRLIYLDHDFRFPFLIDVNNLFGNFIYATRLTFLRGD 457

QY 479 GTLPLAIELSLPHDPDQOQGVSKVYTPAHTG-VEGHVWOLAKAYACVNDSAWHQLISH 537

Db 458 ORLTPLAIELSEPTIQGGLTTAKSKVYTPVPSGVEGWVWELAKAYAVANDSGWHQLVSH 517

QY 538 WLNTHAVIEPVIATNEQLSVVHVPVKLLSPHYRDTLNALAROTLINAGGVFERTVFP 597

Db 518 WLNTHAVMEPVIISTNHLSTVHPVKLLSPHYRDTLNALAROTLINAGGVFERTVFP 577

QY 598 AKYALGSAOVYKSWNFNEQALPADLVKRGVAVDPDQSSPYGVRLLIKDYPAVDGLVIW 657

Db 578 KGFALGSAVVYKDWKFTSQGLPDDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWH 637

QY 658 AIERWVKEYLDIYYPNDGELQRDVELQAWKVEEBAHGLDKDRDWMPRDVTQOLARAC 717

Db 638 AIEQVVEYLAIVYPNDDVLOGDTEVQAWKKEFVCHGDLKADPWPKVQSPVELAKAC 697

QY 718 TTIIVASALHAAVNFQGYVAGYLPNRTASRRPMPPEPGSHDYKKGACQKESADVMVIR 777

Db 698 TTIIVIGSALHAAVNFQGYVAGYLPNRTVSRRRMPPEPGTEEYAEI---ERDPERAFIH 754

QY 778 TITSQFOTILGISLIELLSKSSDEVYLGORDPDRWTSADKALDAFKRGSRLVQENR 837

Db 755 TITSQIQTILGVSLIELLSKSSDEVYLGORDTPE-WTSPDKALEVFKRSDRLVEIESK 813

QY 838 IKTWNDSPDLKNRKGPVEMPYMLLYPNTSDVTGKAGLTAMGIPNSISI 887
 Db 814 VVGWNHDPDLKNRNGPAKFFYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 5

ABG30566

ID ABG30566 standard; protein; 862 AA.

XX

AC ABG30566;
 XX 07-OCT-2002 (first entry)
 DT
 XX Wild type barley low-lipoxygenase 1.
 DE
 XX Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;
 KW brewing; trans-2-nonenal; flavour stability; storage; shelf-life;
 KW low-lipoxygenase 1; barley.
 XX
 OS Hordeum vulgare.
 XX
 XX WO200253721-A1.
 PN
 XX 11-JUL-2002.
 PD
 XX 22-JAN-2001; 2001WO-IB000207.
 PF
 XX 29-DEC-2000; 2000US-00751687.
 PR
 XX 29-DEC-2000; 2000WO-IB002045.
 XX
 XX (CARL-) CARLSBERG RES LAB.
 PA (HEB-) HEINEKEN TECH SERVICES BV.
 PA (BRAS-) BRASSERIES KRONENBOURG SA.
 XX
 PI Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;
 PI Schmitt N, Heistek JC, Van Mechelen JR;
 DR
 DR WPI; 2002-557742/59.
 DR N-PSDB; ABK88515.
 XX
 FT Novel barley plants having low lipoxygenase activity useful in the
 FT production of plant products such as malt or brewed beverages,
 FT particularly beer having increased stability and flavor.
 XX
 PS Example 3; Fig 22A-B; 11:2pp; English.
 XX
 CC The invention describes a barley plant (I) having a mutant lipoxygenase-1
 CC (LOX-1) protein, the plant or plant portion characterised by a reduction
 CC or absence of LOX activity as compared to a non-mutated control, or
 CC comprising a heterologous nucleic acid sequence expressing an antisense
 CC sequence to a transcribed region of barley lox-1 gene, operably linked to
 CC a promoter and a transcription terminator sequence. (I), a plant (II)
 CC produced using (I) or a plant product (III) is useful in the manufacture
 CC of a beverage, preferably malt or beer, for stabilising organoleptic
 CC properties of a brewed product over a measured period of time as compared
 CC to a control brewed product produced using a non-mutated barley plant or
 CC its portion, grain or plant progeny, or plant product, and for the
 CC manufacture of a brewed product having reduced levels of free trans-2-
 CC nonenal over a measured period of time or under conditions of elevated
 CC storage temperature, as compared to a control brewed product produced
 CC using a non-mutated barley plant or its portion, grain or plant product.
 CC Beer with significantly enhanced flavour stability, both during storage
 CC and on exposure to elevated storage temperatures is obtained. These
 CC properties enhance the quality of beer and are useful to extend its shelf
 CC -life and reduce the need to cool beer during transport and storage. This
 CC is the amino acid sequence of the wild type barley low-lipoxygenase 1
 CC (lox-1) protein
 XX
 XX Sequence 862 AA;
 SQ
 Query Match 62.2%; Score 2936.5; DB 5; Length 862;
 Best Local Similarity 63.1%; Pred. No. 7.6e-264;
 Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;
 1 MFWHGVADRLGKNEAWSEKIGTGLVRLVYKKEVLVDGDFNALSILGQVHRLGWDQVAF 60
 1 MLLGLGLDITLTKANKSA---RLKGTVMLEKKNVLDLDFGATIIDGIFLGG--KGVC 54
 61 QLVGATAADPNNGRGKGVKAHLEEAWSLSTADGETVYRVSEFWD--ESQIGPGAVLV 119
 55 QLISSTAVDQNGRGKGVGAEELEQWTSLSPLTTGSEKFGLTDFDVEKLGVPGAIVV 114

QY 120 RNLOHAEFFLKTTLTSGVPGK-GTVVVFVANSVYVPHKLYSQERIFPANTYLPSPKMPAAL 178
 DB 115 NNYHSSEFLKTTTLHDVFGSGNLTFVANSVIYPAANYRYSRVFPFANDTYLPSCMPAAL 174
 QY 179 VPYRQDELKILRGDDNPGFVQEHDRVYVYNDYNDLGDGDPKGEHARPIILGSGSEHYPFR 238
 DB 175 KPYRDELANLRGDDOQGYQEHDRYRYVDVNDLGE-----GRPIILGNSDHPYFR 227
 QY 239 CRTGRHPTKKDPNSESRLFLNLNIYVPRDERFGHLKMSDFLGYSLKTIIEAVLPGLGTF 298
 DB 228 GRTERKPNASDPSLESRLSLE-QIYVPRDEXFGLKTSDFLGYSIKAITQGLLPVARTY 286
 QY 299 VDDTPKEFDSFEDILGLYELGPEAPNPLIAERKKIPSEFLRSILPNSGSHDPLKMPLP 358
 DB 287 VDTTPGEFDSFQDIINLYEGGKLPKVAALBEHRKQFPLQIKDLPLVCG-DLLKLPVP 345
 QY 359 NVTKSDVLKKAPEFKGWRTEDEFAETLAGVNPVILKLTETFPKASTLDPQYGDHTSK 418
 DB 346 HIIQ-----ENQAWRTDEFAEVLAGVNPVITLTFEPPKSSLDPSKFGDHTST 397
 QY 419 ITEAHTHNMGGLSVQNALRNKELFTLDHHDHFMPLYDEINLEGNFIYASRTLLFLKDD 478
 DB 398 ITAEHIEKNLEGLTVQQALESNRLYILDHHDHFMPLYDNNLPGNFIYATLTFLFRGD 457
 QY 479 GTLKPLAIELSLPHPDGQQRGAVSKYVTPAHTG-VEGHVWQLAKAYACVNSAWHQLISH 537
 DB 458 GRUTPLAIELSEPIIQGLTTAKSKYVTPVPSGSEGVWVWELAKAYAVVNSGWHQLVSH 517
 QY 538 WLNTHAVIEPFIATNRQISVVPVHKLSPHYRDTLAINALARQTLINAGGVFERTVFP 597
 DB 518 WLNTHAVMBPFIATNRHLSVTHPVHKLSPHYRDTMTINALARQTLINAGGIFEMTVFP 577
 QY 598 AKYALGMSADVYKSNFNEQALPADLVKRGVAVPQSSPYGVRLTIKDYPIYAVDGLIVW 657
 DB 578 GKPALGMSAVVYKDKWKFTEQGLPDDLKEGMAVEDPSSPYKVLVLLVSDPYAADGLAIWH 637
 QY 658 AIBRWKVEYLDIYPNDEGLQRDVLEQAWKVEVREAHGDLKORDWPMRMTVQQLARAC 717
 DB 638 AIEQVYSEYLAIIYPNNDGLQDTEVQAWKKEVREHGHDKDADAPWPKMQSVPELAKAC 697
 QY 718 TTIIVASALHAAVNPGQYPYAGYLPNRPATASRRPMPPEGSHDYKKLGAGQKAEADWFTIR 777
 DB 698 TTIITGSAALHAAVNPGQYPYAGYLPNRPATASRRPMPPEGSHDYKKLGAGQKAEADWFTIR 754
 QY 778 TTSQQTTLGSLTLEILSKHSDDEVYLGQRDEPRWTSDAKALDAFKRFGSRLVQIENR 837
 DB 755 TITSQITQITIGVSLLEVLKSHSDDEVYLGQRDTPB-WTSDPKALEVFKRFSRLVVEISK 813
 QY 838 IKTMNDSPDLKVRKGVEMVPMYLLPNTSDVTGKAEGLTAMGIPNSISI 887
 DB 814 VVGMHDPBLKVRNGPAKFPYMLLPNTSDHKG-AAAGLTAKGIPNSISI 862
 RESULT 6
 AAU99693
 ID AAU99693 standard; protein; 862 AA.
 XX
 XX AAU99693;
 AC
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX Barley wild-type lipoxygenase 1, LOX-1, mutant #2.
 DE
 KW Barley; plant; enzyme; lipoxygenase-1; LOX-1; transgenic; beer; beverage;
 KW malt; organoleptic property; brewing; trans-2-nonenal; T2N;
 KW elevated storage temperature; flavour stability; shelf-life; mutant;
 XX
 OS Hordeum vulgare.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 368
 FT


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Db 117 AAEFFLKTILDNVPGHGVVANSWIYPAKYRNVNFSSNDTSLPKMAALXPYRD 176
Qy 184 DELKILRGDNDPGYQEHDRVRYDYNDIGDPDKGEEHARPILGSGQEHPPRRCTGR 243
Db 177 DELNLKRGDDQGGPYQEHDRVRYDYNDIGDPDSG--NRPVILGSGPDRPYFRRGTR 234
Qy 244 HPTKDPNSRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP 303
Db 235 KPXTDPTAESRLSLE-NIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP 293
Qy 304 KEFDSFDILGLYELGPEAPNPLIARIRKIPSEFLRSILPNSGSHDHPKMLPNVIRK 363
Db 294 GEFDSFDILGLYELGPEAPNPLIARIRKIPSEFLRSILPNSGSHDHPKMLPNVIRK 351
Qy 364 DVLKKAPEFPGWRTDEEPARETLAGVNPVILKRLTEFPKASTLDPQYGDHSTKITEAH 423
Db 352 D--KKA-----NMTDDEFAREILAGVNPVILKRLTEFPKASTLDPQYGDHSTKITEAH 402
Qy 424 IRHNMGLSVQNALRNKRLFTLDHDFHMPYLDEINELEGNFTYASRTLLFKDQDTLKP 483
Db 403 VERGLEGLTVQQAIDGNLLYVVDHDFHMPYLDEINELEGNFTYASRTLLFKDQDTLKP 461
Qy 484 LAIELSLPH-PDQQRGAHSVKTTPAHT-----GVEGHVWQLAKAYACVNDSAWHQLISH 537
Db 462 LAIELSLPH-PDQQRGAHSVKTTPAHT-----GVEGHVWQLAKAYACVNDSAWHQLISH 521
Qy 538 WLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597
Db 522 WLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 581
Qy 598 AKYALGNSADYKSWNFNEQALPADLVKRGVAVDPQSSPYGRLLIKDYPIYADGLVIW 657
Db 582 RNDALAMSSAFYKDWSPADQALPDDLKRGVAVDPQSSPYGRLLIKDYPIYADGLVIW 640
Qy 658 AIERWKEYLIDITYPNDGELQDVVEQAQWKEVREAHGDLKDRWPRMDTVQQLARAC 717
Db 641 PIEQWATEYLAIYVNDGVVQDAELQAWKEVREAHGDLKDRWPRMDTVQQLARAC 700
Qy 718 TTIWVASALHAANFQGYAGVLPNRPASRRPMPGSHDYKGLGAGQKADWVFIR 777
Db 701 ATTIWIGSALHAANFQGYAGVLPNRPASRRPMPGSHDYKGLGAGQKADWVFIR 757
Qy 778 TITSQFOTILGISLIELILSKSHSDEVVLGQDEPDRWTSDAKALDAFKFGRGLVQIENR 837
Db 758 TITKQMAIVGISLIELILSKSHSDEVVLGQDEPDRWTSDAKALDAFKFGRGLVQIENR 816
Qy 838 IKTNDSFDILKRNKGPVEMPMILLYNTSDVTGKAEGLTAMGIPNSISI 887
Db 817 VVAMNKDPHRRKNRVGPTNFTYLLYNTSDVTGKAEGLTAMGIPNSISI 865

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RESULT 11

AA20670
ID AA20670 standard; protein; 865 AA.

XX AC AA20670;

XX AC AA20670;
DT 24-OCT-2003 (revised)
DT 04-NOV-1992 (first entry)

XX DE Lipoxigenase.

XX KW Temperature; denaturation; rice; pRLC11; enzyme.

XX OS Oryza sativa; (Nihonbare).

XX PN JP04094681-A.

XX PD 26-MAR-1992.

XX PF 13-AUG-1990; 90JP-00211470.

XX

PR 13-AUG-1990; 90JP-00211470.
XX (MITS-) MITSUI GHOSAI SHOKU.
XX WPI; 1992-156052/19.
DR N-PSDB; AAQ24234.
XX Prodn. of protein in E.coli without denaturation - by culturing transformed E.coli at low temp.
XX Disclosure; Fig 1 (1-4); 5pp; Japanese.
XX mRNA was extracted from a rice plant and used to prepare a cDNA library. A clone contg. cDNA encoding the full length lipoxigenase gene was isolated (pRLC11) and used to transform E.coli. The transformant was deposited as FERM P-11635. pRLC11 was then ligated with an expression vector to obtain clone ET3a/RLX2, which was used to transform E.coli BL21(DE3). The obtained clone was deposited as FERM P-11636. This clone was inoculated to ampicillin contg. LB medium, and cultured at 37 degrees C overnight. IPTG was then added, and the mixt. cultured below 20 degrees C, e.g. 18 or 15 degrees C for 16 hrs. Cells were collected and disrupted by ultrasonication to recover the enzyme solution. (Updated on 24-OCT-2003 to standardise OS field)
XX Sequence 865 AA;

Query Match 59.9%; Score 2829.5; DB 2; Length 865;
Best Local Similarity 62.1%; Pred. No. 7.2e-254;
Matches 553; Conservative 113; Mismatches 189; Indels 35; Gaps 17;
Qy 5 GVADRLGKKEANSEKIRGTVRVLKVEVLVDGDFNALLDGVHRILGDDGVAFLVLS 64
Db 4 GIIIGLIG-KNKA----RLKGSILVMKRNALDINDFOATVIERISEFLG--RGVTCQLVS 56
Qy 65 ATAADPNNGSGRGKGVKAAHLEEAUVSLKSTADGETVYRVSVFWD--ESQGPVGAVLVRLNQ 123
Db 57 SSVLPNNNGNRGRVGTSEALQMLTSLPSTTGESKFGVTFEWEVKMGIPGAIIVKNH 116
Qy 124 HAEFLKTLTLEGVPGKGTGVVANSWVYHKLVSQERIFPANDTYLPKMPAALVYRQ 183
Db 117 AAEFFLKTILDNVPGHGVVANSWIYPAKYRNVNFSSNDTSLPKMAALXPYRD 176
Qy 184 DELKILRGDNDPGYQEHDRVRYDYNDIGDPDKGEEHARPILGSGQEHPPRRCTGR 243
Db 177 DELNLKRGDDQGGPYQEHDRVRYDYNDIGDPDSG--NRPVILGSGPDRPYFRRGTR 234
Qy 244 HPTKDPNSRLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP 303
Db 235 KPXTDPTAESRLSLE-NIYVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFFVDDTP 293
Qy 304 KEFDSFDILGLYELGPEAPNPLIARIRKIPSEFLRSILPNSGSHDHPKMLPNVIRK 363
Db 294 GEFDSFDILGLYELGPEAPNPLIARIRKIPSEFLRSILPNSGSHDHPKMLPNVIRK 351
Qy 364 DVLKKAPEFPGWRTDEEPARETLAGVNPVILKRLTEFPKASTLDPQYGDHSTKITEAH 423
Db 352 D--KKA-----NMTDDEFAREILAGVNPVILKRLTEFPKASTLDPQYGDHSTKITEAH 402
Qy 424 IRHNMGLSVQNALRNKRLFTLDHDFHMPYLDEINELEGNFTYASRTLLFKDQDTLKP 483
Db 403 VERGLEGLTVQQAIDGNLLYVVDHDFHMPYLDEINELEGNFTYASRTLLFKDQDTLKP 461
Qy 484 LAIELSLPH-PDQQRGAHSVKTTPAHT-----GVEGHVWQLAKAYACVNDSAWHQLISH 537
Db 462 LAIELSLPH-PDQQRGAHSVKTTPAHT-----GVEGHVWQLAKAYACVNDSAWHQLISH 521
Qy 538 WLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 597
Db 522 WLNTHAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFP 581
Qy 598 AKYALGNSADYKSWNFNEQALPADLVKRGVAVDPQSSPYGRLLIKDYPIYADGLVIW 657
Db 582 RNDALAMSSAFYKDWSPADQALPDDLKRGVAVDPQSSPYGRLLIKDYPIYADGLVACT 640

Amino acid sequence of tobacco lipxygenase-1 (LOX-1).
Lipxygenase-1; LOX-1; enzyme; plant; dioxygenation;
polyunsaturated fatty acid; pentadiene; disease resis-
tobacco; tomato; potato; pepper.

OS Nicotiana tabacum.
 XX WO200299112-A2.
 XX 12-DEC-2002.
 XX 06-JUN-2002; 2002WO-FR001943.
 XX 07-JUN-2001; 2001FR-00007470.
 XX 07-NOV-2001; 2001FR-00014358.
 XX (RHOB-) RHOBIO.
 XX Mene-Saffrane L, Esquerre-Tugaye M, Fournier J, Beffa R;
 PI Grosjean-Cournoyer M;
 XX WPI; 2003-156858/15.
 DR N-PSDB; AB268210.
 XX Reducing sensitivity of plants to diseases and pathogens, by
 PT overexpressing a lipoxygenase, also vectors and cassettes for the process
 PT and transformed plants.
 XX Claim 7; Page 39-41; 47pp; French.
 XX The present sequence represents a lipoxygenase-1 (LOX-1) gene. LOX-1 is
 CC an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids
 CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce
 CC the sensitivity of plants to diseases and attack by pathogens.
 CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi
 CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.
 CC tobacco, tomato, potato and pepper
 XX Sequence 862 AA;
 SQ

Query Match 57.7%; Score 2724.5; DB 6; Length 862;
 Best Local Similarity 59.9%; Pred. No. 4.4e-244;
 Matches 533; Conservativity 111; Mismatches 215; Indels 31; Gaps 11;

QY 1 MFHGVADRLTGKNEAMSEG-KIRGTVRLVKKEVLDVDFNASLLDGVHRLGWDDGVA 59
 DB 1 MFLEXIVDAITGKD-----DGKVKGTVLMKKNVLDFTDINASVLDGVLEFLG--RRVS 53
 QY 60 FQLVSAATADPSNGRGKVGKRAHLEBAVVLKSTADGETVYRVSVFEWDSQ-GIPGAVL 118
 DB 54 LELISSVNADPANGLOGRKSAAYLENLWLTNSTFIAAGESAFRVTFDWDDEFGVPGAFI 113
 QY 119 VRNLQHAFFFLKTLLEGVPGKGTVPFVANSWYVPHKLYSCERIFFFANDTVLPKMPAAL 178
 DB 114 IKNLHFSFEFLKSLTLEVDVPHGKHVFCVNSWYVPAKYKSDRIFFANQAYLPSETPTL 173
 QY 179 VPYRODELKILRGDDNPGPYQEHDRVYRYDNDLGDPPKGEHARFILGSGQEHYPYRR 238
 DB 174 RKYRENELVTLRG-DGTGKLEWDRVYDYYNDLGDPPKQDLSPVLGSGSEYYPYRR 232
 QY 239 CHTGRHPTKOPNSERL-FILNLNIVYPRDERGHLKMSDFLGYSLKTIIEAVLPLGT 297
 DB 233 GRTGRKPTKOPNSERLPLMSLDIYVPRDERGHKLSDFLFAKLSIVQLLPEFKA 292
 QY 298 FVDDTPKEFDSFEDILGYELGPEAFNNPLIAEIRKKIPSEFLRSILPNSGSHDHPKQPL 357
 DB 293 LFDSTHNEFDSFEDVLKLYEGIKLPQGLLKAITDSIFLILKELL-RSDGSEGLPKYPT 351
 QY 358 PNVIKSDVLKKAPEKFGWRDEFARETLAGVNPVIKRLTEPPAKSLTDPROYGDHTS 417
 DB 352 PQVIOED-----KTAWRTDEFGREMLAGVNPVIISRLQEPFPKSKLDPKLYGNQS 403
 QY 418 KITEAHIRHNMGLSVQNALRNKFLFILDHHDHFWPYLDEINELEGNFIVASRTLLFLKD 477
 DB 404 TITREIQLDGLTIDEAIKTNRLFILNHHDLMPYLRLINTSTDKTVASRTLLFLQD 463
 QY 478 DGLTKPLAIELSLPHDPDQCGAGSVKVTPTAHTGVEGHVWOLAKAYACVNDSAWHQLISH 537

464 NGTLKPSAIELSLPHDPDQCGAGSVKVTPTAHTGVEGHVWOLAKAYACVNDSAWHQLISH 523
 538 WLNTHAVIRPFIATNRQLSVVHPVKLLSPHYRDTLNINALAROTLINAGGVFERTVFP 597
 524 WLNTHAAIEFFVIATNRQLSALHPYIKLLPHFRFETMNLAROLLINGGGLLELTVPF 583
 598 AKYALGMSADVYKSNFNFOALPADLVKRGVAVPOSSPYGVRLLLIKIDPYAVDGLVIWM 657
 584 AKYSMEMSAVYKDWYFPEQALPTDLIKRGVAVDESSPLGIRLLITQDYFYAVDGLKWS 643
 658 AIERWVKEYLDIYYPNDGSLQDVELQAWKKEVREAHGDLKDRDWWPMDTVOQLARAC 717
 644 AIKSWTEYCNYYKSSDDAVQKTELQAWKKEVREAHGDLKDRDWWPMDTVOQLIDSC 703
 718 TTIIVASALHAAVNFQYVYAGYLPNRPRTARRPMPPEGSHDYKKGAGKEADWVFIR 777
 704 TITINTIASALHAAVNFQYVYAGYLPNRPRTARRPMPPEGSHDYKKGAGKEADWVFIR 760
 778 TITSQFOTILGISLIEILSKSSDEVILGQRDEPDRWTSDAKALDAFKFSGRLVQIENR 837
 761 TITPQOTILGISLIEILSRHSDDIYLGQRSPF-WTKDQFPLSAFARFGKLSIDEDQ 819
 838 IKTMNDSPDLKVRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
 820 IMQNVDEKWKNSRSGVPYVYLLPPTSEG-----GLTGKIPNSVSI 862

RESULT 15
 ID AAB46803
 XX AAB46803 standard; protein; 857 AA.
 AC AAB46803;
 XX 23-APR-2001 (first entry)
 DT Potato LOX protein.
 XX Potato; LOX protein; lipoxygenase; arachidonic acid; mutant; plant;
 KW 11-arachidonate-lipoxygenase; 11-hydroperoxy-arachidonic acid.
 XX Solanum tuberosum.
 XX WO200104323-A2.
 XX 19-JAN-2001.
 XX 10-JUL-2000; 2000WO-BP06539.
 XX 08-JUL-1999; 99DE-01031819.
 XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.
 PA Feussner I, Hornung E, Rosahl S;
 PI WPI; 2001-081054/09.
 DR New nucleic acid encoding lipoxygenase useful for producing 11-
 XX hydroperoxy- or hydroxy-arachidonic acid.
 XX Disclosure; Fig 3; 18pp; German.
 XX This invention describes a novel nucleic acid (I) encoding a potato
 CC lipoxygenase protein LOX, (II) is new. The invention also describes (1)
 CC (II), a sequence of 857 amino acids (aa), given in the specification; (2)
 CC a vector (III) comprising (I); (3) a host cell (IV) comprising (I) or
 CC (III); (4) a plant or part of a plant comprising (IV); (5) enhancing the
 CC specificity of a plant lipoxygenase for position 11 of arachidonic acid
 CC comprising mutating at least one amino acid of the wild type lipoxygenase;
 CC (6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-
 CC derivative comprises treating arachidonic acid with (II) and further
 CC reducing the obtained hydroperoxy form to the hydroxy group; (7) the
 CC arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy
 CC group at position 11. (II) is useful for producing 11- hydroperoxy-

CC and/or 11-hydroxy-arachidonic acid. The lipoxygenase is specific for
CC position 11 of arachidonic acid

Sequence 857 AA;

Query Match	55.78;	Score	2630.5;	DB	4;	Length	857;
Best Local Similarity	58.9g;	Pred.	No.2.6e-235;				
Matches	511;	Conservative	113;	Mismatches	218;	Indels	25; Gaps
							9;
QY	22	KIRGTVALVKKEVLVDGDFNASLLDGVHRILGWDDGVAFQLVSAATAADPSNGRGKVGKA	81				
Ddb	15	KVKGTVMVMKKNALDFTDLAGSLTDKIPEALG-QKVSEQLISSVQSDPANGLOKHSNP	72				
QY	82	AHLEAVVSLKSTADGETTVRVRSFEWDESGGTPGAIVLRNUQHAEFFTKUTLTLEGVPKG	141				
Ddb	73	AYLENFLTITPLAAGETAFGVTFDWNBEFGVGFAGFIKNTHNEFFLKSTLTLEDVFPHG	132				
QY	142	TUVFVANSWYYPHKLSQERIIPANDTYLPKMPAALVPYRODEKILRLGDNDPGPCQEH	201				
Ddb	133	KVHPVCNSWYPPSFYKSDRIIFANOPYLPSETPELLKYRENELLTLRG-DGTGKREAW	191				
QY	202	DRVTRYDNDLDGDPKGBEHAARPIIGGSQEHPYPRRCRTGRHPTKDPNSESFL-FLLN	260				
Ddb	192	DRIYDYDVNDLGNPDQGEONVRTLTGGADYVFPFRGTGRTPTRTDPKSESIPLITS	251				
QY	261	LNIYVPSDERFGLKMSDFLGYSLKTIIEAVLPTLTGTVDDTPKEFSFDILGLVELGP	320				
Ddb	252	LDIYVPSDERFGLKMSDFLTALKSIVQFIPELHALFDGTPNEFDSFEDVLRLEYGGI	311				
QY	321	EAPNPPLJABIRKKIPSEFLRSLPILNGSHDHPLKMLPNVIKSKDVLKCAPKPFEGMTDE	380				
Ddb	312	KLPGQPLFKALTAAIPLNNMKELLRTDG-EGILRPFTPVLVIK-----DsktAwrtDe	362				
QY	381	EPARETLAGNVPIIKELTEFFPAKSTLPDPROCGDHTSKI TEAHIRHNMGGLSVQNALRNK	440				
Ddb	363	EPAREMLAGNVPIIISRLQEPFPKSPKLDPKPYAGNQNSTITAETHEDKLDUGLTVDNEANN	422				
QY	441	RLFILDHHDHFPLYLDEINELEGNFTYASRTLLFLKDGTCLKLAIELSLPHPDGOORGA	500				
Ddb	423	KLFTLNHHDLVIPYLRRINTTTTK-TYASRTLLFLQDNGLSKPLAIELSLPHPDGDQFGV	481				
QY	501	VSKVYTPAHTGVGHVWOLAKAYACVNDASWHQLISHWLNTHAVIEFPVTATNRQLSVNH	560				
Ddb	482	ISKVYTPSDQGVSSIIWQAKAYAVNDSGVHQHLISHWLNTHAVIEFPVTATNRQLSVNL	541				
QY	561	PVHKLSPHYRDPTLINALAROTLINAGGVPERTVFPKAYALGMSADVYKSNWFNEOALP	620				
Ddb	542	PIHKLLYPHPRDTMNINAMARQLINNAGGVLBSTVFPSPKFAMENSAVVYKDWVPDQALP	601				
QY	621	ADLVKRGVAVPDOSSPGYVRLLIKOYPYAVDGLVTWAIERWKVEYLDITYPNDDELQRD	680				
Ddb	602	ADLVKRGVAVEDSSSPHGVRLLITEDYPYAVDGLETSASKWVTDYCSFYGSDSEELIKD	661				
QY	681	VELQAWWKEVREBAHGDLDKRDWWPRMDTVQQBARACTIIIWASALHAAVNFQCPYAG	740				
Ddb	662	NELQAWWKELVREVCHGDGKNEPWPMETPQELIDSCITIIWASALHAAVNFQCPYAG	721				
QY	741	YLPNRPTASRRPMPEPGSHDYKKLGAGOKADMVIRTITSQFOITLIGISLIETLSKHSS	800				
Ddb	722	YLPNRPTVSRRFMPEPGTPEYSEL---KCNPKDAFLKTIITAOQLTLGVSLIETLSRHTT	778				
QY	801	DEVVLGORDEPDRWTSDAKALDAPKXFGSRSLVQIENRIKTWNSDPDKNKRGVEMPYML	860				
Ddb	779	DEIYLGORSPE-WTKDKEPLAAPDKFKGUKLTDIEKQIIRQNGNIUITSAGPVNAPYTL	837				
QY	861	LYPNTSDVTGKAEGLTAMGIPNSISI	887				
Ddb	838	LFPTSBG-----GLTGKGIENSYSI	857				

Search completed: March 23, 2004, 06:59:05
Job time : 92 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 06:57:53 ; Search time 26 seconds
(without alignments)
1761.240 Million cell updates/sec

Title: US-10-059-909-16
Perfect score: 4723
Sequence: 1 MFHGVADRLTGKKNKAWSE.....VTGEKAEGLTANGIPNSISI 887

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3049	64.6	864	4	US-09-810-268-3
2	2936.5	62.2	862	4	US-09-751-687-9
3	2929.5	62.0	862	4	US-09-751-687-12
4	2860	60.6	864	4	US-09-751-687-18
5	2491.5	52.8	857	4	US-09-751-687-17
6	2486	52.6	865	4	US-09-751-687-16
7	2355.5	49.9	839	4	US-09-751-687-15
8	513.5	10.9	676	3	US-09-061-768A-2
9	513.5	10.9	676	4	US-09-764-246-2
10	513	10.9	556	4	US-09-547-435-6
11	513	10.9	711	4	US-09-547-435-2
12	513	10.9	867	4	US-09-547-435-24
13	507	10.7	677	3	US-09-061-768A-4
14	507	10.7	677	4	US-09-764-246-4
15	503.5	10.7	701	3	US-09-087-727-2
16	503.5	10.7	701	4	US-09-853-053-2
17	485.5	10.3	692	4	US-09-252-991A-19668
18	475	10.1	582	3	US-09-413-814-83
19	430	9.1	663	4	US-09-641-638-653
20	427	9.0	460	4	US-09-547-435-12
21	427	9.0	615	4	US-09-547-435-10
22	427	9.0	662	3	US-09-061-768A-25
23	427	9.0	662	4	US-09-764-246-25
24	427	9.0	771	4	US-09-547-435-28
25	380.5	8.1	291	4	US-09-547-435-14
26	294.5	6.2	195	4	US-09-547-435-20
27	253.5	5.4	334	4	US-09-547-435-8

28	253.5	5.4	489	4	US-09-547-435-4	Sequence 4, Appli
29	253.5	5.4	645	4	US-09-547-435-26	Sequence 26, Appl
30	139	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
31	121	2.6	69	4	US-09-547-435-16	Sequence 16, Appl
32	118	2.5	560	4	US-09-252-991A-22343	Sequence 22343, A
33	111.5	2.4	1675	4	US-09-540-236-1994	Sequence 1994, A
34	111	2.4	943	4	US-09-540-236-3458	Sequence 3458, Ap
35	111	2.4	982	4	US-09-540-236-12	Sequence 12, Appl
36	111	2.4	1231	4	US-09-107-532A-5150	Sequence 5150, Ap
37	109.5	2.3	883	2	US-08-353-492-2	Sequence 2, Appli
38	108.5	2.3	640	4	US-09-687-538B-2	Sequence 2, Appli
39	108.5	2.3	751	4	US-09-540-236-2320	Sequence 2320, Ap
40	108.5	2.3	986	4	US-09-403-618A-5	Sequence 5, Appli
41	107.5	2.3	949	4	US-09-623-326-11	Sequence 11, Appl
42	106.5	2.3	423	1	US-08-844-064-7	Sequence 7, Appli
43	106.5	2.3	423	3	US-09-009-433-7	Sequence 7, Appli
44	106.5	2.3	1007	4	US-09-252-991A-28773	Sequence 28773, A
45	106.5	2.3	2311	4	US-08-934-386-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-810-268-3
; Sequence 3, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 864
; ORGANISM: Zea mays
US-09-810-268-3

Query Match	64.6%	Score	3049	DB	4	Length	864
Best Local Similarity	66.2%	Pred. No.	4.8e-285				
Matches	585	Conservative	100	Mismatches	175	Indels	24
Gaps							10
Qy	5	GVADRLTGKKNKAWSEGGKIRGT	VLVKKVLDVGFNLSLLDGVHRLGDDGVAFQVLS	64			
Db	4	GIIDGUTGANKA	-----RLKGVLMKRVLDNDFGATVDSISEFLG--KGVTCQLIS	57			
Qy	65	ATAADPSNGRGKVGKAAHLEAVVSLKSTADGETVYRVSVFWD-ESOGIPGAVLRNLQ	123				
Db	58	STLVANNRGRVGAENLEQLTSLP	SLTTGSGKFGVTFDWEVKLGVPAGVVVKNH	117			
Qy	124	HAFFELKTLTSGVCKGTWVFVANSWYVPHKLYSQERIFFANDTYLBSKMPAALVPYRQ	183				
Db	118	AAEFFKTLTLDVPGRGAVTFVANSWYVPAKRYNRVFFNSNDTYLBSQMPAALPKPRD	177				
Qy	184	DELKILRGDDNPGPYQEHDRVRYDYNDLGDPDFDKGESHARILGSGSEHPYPRRCRTGR	243				
Db	178	DELNLRGDDQGPQYQEHDRVRYDYNDLGDPDFDGG--NPRILGGSADHPYPRRCRTGR	235				
Qy	244	HPTKDPNSESRLFLNLNIYVPRDRGHLKMSFLGYSKLTIIIEAVLPTLTGTVDDTP	303				
Db	236	KPTKDPNDSRLSLVE-QIYVPRDRFGHLKMSDFLGYSIKAITQGIIPAVRTVDTTP	294				
Qy	304	KEFDFSPEDILGIELGPGRAPNPLIAEIRKIPSEFLRSILPFGSHDHPKMPLENIKVS	363				
Db	295	GEFDSFQDIINIYEGGKIPKIQALEDMKLPFLQIVKDLFPAGG-DYLLKLPPIQIIQE	353				

QY 364 DVLKAPKFKGRTDEEFABETLAGVNPVLIKLTTEPPAKSTLDPQYGDHTSKITEAH 423
Db 354 D-----KNAWRTDEFAREVLAGVNPVITLTPFPKSTLDPKSGYDHTSKITIAEH 405
QY 424 TRHNGGVSQNALRNKRLFLDLHDHFMFYLDEINELEGFIYASRTLLFLKDDGTLKP 483
Db 406 TEKNLEGTVOQALDGNRLYLIDHHDREMPFLIDVNNLEGNFIYATRTLPFLRGDGLAP 465
QY 484 LAIELSLPHPDQQRGAVSKVYTPAHTGVEGHVQCLAKAYACVNDSSAWHOLISHLWNTA 543
Db 466 LAIELSEPIYDGLTVAKSKVYTPASSGVEAWVQCLAKAYAVVNDSSGHWQLVSHLWNTA 525
QY 544 VIEPVIATNRQLSVVPHKLLSPHYRDTLNALARQTLINAGGVFERTVPPAKYALG 603
Db 526 VMEPVIATNRQLSVTHPVHKLSSHPFRDTMTINALARQTLINAGGVFERTVPPAKYALG 585
QY 604 MSADVYKSWNEQALPADLVKRGVAVDPDQSSPYGVRLIKDYPAVDGLVWATERWV 663
Db 586 MSSVVYKSWNTTEQGLPADLVKRGVAVDPDQSSPYGVRLIKDYPAVDGLVWATERWV 645
QY 664 KEYLDIYPNDGELQDVELQAWKKEVREEAHGDLKDRDWMRMDTVQOLARACTIIW 723
Db 646 GEYLAIVYDDGALRGDEELQAWKKEVREVGHDHDKDAPWPKMQAVSELASACTIIWI 705
QY 724 ASALHAAVNFGQYVAGYLPNRPASRRPMPPEGSHDYKKGACQKADWVFTITISQF 783
Db 706 ASALHAAVNFGQYVAGYLPNRPASRRPMPPEGSHDYKKGACQKADWVFTITISQI 762
QY 784 QTLIGISLIEILSKHSSDEVYLGORDPDRWTSDAKALDAFKRFGSLVQIENRIKTMND 843
Db 763 QTLIGISLIEILSKHSSDEVYLGORDPDRWTSDAKALDAFKRFGSLVQIENRIKTMND 821
QY 844 SPDLKNRKGVPVEMPMYLLYPNTSDVTGKABGLTAMGIPNSISI 887
Db 822 DPQLRNRNGPAFFPMYLLYPNTSDHSG--AAAGLTAKGIPNSISI 864

RESULT 2
US-09-751-687-9
; Sequence 9, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 862
; TYPE: PR1
; ORGANISM: Hordeum vulgare
US-09-751-687-9

Query Match 62.2%; Score 2936.5; DB 4; Length 862;
Best Local Similarity 63.1%; Pred No. 3.5e-274;
Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY 1 MFWHGVADRLTGKNEAWSBKIGTVRLVKKEVLDVGFNASLLDGVHRLGMDGVAF 60
Db 1 MLLGGLIDTLTGANKSA---RLKGTIVLMKQVLDLNDPFGATIIDIGBFLG--KGVTC 54
QY 61 QLVSAATADPSNGRGKVGKAAHLEAVSISKADGETVYRVSEFWD--ESQIGPGLV 119
Db 55 QLISSTAVQDNGRGKVGAAELQEWVSLDPSLTGSEKFGLTDFWEVEKGVPGAIW 114
QY 120 RNLOHAEFFLTKLTLEGVPGK-GTVVFVANSWYVPHKLYSQERIFFFANDTLPKMKPAAL 178

Db 115 NYHSSEFLKLTITLHDVPGSRGNLTFVANSWYVPAAYRYSRVFANDTLPKMKPAAL 174
QY 179 VYPRODELKILRGDNPBGYQEHDRVYRYDYNDLGDPKGBEHPILGSGQEHYPFR 238
Db 175 KEYRDDLENLRGDDQCGFYQEHDRYRYDYVDYNDLGE-----GRPILGNSDHPYPR 227
QY 239 CRTGRHPTKKDPSNSRLFLNLNIYVPRDERFGLHKMSDFLGYSLKTKTIEAVLPTLGT 298
Db 228 GTERKPNASDPSLSRSLLE-QIYVPRDEKFGHLKTSDFLGYSIKAITQGIILPAVRY 286
QY 299 VDTTPKFPSPDIILGYELGPEAPNPLIAIRKIPSEFRLSRSLPNSGSHDHPKMLP 358
Db 287 VDTTPKFPSPDIILGYELGPEAPNPLIAIRKIPSEFRLSRSLPNSGSHDHPKMLP 345
QY 359 NIKSDVLKCAPEFPGWRTDEPARETLAGVNPVLIKLTTEPPAKSTLDPQYGDHTSK 418
Db 346 HIQ-----ENQAWRTDEPARETLAGVNPVLIKLTTEPPAKSTLDPQYGDHTSK 397
QY 419 ITEAHRNMGSLVONALRNKRLFILDHDFHMPYLDEINELEGNFIYASRTLLFLKDD 478
Db 398 ITEAHEIKNLEGLTVQALLESNRLYLDHDFHMPFLIDVNNLPGNFIYATRTLPFLRGD 457
QY 479 GTLKPLAIELSLPHPDQQRGAVSKVYTPAHTG-VEGHVWOLAKAYACVNDSSAWHOLISH 537
Db 458 GRLTPLAIELSEPIIOGGLTTAKSKVYTPVPSGVEGWVWELAKAYAVVNDSSGHWQLVSH 517
QY 538 WLNTHAVIEPFIATNRQLSVVPHKLLSPHYRDTLNALARQTLINAGGVFERTVFP 597
Db 518 WLNTHAVIEPFIATNRQLSVVPHKLLSPHYRDTLNALARQTLINAGGVFERTVFP 577
QY 598 AKYALGMSADVYKSWNEQALPADLVKRGVAVDPDQSSPYGVRLIKDYPAVDGLVW 657
Db 578 KGFALGMSADVYKSWNEQALPADLVKRGVAVDPDQSSPYGVRLIKDYPAVDGLVW 637
QY 658 AIERWVKEYLDIYPNDGELQDVELQAWKKEVREEAHGDLKDRDWMRMDTVQOLARAC 717
Db 638 AIEQVSEYLAIVYENDGVLODTEVQAWKKEVREVGHDLDKADAPWPKMQSVPELAKAC 697
QY 718 TTIIVASALHAAVNFGQYVAGYLPNRPASRRPMPPEGSHDYKKGACQKADWVFR 777
Db 698 TTIIVIGSALHAAVNFGQYVAGYLPNRPASRRPMPPEGSHDYKKGACQKADWVFR 754
QY 778 TITSQFQITLIGISLIEILSKHSSDEVYLGORDPDRWTSDAKALDAFKRFGSLVQIENR 837
Db 755 TITSQIQTIIIGVLSLLEVLKSHSSDELYLGORDTPE-WTSDPKALEVFKRFSRLVEIESK 813
QY 838 IKTMNDSPDLKNRKGVPVEMPMYLLYPNTSDVTGKABGLTAMGIPNSISI 887
Db 814 VVGNNHDPKLRNGPAFFPMYLLYPNTSDHSG--AAAGLTAKGIPNSISI 862

RESULT 3
US-09-751-687-12
; Sequence 12, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12
; LENGTH: 862
; TYPE: PR1
; ORGANISM: Hordeum vulgare
; FEATURE:

;	NAME/KEY: variation	62.0%;	Score 2929.5;	DB 4;	Length 862;
;	LOCATION: (368)..(368)	Best Local Similarity	63.0%;	Pred. No. 1.7e-273;	
;	OTHER INFORMATION: "Xaa" is an acidic, basic, or polar amino acid	Matches 561;	Conservative 110;	Mismatches 188;	Indels 31;
US-09-751-687-12					Gaps 12;
Qy	1 MFHWGVADRLTGKKEAWSEGGKRGITVPLVKKEVLVDGDFNASLLDGVHRLHGDDGVAF	60			
Db	1 MLGLGLDITLTGANKSA-----RLKGTVMRMKRNLDLNDFGATIDIGIGFELG--KGVT	54			
Qy	61 QLVSATAADPSNGGRGKVKGAHLEAEVYSLSKTADGETVYRVSPFEMD--ESQIGIPGAVLV	119			
Db	55 QLISSSTAVDQDNGGRGKVGAEAELEQWTSLSPLTTGSGFKGLTFDMEVEKVLGVGEAVV	114			
Qy	120 RNLQHAFFFLKTLLEGVPGK-GTVVFVANSWVPHKLYSOERFFANDTVLPKMPAAL	178			
Db	115 NNYHSSFFLLKTIHLDPVGRGNLTFVANSWIVPAANYRVSRVFFANDTVLPQMPAAL	174			
Qy	179 VPYQDELKILRGDDNPGPYQEHDRVRYDYNDLGPDKGEEHARFILGSGQSHHPYPR	238			
Db	175 KPYRDDLRNLRGDDQDQPGYQEHDRIVRYDYNDLGE-----GRPLIGNSDHPYPR	227			
Qy	239 CRTGRHPTKDPNSESRLFLNLNLNLYVPRDRFGLKMSDFLGSYSLKTIKTLVAVLPTLGTF	298			
Db	228 GRTERKWNASDPSLESRLSLE-QIYVPRDRSKFGLKTSDFLGSYSLKTIKTLVAVLPTLGTF	286			
Qy	299 VDDTPKDFDPSDELILGYELGPEAPNNPLIAIRKIPSEFLRSILPNGSHDHPKMLPL	358			
Db	287 VDTTFGBFDSDQDINLYYEGGIKPKVAALFEELRKQFPLOIKDOLLVPGG-DSLLKLPVP	345			
Qy	359 NVIKSDVLKAPKPFKWRITDEEFARETLAGVNPVTKRLTEFPKASTLDPROYGDHTSK	418			
Db	346 HIIQ-----ENKQWRITDEEFAREVLAXVNPVMTLRTTEFPKSSLDPSKSGDHTST	397			
Qy	419 ITEAHIRHNGGLSVQNALNRKRLFILDHHDHFMPIYDEINELBGNFIYASRTLLFLKDD	478			
Db	398 ITAEHIEKNLEGLTVQQALESNRILYIILHHDHFMPIYDINVLNPGNFIYATRTLLFLRGD	457			
Qy	479 GTLKPLALELSLPHDPDQQRGAVSKVTPAHTG-VEGHVWQLAKAYACVNDSSAMHQLISH	537			
Db	458 GRULTPLALELSEPIIQGLTTAKTSKVTPVPSSGVEGVWVELAKAYAVVNDSSGHWQLVSH	517			
Qy	538 WLNTHAVIEBPVIATNQLSVVHVHKLSPHYRDTLINALAQTLINAGGVFERTVFP	597			
Db	518 WLNTHAVNEBPVISTNRHLSVTHBHVHKLSPHYRDTLINALAQTLINAGGVFERTVFP	577			
Qy	598 AKYALGMSADYKYSWNFEQALPADLVKRGVAVPDQSSPYGVRLIKDYYPVAVDGLVIW	657			
Db	578 GKFAIGMSAVVYKDWKFTQQLPDDLKRGWAVEDPSSPKVRLVSDYPIYAADGLAIWH	637			
Qy	658 AIERAWKEYLIDYYPNDGELQROVELCAWKKEVREEAHGLKORDWPRMDTVQOLARAC	717			
Db	638 AIEQVSEYLAIYPNDGVTLQDTEVQAQWKKEVREHGLKORDWPRMDTVQOLARAC	697			
Qy	718 TTIIVASALHAAVNFCQYPYAGVLPNRPATASRRMPPEGSHDYKYLGAQCKEAMVFI	777			
Db	698 TTIIVISALHAAVNFCQYPYAGVLPNRPATASRRMPPEGSHDYKYLGAQCKEAMVFI	754			
Qy	778 TITSQFOTILGISLIEILSKHSDDEVYLGORDSPDRWTSKADALDAFKFGSLVOIENR	837			
Db	755 TITSQIOTIIGVSLLEVLKSHSDDEVYLGORDTPE-WTSDPKALEVFKRSDRLVLEISK	813			
Qy	838 IKTNWSDPDLKNRKGPVEMPYMLLYNPTNSDVTEKAEGLTAMGIPNSISI	887			
Db	814 VGMNHDPKLNKRGPAKFFYMLLYNPTNSDPKG-AAAGLTAKGIPNSISI	862			

RESULT 4
US-09-751-687-18
; Sequence 18, Application US/09751687

[illegible]

Db 704 WTGSALHAAYNFGQYPYSGYHNPSPASRRPMPVQSGSEYAEVL---ERDEKAFIRITIS 760
Qy 782 QFQITILGISLILILSKSSDEVYLGQRDEPRDWTSDAKALDAPKRGSRVLQIENRIKTM 841
Db 761 QFHALVGSILMEILSKSSDEVYLGQRDTP-AWTSDAKALEAFKRGAKLEGIEKQVAM 819
Qy 842 NDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNPSISI 887
Db 820 NSDPLKNRKGPVEMPYMLLYPNTSDHTGQ-AEGLTARGIPNPSISI 864

RESULT 5
US-09-751-687-17
; Sequence 17, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhaug, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-17

Query Match 52.8%; Score 2491.5; DB 4; Length 857;
Best Local Similarity 55.3%; Pred. No. 3.4e-231;
Matches 487; Conservative 135; Mismatches 210; Indels 49; Gaps 14;

Qy 22 KIRGTVLVKKVLDV-----DFNASLLDGVHRLTGDDGVAFOLVATAA 68
Db 11 KIKGTVLMKKNVLDVNSVTSVGGIIOGGLDVGSLDITLTAFLG--RSVALQLI 68
Qy 69 DPSNGRGKVGKAAHLEAVVSLKSTADGETVYRVSVFDESGIGPAVLVRLQHAEPF 128
Db 69 DAN--GKGLGKATFLEGIITSLPTLGAGQSAFKINFEWDDGGIGPAVKNFMOTEFF 126
Qy 129 LKTLTLEGVPGKGVVAVNSVYVPHKLYSQEIRIFANDTLPKMPAALVPYRQDELAKI 188
Db 127 LVSLTLEIDPNHGSIFHVCNSWIYNAKLFKSDRIFFANQTYLSETPAPLVKTRBEELN 186
Qy 189 LRGDNPQPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPYRRCRTGRHPTKK 248
Db 187 LRG-DGTRGERKEWERIYDYVDYNDLGDPPDKGEEHARFVLGGNDTFYPYRRCRTGRKPTRK 245
Qy 249 DPNSERLFLNLNIVYPRDERCHLKMDSFLGYSIKTIEAVLPLTGFVD--DTPKEF 306
Db 246 DPNSER-----SNDVLPDEAFGHLSKSDFLTGLKSVSQNVLPPLQSAFDLNFPPREF 301
Qy 307 DSFEDILGLYELGPEAPNNPLIAEIRKIPSEELRSLPNSGSHDHPKPLPNIKSDVL 366
Db 302 DSPDEVHGLYSGGKLPD--IISKIS---PLPVKGEIFRTDG-EQALKFPFPKVIQVS-- 354
Qy 367 KXAPFPGWRTDEEPARELAGVNPVILKLTPEPAKSTLDPROQGDHTSKITEAHIRH 426
Db 355 -----KSAMWTDEEPARELAGVNPVILKLTPEPAKSTLDPROQGDHTSKITEAHIRH 408
Qy 427 NMGLSVQNALRNKRLFLDHHDFMYPYLDIENLEGNFTYASRTLLFLKDDGTLKPLAI 486
Db 409 NLEGLTVDEALQNKRLFLDHHDFMYPYLDIENLEGNFTYASRTLLFLKDDGTLKPLAI 467
Qy 487 ELSLPHPDQQRGAVSKYTPATGVGEHWQAKAYACVNDGAMQOLISHMLNTHAVIE 546
Db 468 ELSLPHPDQQRGAVSKYTPATGVGEHWQAKAYACVNDGAMQOLISHMLNTHAVIE 527

Qy 547 PVVATNRQLSVHVPVKLLSPHYRDTLINALAQTLINAGGVFEETVPKAYALGNSA 606
Db 528 PFVATNRQLSVHVPVKLLSPHYRDTLINALAQTLINAGGVFEETVPKAYALGNSA 587
Qy 607 DVIKSWNFNEQALPADLVKRGVAVFDOSPPYGVALLIKDYPYAVDGLVIMWAIERWKEY 666
Db 588 VVYKDWFTDQALPADLVKRGVAVFDOSPPYGVALLIKDYPYAVDGLVIMWAIERWKEY 647
Qy 667 LDIVYPNDGELORDVELQAWKVEYBEAHGDLKDRDWMFMDTVQQLARACTTIIWASA 726
Db 648 VLYIYKSDTTLREDEPELQACWKLVEVCHGDKKNEPMPKMTREELVEACALIIWASA 707
Qy 727 LHAAVNFQYYPYAGYLNRPRTASRRPMPPEPGSHDYKKGAGQKXADVFIRITISQFTI 786
Db 708 LHAAVNFQYYPYAGYLNRPRTASRRPMPPEPGSHDYKKGAGQKXADVFIRITISQFTI 764
Qy 787 LGISLIEILSKSSDEVYLGQRDEPRDWTSDAKALDAPKRGSRVLQIENRIKTMNDSPD 846
Db 785 IDLSVIEILSKSSDEVYLGQRDEPRDWTSDAKALDAPKRGSRVLQIENRIKTMNDSPD 823
Qy 847 LKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNPSISI 887
Db 824 LNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNPSISI 857

RESULT 6
US-09-751-687-16
; Sequence 16, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhaug, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-16

Query Match 52.6%; Score 2486; DB 4; Length 865;
Best Local Similarity 54.5%; Pred. No. 1.2e-230;
Matches 487; Conservative 137; Mismatches 196; Indels 74; Gaps 15;

Qy 22 KIRGTVLVKKVLDV-----VGDEN-----ASLLDGVHRLTGDDGVAFOLV 63
Db 18 KIKGTVLMKKNVLDVNSVADLTGKNGVGLLGTGLNVVSTGLDNLTAFLG--RSVALQLI 75
Qy 64 SATAADPSNGRGKVGKAAHLEAVVSLKSTADGETVYRVSVFDESGIGPAVLVRLQ 123
Db 76 SAT--KPLANGKVGKDTFLEGIIVSLPTLGAGESAFNIQFWEDESMGIPGAFIKNYM 133
Qy 124 HAEFLKTLTLEGVPGKGVVAVNSVYVPHKLYSQEIRIFANDTLPKMPAALVPYRQ 183
Db 134 QVEFYKSLTLEVDVNGQITRFVCSNWNVTKLYSVIRIFANHTYVPSETPAALVGRE 193
Qy 184 DELKILRGDDNPQPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPYRRCRTGR 243
Db 194 BELKILRG-DGKGERKEHRIYDYVDYNDLGDPPDKGEEHARPIILGSGQEHYPYRRCRTGR 252
Qy 244 HPTKDPNSERLFLNLNIVYPRDERCHLKMDSFLGYSIKTIEAVLPLTGFVD--D 301
Db 253 YETRQDQNSEK-----PGEVTVPRDENFGLHKSDFLGYKLSQVLPFAFESVFDLNF 307
Qy 302 TPKEFSDPEDILGYELGPEAPNNPLIAEIRKIPSEELRSLPNSGSHDHPKPLPNIKSDVL 353

Db 308 TPNEEDSFQDVRDLHEGG-----IKLPTEVISTIMPLPVVKEILFRDGBQVL 354
QY 354 KNPENLVKSVLKKAPKFKGWRTEDEFARETAGVNPVIAIKRTEPPAKSTLDPROYG 413
Db 355 KPPPHVQVS-----KSAMMTDEEFAREWAGVNPVIRGLQEPFPPKSNLDPTIYG 406
QY 414 DHTSKITEAHIRHNMGGLSVQNALRNKRLFLDHDHMPYLDDEINELEGNFIYASRTLL 473
Db 407 BOTSKITADAL--DUGQTVDEALASRLFLMDYHDVFMPIRIRINOTYAK-AYATRTIL 463
QY 474 FLKDDGTILKPLAIELSLPHDPDQOQRGAVSVYTPAHTGVEGHVQMLAKAYACVNDSSAHQ 533
Db 464 FLRENGTLKPAVIELSLPHDPAGDLGSAVSQVLPKAGEVESTIWLAKAYVVVNDSCVHQ 523
QY 534 LISHNLNTHAVTEPEVIATNROLSUVVPHVKLLSPHYRDTNINALAROTLINAGVFER 593
Db 524 LMSHNLNTHAVTEPIATNRHLSALHPYKLLTTPHYRDTNINALARQSLINADGIEK 583
QY 594 TVFPKALGMSADYKSWNFNEQALPADLVKRGVAVPDQSPYGVRLIKDYPIYAVDGL 653
Db 584 SFLPKSHVEMSSAVYKXWVFTDQALPADLKRGAIKDPSAPGRLALLIEDIYAVDGL 643
QY 654 VVWIAERWVKEYLDIYPNDGELQDVELQAWKEVREBAHGDLDKRDWWRMDTVQOL 713
Db 644 ELWAAIKTWQVQVSLYARDDVVKPDSELOQWKEAVEKGHGDLDKDPWPKLQTIIEEL 703
QY 714 ARACTTIWIASALHAAVNFQYPVAGVLPNRPRTASRRPMPPEPGSHDYKKLGAGQKADM 773
Db 704 VEICTIIWIASALHAAVNFQYPVGGPILNRPRTSSRRLLEKGTPEYEMVKSHQKA-- 761
QY 774 VPIRTISQPTILGISILSILSKHSDDEVYLGQDPEPRWTSDAKALDAPKRGSLVQ 833
Db 762 -YLRTISKFTQVLDSVIELSRHASDEVYLGQDNP-HWTSDSKALQAFQKGNLKE 819
QY 834 IENRIKTWNSDPLKRNKRGVEMPMVLLYPNTSDVTEKAGLTAMGIPNSISI 887
Db 820 IEEKLARNQDSLSNRLGPVQLPYTLHPN-----SEGLTCRGIPNSISI 865

RESULT 7
US-09-751-687-15
; Sequence 15, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751.687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Glycine max
US-09-751-687-15

Query Match 49.9%; Score 2355.5; DB 4; Length 839;
Best Local Similarity 53.4%; Pred. No. 4.5e-218;
Matches 465; Conservative 140; Mismatches 223; Indels 43; Gaps 14;

QY 22 KIRGTVRVKEVLDVGDGDFNLSLDGVRILGWDGVAQVQLVATADPSNGRGKVGKA 81
Db 7 KIRGTVRLMPKNEVNP-DGSAVDNINAFIG--RSVSLQLISATKADAH--GKGKVGKD 61
QY 82 AHLEEAUVVLSKSTADGETVYKVSPEWDESQICPAVLVRNLQHAEPFLKTLLEGVPGK 141
Db 62 TFLGINTSPTLGAESAFAFNHFENDGSMGIPQAFYIKMYQVFFPKSLTLEAISNQ 121

QY 142 TVVVFANSWYPHKLYSQERIFPANDTYLPKMPAALVPYRQDELKILGDDNPGYQBH 201
Db 122 TIRFVCNSWYNTKLYKSVIRIFANHTYVSETPAPLVSYRBEELKSLRG-NGTGRKEY 180
QY 202 DRVYRDYNDLGDGPKGEEHARPLGGQEHPPYPERCETGRHPTKKDQNSBSR--LFL 259
Db 181 DRIYDVNDJGNPKSEKJARPVUGSGSTFPYPRGRGTGRGPTVTDNTKQGEVF-- 238
QY 260 NLNIYPRDERFGHLKMSDFLGYSKXTIIEAVLPTLTGTVD--DTPKPSDFEDILGLYE 317
Db 239 ---YVPRDENLGHLSKDALEIGTKLSQIQVAPESAFDLKSTPIEPHSTQDVHDLVE 294
QY 318 LGPEAPNNPLIAIRKIPSEFLRSILPNSHDHPLKMPLPNVIKSDVLKKAPEKFGHR 377
Db 295 GGKLPDRDVIPTIIPVKEIYRT-----DQGHILKFPQPHVQVS-----QSAW 341
QY 378 TDEEFARETAGVNPVIAIKRTEFFPAKSTLDPQYGDHTSKITEAHIRENMGLSQNAL 437
Db 342 TDEEFAREMIAGVNPVIRGLEEFFPKSNLDPAIYDQSSKITADSL--DLGYTMDAL 399
QY 438 RNKRLFLDHDHFMPLDDEINELEGNFIYASRTLLFLKDDGTILKPLAIELSLPHDPQO 497
Db 400 GSRRLFMLDYHDFIMPYVRQINQANSAKYATRTILFLREDGTLPVAIELSLPHSAGDL 459
QY 498 RGAVSXVYTPAHTGVEGHVQMLAKAYACVNDSSAHQILSHWLNTEAVIEPFFVIATNRQLS 557
Db 460 SAAVSQVLPKAGEVESTIWLAKAYVINDSCYQLMSHNLNTHAAKEPFFVIATNRHLS 519
QY 558 VHPVHKLSPHYRDTNINALAROTLINAGVFERVTPPAKYALGMSADYKSWNFNEQ 617
Db 520 VLHPITYKLTTPHYRNMNINALARQSLINANGIETTFPLPSKYSVEMSSAVYKXWVFTDQ 579
QY 618 ALPADLVKRGVAVPDQSPYGVRLIKDYPIYAVDGLVIAWATERWVKEYLDIYPNDGEL 677
Db 580 ALPADLVKRGVAVPDQSPYGVRLIKDYPIYAVDGLVIAWATERWVKEYLDIYPNDGEL 639
QY 678 QRDVELQAWKEVREBAHGDLDKRDWWRMDTVQOLARACTTIWIASALHAAVNFQY 737
Db 640 KNDSELOQWKEAVEKGHGDLDKDPWPKLTLEDLVEVCLIIWIASALHAAVNFQY 699
QY 738 YAGVLPNRPRTASRRPMPPEPGSHDYKKLGAGQKADMVPIRTITTSQFTILGSLIEILSK 797
Db 700 YGGLINRPTASRRLLPEKGTPEYEMINNHEKA---YLRTISKLPILISUSVIELIST 756
QY 798 HSDDEVYLGQDPEPRWTSDAKALDAPKRGSLVQIENRIKTWNSDPLK-NRKGVPVEM 856
Db 757 HASDEVYLGQDNP-HWTSDSKALQAFQKGNLKEIEKLVRRNNDPSLQGNRLGPVL 815
QY 857 PYMLLYPNTSDVTEKAGLTAMGIPNSISI 887
Db 816 PYTLLYPSE-----EGLTPRGIPNSISI 839

RESULT 8
US-09-061-768A-2
; Sequence 2, Application US/09061768A
; Patent No. 6204037
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; APPLICANT: BOEGLIN, WILLIAM E.
; APPLICANT: JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSES: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible

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; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,768A
; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-09-061-768A-2

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Query Match      10.9%; Score 513.5; DB 3; Length 676;
Best Local Similarity 31.2%; Pred. No. 2.7e-40;
Matches 164; Conservative 74; Mismatches 193; Indels 95; Gaps 17;

QY 376 WRTDEEFARETLAGNPNVILKELTEFFPAKSTLDPROYGDHTSKITEAHIRNMG-GLSVQ 434
Db 232 WOEDAFFASQFLNGLNPLIRCHYLP-----KNFPVTDAMVASLLPGGTSQ 279
QY 435 NALNRKRLFIIDHDFHMFYDEI--NELEG--NFIYASRTLLFLKDD-GTLKPLAIELS 489
Db 280 AELEKGSFLVDH-----GILSGIQTNVINGKPKQPSAAPMTLLYQSPCGPLPLAQLS 334
QY 490 LPHPPQOORGAVSKYVTPAHTGVEGVWQAKAYACVNDSSAWHQLISHWLNTHAVIEPV 549
Db 335 -----QTPGNSPIFLPTDDKWD---WLLAKTWVRNAEFSFHEALTHLLSHLLPEVFT 385
QY 550 IATNRQLSVHVPVHKLSPHYRDTLINALARQTLINAGGVFERTVFPKVALGMSADVY 609
Db 386 LATLQLPCHPLFKLLIPHTRYTLHINTLARELLIVPGQVVDST-----GIGIEGF 438
QY 610 -----KSNWFNEQALPADLVKRGVAVPQSSPYGVRLLIKDYPAVDGLVWIAIER 661
Db 439 SELIQRMKQLNYSLLCLPEDIRTRGVED-----IPGYIYRDDGMQIWGAYER 486
QY 662 WYKEYLDIYYPNDGELQDVELQAWKVEVBEAHGDLKDRDWPMDTVQOLARACTTII 721
Db 487 FVSEIIGIYPSDESQVDDRELQAVREIFSKGFLNQESSGIPSSLETREALVQVYTWVI 546
QY 722 WVASALHAANFGQVYAGYLPNPTASRRRPMPEGSHDYKKGAGQKEADWVFIRITTS 781
Db 547 FTCSAKHAASAGQPDSCAMNPLPPSMLPPP-----TSKGLATCEG---FIATLPP 596
QY 782 QFTILGISLLEILSKHSSDEVILQORDEPRWTSDAKALDAFKRFGSLVQIENRIKTM 841
Db 597 VNATCDVILALWLSKEGDRPLG--TYPDEHTEAPRPSIATFOSRLAQISRGIOER 654
QY 842 NDSPDLKVRKGFVEMPYMLLYPNTSDVTGEKAELGTAMGIPNSISI 887
Db 655 N-----RGVL-LPYTYLDPEL-----IENSYSI 676

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RESULT 9

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US-09-764-246-2
; Sequence 2, Application US/09764246
; Patent No. 6649355
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.

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; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-764-246-2

```

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Query Match      10.9%; Score 513.5; DB 4; Length 676;
Best Local Similarity 31.2%; Pred. No. 2.7e-40;
Matches 164; Conservative 74; Mismatches 193; Indels 95; Gaps 17;

QY 376 WRTDEEFARETLAGNPNVILKELTEFFPAKSTLDPROYGDHTSKITEAHIRNMG-GLSVQ 434
Db 232 WOEDAFFASQFLNGLNPLIRCHYLP-----KNFPVTDAMVASLLPGGTSQ 279
QY 435 NALNRKRLFIIDHDFHMFYDEI--NELEG--NFIYASRTLLFLKDD-GTLKPLAIELS 489
Db 280 AELEKGSFLVDH-----GILSGIQTNVINGKPKQPSAAPMTLLYQSPCGPLPLAQLS 334
QY 490 LPHPPQOORGAVSKYVTPAHTGVEGVWQAKAYACVNDSSAWHQLISHWLNTHAVIEPV 549
Db 335 -----QTPGNSPIFLPTDDKWD---WLLAKTWVRNAEFSFHEALTHLLSHLLPEVFT 385
QY 550 IATNRQLSVHVPVHKLSPHYRDTLINALARQTLINAGGVFERTVFPKVALGMSADVY 609
Db 386 LATLQLPCHPLFKLLIPHTRYTLHINTLARELLIVPGQVVDST-----GIGIEGF 438
QY 610 -----KSNWFNEQALPADLVKRGVAVPQSSPYGVRLLIKDYPAVDGLVWIAIER 661
Db 439 SELIQRMKQLNYSLLCLPEDIRTRGVED-----IPGYIYRDDGMQIWGAYER 486
QY 662 WYKEYLDIYYPNDGELQDVELQAWKVEVBEAHGDLKDRDWPMDTVQOLARACTTII 721
Db 487 FVSEIIGIYPSDESQVDDRELQAVREIFSKGFLNQESSGIPSSLETREALVQVYTWVI 546
QY 722 WVASALHAANFGQVYAGYLPNPTASRRRPMPEGSHDYKKGAGQKEADWVFIRITTS 781
Db 547 FTCSAKHAASAGQPDSCAMNPLPPSMLPPP-----TSKGLATCEG---FIATLPP 596
QY 782 QFTILGISLLEILSKHSSDEVILQORDEPRWTSDAKALDAFKRFGSLVQIENRIKTM 841

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Db 597 VNATCDVILALWLLSKPGDQRLG--TYPDEHTEAPRRSIAFQSLRAQISRGIOER 654
QY 842 NDSPLDKNEKGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 655 N-----RGLV-LPYTYLDPPL-----IENSVSI 676

RESULT 10

US-09-547-435-6
; Sequence 6, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-6

Query Match 10.9%; Score 513; DB 4; Length 556;
Best Local Similarity 29.3%; Pred. No. 2,1e-40;
Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;
QY 376 WRTDEEFARETLAGVNPVILKLTETPAKSTLDPQYGDHTSKITEAHIRNMG-GLSVQ 434
Db 113 WCEDHFFGYQYLVNPNVLMHCISLPSK-----LPVTNDMVAPLLGQDTCLQ 160
QY 435 NALNRKRLFLDHHDFMPYLDE--INLEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
Db 161 TELERGNIFLADYV-----ILAEAPTHCLNGRQQYVAAPLCLLWLSPOGALVPLAIQLSQ 215
QY 490 LPHPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDASAMHQLISHLWNTHAVIEPVFV 549
Db 216 TPGPD-----SPIFLPTDSEWD---WLLAKTWVNSEFLVHENTHFLCTHLLCEAFA 265
QY 550 IATNQLSVVPHVKLLSPHYRDTLINALARQTLINAGGVFERTVPPAKYALGMSADYV 609
Db 266 MATRLQLPLCHPIYKLLLPHTRYTLQVNTIARATLNPGLVDQVT-----SIGRQGLIY 320
QY 610 -----KSNWFNEQALPADLVKRGVAVPDQSPYGVRLLIKDYPAVDGLVWIAERWV 663
Db 321 LMSTGLAHFTYTNFCLPDSLARGV-----LAIPNYHYRDDGLKIWAIESFV 368
QY 664 KEYLDIYYPNDGELORDVELQAWKEVREBAHGDLDKORDWPRMDTVQQLARACTTIWV 723
Db 369 SEIVGYIYPSDASVQDSQLQWGTGEIIFAQFLGRESGFPRLCTPGEMVKFLTAIFN 428
QY 724 ASALHAANVFGQYPYAGYLPNRPASRPMPE-PGSHDYKKGAGQKEADWVFRTITSQ 782
Db 429 CSAQHAANVSGQHDGAWNPAPSSMRQPPQTKGTTLK-----TYLDTLPEV 477
QY 783 FTILGISLIEILSKHSSDEVILQGRDEPDRTSDAKALDAFKRGSRLVQIENRIKTMN 842
Db 478 NISCNLLFLWLSQSPKQDRPLG--TYPDEHTEAPRRSIAAFQSLRAQI----- 527
QY 843 DSPDLKNRKGPMVPMYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 528 -SRDIQERNQGLALPYTYLDPPL-----IENSVSI 556

RESULT 11

US-09-547-435-2
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

; Sequence 2, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-2

Query Match 10.9%; Score 513; DB 4; Length 711;
Best Local Similarity 29.3%; Pred. No. 3.3e-40;
Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;
QY 376 WRTDEEFARETLAGVNPVILKLTETPAKSTLDPQYGDHTSKITEAHIRNMG-GLSVQ 434
Db 268 WCEDHFFGYQYLVNPNVLMHCISLPSK-----LPVTNDMVAPLLGQDTCLQ 315
QY 435 NALNRKRLFLDHHDFMPYLDE--INLEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
Db 316 TELERGNIFLADYV-----ILAEAPTHCLNGRQQYVAAPLCLLWLSPOGALVPLAIQLSQ 370
QY 490 LPHPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDASAMHQLISHLWNTHAVIEPVFV 549
Db 371 TPGPD-----SPIFLPTDSEWD---WLLAKTWVNSEFLVHENTHFLCTHLLCEAFA 420
QY 550 IATNQLSVVPHVKLLSPHYRDTLINALARQTLINAGGVFERTVPPAKYALGMSADYV 609
Db 421 MATRLQLPLCHPIYKLLLPHTRYTLQVNTIARATLNPGLVDQVT-----SIGRQGLIY 475
QY 610 -----KSNWFNEQALPADLVKRGVAVPDQSPYGVRLLIKDYPAVDGLVWIAERWV 663
Db 476 LMSTGLAHFTYTNFCLPDSLARGV-----LAIPNYHYRDDGLKIWAIESFV 523
QY 664 KEYLDIYYPNDGELORDVELQAWKEVREBAHGDLDKORDWPRMDTVQQLARACTTIWV 723
Db 524 SEIVGYIYPSDASVQDSQLQWGTGEIIFAQFLGRESGFPRLCTPGEMVKFLTAIFN 583
QY 724 ASALHAANVFGQYPYAGYLPNRPASRPMPE-PGSHDYKKGAGQKEADWVFRTITSQ 782
Db 584 CSAQHAANVSGQHDGAWNPAPSSMRQPPQTKGTTLK-----TYLDTLPEV 632
QY 783 FTILGISLIEILSKHSSDEVILQGRDEPDRTSDAKALDAFKRGSRLVQIENRIKTMN 842
Db 633 NISCNLLFLWLSQSPKQDRPLG--TYPDEHTEAPRRSIAAFQSLRAQI----- 682
QY 843 DSPDLKNRKGPMVPMYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 683 -SRDIQERNQGLALPYTYLDPPL-----IENSVSI 711

RESULT 12

US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: 7705.0009-00000
 ; CURRENT APPLICATION NUMBER: US/09/547,435
 ; CURRENT FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 867
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-547-435-24

Query Match 10.9%; Score 513; DB 4; Length 867;
 Best Local Similarity 29.3%; Pred. No. 4.6e-40;
 Matches 154; Conservative 85; Mismatches 192; Indels 94; Gaps 16;
 QY 376 WRTDEEFARETLAGVNPVILKLETFEPAKSTLDRPQYGDHSTKITEAHIRHNG-GLSVQ 434
 DB 424 WCEHFFQYQYINGVNPMLHCISLSFSK-----LPVNDMVAFLGQDTCLQ 471
 QY 435 NALRNKRLFIIDHDFHMFYLDL--INELEG--NFIYASRTLLFLKDDGTLKPLAIELS- 489
 DB 472 TELERGNIFLADYV-----ILAEAPTECLNGRQQYVAAPLCLLWLSPOGALVPLAQLSQ 526
 QY 490 LPHDPGQORGAVSKVYTPAHTGVEGHVWOLAKAYACVNDSAWHQLISHWLNTHAVIEPV 549
 DB 527 TPGPD-----SPFLPTDSEWD---WLLAKTWVRNSEFLVHENTHFLCTHLLCEAFA 576
 QY 550 IATNRQLSVHVPVKHLSPHRYDTLNINALAROTLINAGGVFERVTPPAKALMGADVY 609
 DB 577 MATLRQLPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVT-----SIGRQGLIY 631
 QY 610 -----KSWNFNEQALPADLVKRGVAVDPDQSSPGVGLLLIKDYPVAVDGLVWATERWV 663
 DB 632 LMSTGLAHFTYTNFLCPDLSFARGV-----LAIPNHYRDDGLKIWAIESFV 679
 QY 664 KEYLDIYPNDGELQRDVELQAWKVEYREAHGDLKDRDWPMDTVQQLARACTTIHW 723
 DB 680 SEIVGYIYPSDASVQDSQSELQATGEIFQAQFLGESSGPPSLRCTPGEVWVKTALIFN 739
 QY 724 ASALHAAVNFGQYAGVLPNRPASRPMPE--PGSHDYKKLGGAGKEADWVIRITISQ 782
 DB 740 CSAQHAAVNSQCHDFGAWMPNAPSQRPPQPTKGTTLK-----TYLDTLPEV 788
 QY 783 FQTILGISLILSHSSDEVYLQORDEPDRWTSDAKALDAFKRFGSLVQIENRIKTN 842
 DB 789 NISCNLLFLWLVQEPKQRPGLG--TYPDEHTEAPRPSIAAFQSLRAQI----- 838
 QY 843 DSPDLKNRKGVPMPYMLLYPNTSDVTGKAEGLTANGIPNSISI 887
 DB 839 -SRDIQERNQGLALPYTYLDPPPL-----IENSVSI 867

RESULT 13
 US-09-061-768A-4
 ; Sequence 4, Application US/09061768A
 ; Patent No. 6204037
 ; GENERAL INFORMATION:
 ; APPLICANT: BRASH, ALAN R.
 ; APPLICANT: BOEGLIN, WILLIAM E.
 ; APPLICANT: JISAKA, MITSUO
 ; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: ARLES A. TAYLOR, JR.
 ; CITY: DURHAM
 ; STATE: NORTH CAROLINA
 ; COUNTRY: USA
 ; ZIP: 27707
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
 ; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1
 ; SOFTWARE: WORD PERFECT 6.1 and ASCII
 ; CURRENT APPLICATION DATA: US/09/061,768A
 ; APPLICATION NUMBER: US/09/061,768A
 ; FILING DATE: APRIL 16, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA: NONE
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ARLES A. TAYLOR, JR.
 ; REGISTRATION NUMBER: 39,395
 ; REFERENCE/DOCKET NUMBER: 1242/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 493-8000
 ; TELEFAX: (919) 419-0383
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 677 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-09-061-768A-4
 Query Match 10.7%; Score 507; DB 3; Length 677;
 Best Local Similarity 29.8%; Pred. No. 1.1e-39;
 Matches 160; Conservative 83; Mismatches 192; Indels 102; Gaps 20;
 QY 369 APEFPGF-WRTDEEFARETLAGVNPVILKLETFEPAKSTLDRPQYGDHSTKITEAHIRHN 427
 DB 225 AAEYVFAHQEDAFASQFLNGINPVLRRCHSLP-----NNFPTDEMVAVP 272
 QY 428 MG-GLSVQNALRNKRLFIIDH-----HDHMFYLDLNELEG--NFIYASRTLLFLKD- 477
 DB 273 LGPGGTSLOALEKSGSLFLVDHGILSGVH-----TNILNGKPFQFSAAPMTLLHQSSG 323
 QY 478 DGTFLKPLAIEL-SLPHDPGQORGAVSKVYTPAHTGVEGHVWOLAKAYACVNDSAWHQLIS 536
 DB 324 SGPLIPALIQLKQTGPD-----NPIFLSDDTWD---WLLAKTWVRNSEFYIHEAVT 373
 QY 537 HWLNTHAVIEPVVATNRQLSVHVPVKHLSPHRYDTLNINALAROTLINAGGVFERVTF 596
 DB 374 HLLHAHLIPEVALATLRLQPRCHPLKLLPHRYTLHINTLARELLVAFGLKIDKS-- 431
 QY 597 PAKYALGNSADYVK---SWNFNEQALPADLVKRGVAVDPDQSSPGVGLLLIKDYPVAVDG 652
 DB 432 -TGLGTGFGFSDLIKRNMEQLNYSVLCLPEDIRAKGED-----IPGYRRDDG 478
 QY 653 LVINWAIERWVKEYLDIYPNDGELQRDVELQAWKVEYREAHGDLKDRDWPMDTVQQL 712
 DB 479 MQIWGAIKSFVSEIVSYVPSDTSVQDDQELQAWVREIFSGFLGREGSSGMPSLDITREA 538
 QY 713 LARACTTIWVASALHAAVNFGQYAGVLPNRPASRPMPEPGSHDYKKLGGAGKEAD 772
 DB 539 LVQYLITWIFTCSAKHAAVSSGQFDSQVMMNLPPTMQLPPP-----TSKGQARPE 589
 QY 773 MYFIRITTSQFOTILGISLILSHSSDEVYLQORDEPDRWTSDA--KALDAFKRFGSR 830
 DB 590 S-FIATLPAVNSSSVHIALMLLSAEPGQRPGLGHPD-EHFTEDAPRPSIAAFQSLRAQI--K 644
 QY 831 LVQIENRIKTNWSDPLKNRKGVPMPYMLLYPNTSDVTGKAEGLTANGIPNSISI 887
 DB 645 LIQI-----SKGIERNRGALPYTYLDPPPL-----IENSVSI 677

RESULT 14
 US-09-764-246-4
 ; Sequence 4, Application US/09764246
 ; Patent No. 6649355
 ; GENERAL INFORMATION:
 ; APPLICANT: BRASH, ALAN R.
 ; APPLICANT: BOEGLIN, WILLIAM E.

JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,246
FILING DATE: 17-Jan-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-764-246-4
Query Match 10.7%; Score 507; DB 4; Length 677;
Best Local Similarity 29.8%; Pred. No. 1.1e-39;
Matches 160; Conservative 83; Mismatches 192; Indels 102; Gaps 20;
QY 369 APEKFG-WRTDEPARETLGAVNPVILKLTETEPKSTLDPKGYGHTSKITEAHRN 427
DB 225 AAEYFAHQSDAFASQFLNGINPVLIRCHSLP-----NNPVTDEMVPV 272
QY 428 MG-GLSVQNALRNKELFLD-----HDHFMPLYLDEINELEG--NFIYASRTLLFLKD- 477
DB 273 LQPGTSLQAELEKSLFLVDHGILSGVH-----TNILNGKPPQPSAAPTLLHQSSG 323
QY 478 DGTLLPLAIEL-SLPHPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDSSAWHQLIS 536
DB 324 SGPLLPALQKQTGPD-----NPIFLPSDDTDW---WLLAKTWVRNSEFYIHEAVT 373
QY 537 HWLNTHAVIEPFIATNRQLSVVHPVKLLSPHYRDTLINALARQTLINAGGVFERTVF 596
DB 374 HLLHAFLPEVPALATLQLRCHPLFKLLPHIRYTLHINTLARELLVAPGKLIDKS-- 431
QY 597 PAKYALGMSADVYK-----SWNFNEQALPADLVKRGVAVDDOSSPYGVRLLIKDYPIAVDG 652
DB 432 -TGLGTGFSGLIKRMEQLNYSVLCLPEDIRARGVED-----IPGYIYRDDG 478
QY 653 LVIMWAIERWKEYLDIYPNDGELQDVELQAWKVEBHAHGLDKORDWPRMDTVQ 712
DB 479 MQIWAIRKISFVSEIYIYPEDTSVQDDQELQAWREIFSGFLGRSSGNPSLLDTREA 538
QY 713 LARACTTIWASALHAANVFGQYVYAGYLPNRPPTASRRPMPFEGSHDYKGLGAGKEAD 772
DB 539 LVQYITWTFVTSKAAHAASVSSQFDCSCVMNLPPTMLPPP-----TSRQGARPE 589
QY 773 MVFIRITISQFTILIGISLIELSKSSDSEVVLGQDPEDEWTSDA--KALDAFKRFSR 830

DB 590 S-FIATLPVNSSYHIIALWLLSAEPGDQRLGHVPD-EHFTEDAPRRSVAAFQ---K 644
QY 831 LVQIENRIKTMNDSPDLKNRKGVEVPMPLLYPNTSDVTGKAEGLTAMGIPNSISI 887
DB 645 LIQI-----SKGIRERNEGLALPYTLDPP-----IENSVSI 677
RESULT 15
US-09-087-727-2
; Sequence 2, Application US/09087727A
; Patent No. 6103496
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-727-2
Query Match 10.7%; Score 503.5; DB 3; Length 701;
Best Local Similarity 26.0%; Pred. No. 2.6e-39;
Matches 205; Conservative 108; Mismatches 249; Indels 227; Gaps 36;
QY 130 KTLTLEGVKGKTVVVFVANSWVPHKLYSQERIFPANDTYLPSKMPAALVPRDELKIL 189
DB 109 ETALAREATGKTA-----DDSLP-----VLEHKKBEIRA- 139
QY 190 RGDNDPGYQEHDRVYDYNDLGDPKGESHARPILGG--SQEH--PYPRCCTGRHP 245
DB 140 -----KQDFY-----HWRVFLGLPSYVHIFSYRPPVRRHNP 172
QY 246 TKKDPNSESRLFLNLNIYVPRDRFGLHKMSDFLGYSKLTIEAVLPTLGFVDDTPKE 305
DB 173 NRPEWNG-----YIPGFPIINPKATKFLNLNL-----YSLFKTASFFV----- 212
QY 306 FDSFEDILGLYELGPEAPNPLIAEIRKKIPDEF-----LRSILPNGSHDHPKMLP 358
DB 213 -----RLGPA-----LAFKRGLLDCKHSHKRLKIRKIPGK----- 246
QY 359 NVIKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVILKLTETEPKSTLDPKGYGHTSK 418
DB 247 --KSVVSEYVAEH--WAEDTFPGVQVLYNGVNPGLIRRCTRIPDK-----PP 288
QY 419 IYEAHTRHNMG-GLSVQNALRNKRLFILDDHDFMPLYLDEINELEGNTFY--ASRTLLPL 475
DB 289 VTDDWVAPFLGSGTCLQAELEKGNILYADY--RIMEGIPTV--ELSGRQKHHCAPCLCLHF 345
QY 476 KDDGTLLPLAIELS-LPHPDQQRGAVSKVYTPAHTGVEGHVWQAKAYACVNDSSAWHQL 534
DB 346 GPEGKMPATIQLSQTPGPD-----CPIFLPSDSEWD---WLLAKTWVRYAEFVSHEA 395
QY 535 ISHLNTHAVIEPFIATNRQLSVVHPVKLLSPHYRDTLINALARQTLINAGGVFERTVF 594
DB 396 IAHLETHLIAFAFCLALLRNLPMCHPELYKLLIPIHTRYTVQINSIGRAVLLNEGLL----- 451
QY 595 VPPAKYALGMSADV-----YKSNFNEQALPADLVKRGVAVDDOSSPYGVRLLIK 644
DB 452 -----SAKWSLGVGEFAGVWVRALSELTYDSLPLNDPVERGV---QDLP----- 494
QY 645 DYPYAVDGLVIMWAIERWKEYLDIYPNDGELQDVELQAWKVEBHAHGLDKORD-- 702
DB 495 GYYRDRDSLAVWNALEKYYVTEIITYYPSDAAVEGDPQLQSWVQIFKEC---LIGRESS 551
QY 703 WMPR-MDTVQQLARACTTIWASALHAANVFGQYVYAGYLPNRPPTASRRPMPFEGSHDY 761

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Db      552 GFPRCLRTVPELIRVTVIIVTCSAKHAANTGQMEFTAMNPFASVRNP-----PI 604
Qy      762 KKLGGAGQKEADMVFIRTTTSOFQILGSLIEILSKSSSDEVYLGQRDEPD-RWTSDA-- 818
Db      605 QTKGLTTLE---TFMDTLPDVKTTCITLLVLWLTLSREFDDRRPLGH--FPDIHFVEEAPR 659
Qy      819 KALDAFKRFGSRLVQIENRIKTMNDSPLKMRKGPVEMPYMLLYPNTSDVTGEKAELTA 878
Db      660 RSIEAFRQ---RLNQI-----SHDIRQNKCLPIPIYYLDP----- 692
Qy      879 MGIPNSISI 887
Db      693 VLIENSISI 701

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Search completed: March 23, 2004, 07:02:07
 Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 07:01:04 ; Search time 333 Seconds
(without alignments)
689.770 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFHGVADRLTGKKNKEAWSE.....VTGKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4723	100.0	887	14	US-10-059-909-16
2	4723	100.0	887	14	Sequence 16, Appl
3	4723	100.0	887	14	Sequence 22, Appl
4	4575	96.9	897	12	US-10-132-350-24
5	4498	95.2	926	12	US-10-425-114-39463
6	4487	95.0	887	14	Sequence 39463, A
7	4487	95.0	887	14	Sequence 69756, A
8	3039	64.3	864	14	US-10-132-350-18
9	2958	62.6	873	14	Sequence 18, Appl
10	2958	62.6	873	14	Sequence 20, Appl
11	2958	62.6	873	14	Sequence 10, Appl
12	2958	62.6	891	12	US-10-132-350-2
13	2936.5	62.2	862	10	US-10-132-350-4
14	2929.5	62.0	862	10	US-10-425-114-62915
15	2860	60.6	864	10	Sequence 9, Appl
					Sequence 12, Appl
					Sequence 16, Appl

Sequence 14, Appl
Sequence 16, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 213159, A
Sequence 45828, A
Sequence 54419, A
Sequence 215976, A
Sequence 45769, A
Sequence 54429, A
Sequence 55253, A
Sequence 17, Appl
Sequence 239573, A
Sequence 16, Appl
Sequence 12, Appl
Sequence 220216, A
Sequence 215973, A
Sequence 45631, A
Sequence 62385, A
Sequence 258944, A
Sequence 242598, A
Sequence 57554, A
Sequence 54555, A
Sequence 151512, A
Sequence 57794, A
Sequence 161981, A
Sequence 57755, A
Sequence 45728, A
Sequence 62362, A
Sequence 151513, A

ALIGNMENTS

RESULT 1

US-10-059-909-16
; Sequence 16, Application US/10059909
; Publication No. US20030074693A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Kinney, Anthony
; APPLICANT: Klein, Theodore
; APPLICANT: Lee, Jian Ming
; APPLICANT: Pearlstein, Richard
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Shen, Jennie
; APPLICANT: Thorpe, Cathy
; APPLICANT: Tingey, Scott
; APPLICANT: Wang, Zude
; TITLE OF INVENTION: Plant Lipoxigenases
; FILE REFERENCE: BBI333 US CIP
; CURRENT APPLICATION NUMBER: US/10/059,909
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/501,422
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,597
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-059-909-16

Query Match 100.0%; Score 4723; DB 14; Length 887;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFHGVADRLTGKKNKEAWSEKIRGTVRLVKKEVLVDGDNASLLDGVHRLGWDGVAF 60

DB 1 MFHGVADRLTGKKNKEAWSEKIRGTVRLVKKEVLVDGDNASLLDGVHRLGWDGVAF 60

QY 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEDWESQGIPIGAVLVR 120
Db 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEDWESQGIPIGAVLVR 120
QY 121 NLOHAEFFLKTTLTLEGVPGKGTVPVANSWYYPHKLVSQERIFPANDTYLPSKMPAALVP 180
Db 121 NLOHAEFFLKTTLTLEGVPGKGTVPVANSWYYPHKLVSQERIFPANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYRVDYNDLGDGPKGEBHARPILGGSQEHYPYPRCR 240
Db 181 YRQDELKILRGDDNPGPYQEHDRVYRVDYNDLGDGPKGEBHARPILGGSQEHYPYPRCR 240
QY 241 TGRHPTKDDPNSESRLLFLNINIVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
Db 241 TGRHPTKDDPNSESRLLFLNINIVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
QY 301 DTPKEFDSFEDILGLYELGPEAPNPLIAERKKIPSEFLRSILPNSHSHDPLKMPLPNV 360
Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAERKKIPSEFLRSILPNSHSHDPLKMPLPNV 360
QY 361 IKSDVLKKAPEFKFGWRTDEFAFETLAGVNPVVIKLTTFPPAKSTLDPQYGDHTSKIT 420
Db 361 IKSDVLKKAPEFKFGWRTDEFAFETLAGVNPVVIKLTTFPPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVONALRNKELFLDHDHDFMPYLDINELEGNFYASRTLLFLKDDGT 480
Db 421 EAHIRHNMGGLSVONALRNKELFLDHDHDFMPYLDINELEGNFYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHDPGQQRGAVSVKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 481 LKPLAIELSLPHDPGQQRGAVSVKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
QY 541 THAVIEPFIATNRQLSVHPVHKLLSPHYRDTLNINALAROTLINAGGVFERTVFPKY 600
Db 541 THAVIEPFIATNRQLSVHPVHKLLSPHYRDTLNINALAROTLINAGGVFERTVFPKY 600
QY 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRELLIKDYPYAVDGLVWMAIE 660
Db 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRELLIKDYPYAVDGLVWMAIE 660
QY 661 RWKEYLIDYYPNDGELQRDVELQAWWKEVREBAHGLDKORDWPRMDTVQQLARACTTI 720
Db 661 RWKEYLIDYYPNDGELQRDVELQAWWKEVREBAHGLDKORDWPRMDTVQQLARACTTI 720
QY 721 IWASALHAAVNFQYFAGYLPNRPPTASRRPMPPEPGSHDYKKGAGQKEADWVFIRTT 780
Db 721 IWASALHAAVNFQYFAGYLPNRPPTASRRPMPPEPGSHDYKKGAGQKEADWVFIRTT 780
QY 781 SQFOTILGISLIELSKHSSDEVYLGQDEPDRWTSDAKALDAFKFGSRLVQIENRIKT 840
Db 781 SQFOTILGISLIELSKHSSDEVYLGQDEPDRWTSDAKALDAFKFGSRLVQIENRIKT 840
QY 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

RESULT 2

US-10-132-350-22
; Sequence 22, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: of Use
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286, 889

; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-22

Query Match 100.0%; Score 4723; DB 14; Length 887;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFWHGVADRLTGKKNKEAMSEKIRGTVPLAVKKEVLDVGDVFNASLLDGVHRLGDDGVAF 60
Db 1 MFWHGVADRLTGKKNKEAMSEKIRGTVPLAVKKEVLDVGDVFNASLLDGVHRLGDDGVAF 60
QY 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEDWESQGIPIGAVLVR 120
Db 61 QLVSAATAADPSNGGRGKVGKAAHLEAAVSLKSTADGETVYRVSVFEDWESQGIPIGAVLVR 120
QY 121 NLOHAEFFLKTTLTLEGVPGKGTVPVANSWYYPHKLVSQERIFPANDTYLPSKMPAALVP 180
Db 121 NLOHAEFFLKTTLTLEGVPGKGTVPVANSWYYPHKLVSQERIFPANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYRVDYNDLGDGPKGEBHARPILGGSQEHYPYPRCR 240
Db 181 YRQDELKILRGDDNPGPYQEHDRVYRVDYNDLGDGPKGEBHARPILGGSQEHYPYPRCR 240
QY 241 TGRHPTKDDPNSESRLLFLNINIVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
Db 241 TGRHPTKDDPNSESRLLFLNINIVPRDERFGLKMSDFLGYSLKTIIEAVLPTLGTFTVD 300
QY 301 DTPKEFDSFEDILGLYELGPEAPNPLIAERKKIPSEFLRSILPNSHSHDPLKMPLPNV 360
Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAERKKIPSEFLRSILPNSHSHDPLKMPLPNV 360
QY 361 IKSDVLKKAPEFKFGWRTDEFAFETLAGVNPVVIKLTTFPPAKSTLDPQYGDHTSKIT 420
Db 361 IKSDVLKKAPEFKFGWRTDEFAFETLAGVNPVVIKLTTFPPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVONALRNKELFLDHDHDFMPYLDINELEGNFYASRTLLFLKDDGT 480
Db 421 EAHIRHNMGGLSVONALRNKELFLDHDHDFMPYLDINELEGNFYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHDPGQQRGAVSVKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 481 LKPLAIELSLPHDPGQQRGAVSVKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
QY 541 THAVIEPFIATNRQLSVHPVHKLLSPHYRDTLNINALAROTLINAGGVFERTVFPKY 600
Db 541 THAVIEPFIATNRQLSVHPVHKLLSPHYRDTLNINALAROTLINAGGVFERTVFPKY 600
QY 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRELLIKDYPYAVDGLVWMAIE 660
Db 601 ALGMSADYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRELLIKDYPYAVDGLVWMAIE 660
QY 661 RWKEYLIDYYPNDGELQRDVELQAWWKEVREBAHGLDKORDWPRMDTVQQLARACTTI 720
Db 661 RWKEYLIDYYPNDGELQRDVELQAWWKEVREBAHGLDKORDWPRMDTVQQLARACTTI 720
QY 721 IWASALHAAVNFQYFAGYLPNRPPTASRRPMPPEPGSHDYKKGAGQKEADWVFIRTT 780
Db 721 IWASALHAAVNFQYFAGYLPNRPPTASRRPMPPEPGSHDYKKGAGQKEADWVFIRTT 780
QY 781 SQFOTILGISLIELSKHSSDEVYLGQDEPDRWTSDAKALDAFKFGSRLVQIENRIKT 840
Db 781 SQFOTILGISLIELSKHSSDEVYLGQDEPDRWTSDAKALDAFKFGSRLVQIENRIKT 840
QY 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 841 MNDSPLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

Db 841 MNDSPDLKURKGPVEMPYMLLPNTSDVTGKAEGLTAMGIPNSISI 887

RESULT 3

US-10-132-350-24
 ; Sequence 24, Application US/10132350
 ; Publication No. US20030166855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Acevedo, Pedro A. Navarro
 ; APPLICANT: Duvick, Jonathan P.
 ; APPLICANT: Koloniets, Mikhailo V.
 ; APPLICANT: Simmons, Carl R.
 ; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
 ; FILE REFERENCE: 35718/246439
 ; CURRENT APPLICATION NUMBER: US/10/132,350
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/286,889
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/305,366
 ; PRIOR FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 887
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-10-132-350-24

Query Match 100.0%; Score 4723; DB 14; Length 887;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPWGVADRLTGKKEAWSEGKIRGTVLVKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 60
 Db 1 MPWGVADRLTGKKEAWSEGKIRGTVLVKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 60
 Qy 61 QLVSAATAADPSNGRGKVGKAAHLEAEVVSLSKSTADGETVYRVSFENDESOGIPGAVLR 120
 Db 61 QLVSAATAADPSNGRGKVGKAAHLEAEVVSLSKSTADGETVYRVSFENDESOGIPGAVLR 120
 Qy 121 NLQHAFFLKTLLTLEGVPGKGVTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
 Db 121 NLQHAFFLKTLLTLEGVPGKGVTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
 Qy 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPRRCR 240
 Db 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPRRCR 240
 Qy 241 TGRHPTKDDPNSESLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIIEAVLPTLGTFTVD 300
 Db 241 TGRHPTKDDPNSESLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIIEAVLPTLGTFTVD 300
 Qy 301 DTPKEFDSFEDILGLYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHDHPKMPLPNV 360
 Db 301 DTPKEFDSFEDILGLYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHDHPKMPLPNV 360
 Qy 361 IKSDVLKCAPFKGWRDEEFARETLAGVNPVILKLTTEPPAKSTLDPQYGDHSTKIT 420
 Db 361 IKSDVLKCAPFKGWRDEEFARETLAGVNPVILKLTTEPPAKSTLDPQYGDHSTKIT 420
 Qy 421 EAHIRHNMGGLSVQNALNKFLPILDDHDPMPYLDEINELEGNFIYASRTLLFLKDDGT 480
 Db 421 EAHIRHNMGGLSVQNALNKFLPILDDHDPMPYLDEINELEGNFIYASRTLLFLKDDGT 480
 Qy 481 LKPLAIELSLPHDPQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHLN 540
 Db 481 LKPLAIELSLPHDPQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHLN 540
 Qy 541 THAVIEPPVIATNRQLSVVPHVKLLSPHYRDTLLINALARQTLINAGGVFERVTPPAKY 600
 Db 541 THAVIEPPVIATNRQLSVVPHVKLLSPHYRDTLLINALARQTLINAGGVFERVTPPAKY 600

Qy 601 ALGMSADVYKSNFNECALPADLVKGVAVPDQSSPYGYVRLIKDYPYAVDGLVIWIAIE 660
 Db 601 ALGMSADVYKSNFNECALPADLVKGVAVPDQSSPYGYVRLIKDYPYAVDGLVIWIAIE 660
 Qy 661 RWVKEYLDIYYPNDGELQORDVELQAWWKEVREAHGDLKDRDWWPRMDTVQQARACTTII 720
 Db 661 RWVKEYLDIYYPNDGELQORDVELQAWWKEVREAHGDLKDRDWWPRMDTVQQARACTTII 720
 Qy 721 IWVASALHAAVNFGQYPYAGYLPNRTASRRPMPERPGSHDYKKGAGOKEADMVFTRTIT 780
 Db 721 IWVASALHAAVNFGQYPYAGYLPNRTASRRPMPERPGSHDYKKGAGOKEADMVFTRTIT 780
 Qy 781 SQFQTILGISLIBILSKHSSDEVYLQORDEPDRWTSDAKALDAFKFSGSRLVQIENRIKT 840
 Db 781 SQFQTILGISLIBILSKHSSDEVYLQORDEPDRWTSDAKALDAFKFSGSRLVQIENRIKT 840
 Qy 841 MNDSPDLKURKGPVEMPYMLLPNTSDVTGKAEGLTAMGIPNSISI 887
 Db 841 MNDSPDLKURKGPVEMPYMLLPNTSDVTGKAEGLTAMGIPNSISI 887

RESULT 4
 US-10-425-114-39463
 ; Sequence 39463, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 39463
 ; LENGTH: 897
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700202892_FLI pep
 US-10-425-114-39463

Query Match 96.9%; Score 4575; DB 12; Length 897;
 Best Local Similarity 97.1%; Pred. No. 0;
 Matches 861; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MPWGVADRLTGKKEAWSEGKIRGTVLVKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 60
 Db 11 MDWGRTEQALTGKKEAWSEGKIRGTVLVKEVLDVGDVFNASLLDGVHRIILGWDDGVAF 70
 Qy 61 QLVSAATAADPSNGRGKVGKAAHLEAEVVSLSKSTADGETVYRVSFENDESOGIPGAVLR 120
 Db 71 QLVSAATAADPSNGRGKVGKAAHLEAEVVSLSKSTADGETVYRVSFENDESOGIPGAVLR 130
 Qy 121 NLQHAFFLKTLLTLEGVPGKGVTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
 Db 131 NLQHAFFLKTLLTLEGVPGKGVTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 190
 Qy 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPRRCR 240
 Db 191 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDPPDKGEEHARPIILGSGQEHYPRRCR 250
 Qy 241 TGRHPTKDDPNSESLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIIEAVLPTLGTFTVD 300
 Db 251 TGRHPTKDDPNSESLFLNLNIYVPRDERFGLKMSDFLGYSLKTIIIEAVLPTLGTFTVD 310
 Qy 301 DTPKEFDSFEDILGLYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHDHPKMPLPNV 360
 Db 311 DTPKEFDSFEDILGLYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHDHPKMPLPNV 370

QY 361 IKSDVLKAPFKFGWRTDEEFARETLAGVNPVLIKELTEFPFAKSTLDPQYGDHTSKIT 420
Db 371 IKSDVLKAPFKFGWRTDEEFARETLAGVNPVLIKELTEFPFAKSTLDPQYGDHTSKIT 430
QY 421 EAHIRHNNGGISVQNALRNKELFLDHDHDFMPVLDINELEGNFYASRTLLFLKDDGT 480
Db 431 EAHIRHNNGGISVQNALRNKELFLDHDHDFMPVLDINELEGNFYASRTLLFLKDDGT 490
QY 481 LKPLAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 491 LKPLAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 550
QY 541 THAVIEPVIATNQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
Db 551 THAVIEPVIATNQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 610
QY 601 ALGMSADVKSNNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWMAIE 660
Db 611 ALGMSADVKSNNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWMAIE 670
QY 661 RWKEYLDIYYPNDGELQRDVELQAWKVEEBAHGLDKORDWMPMDTVQQLARACTTI 720
Db 671 RWKEYLDIYYPNDGELQRDVELQAWKVEEBAHGLDKORDWMPMDTVQQLARACTTI 730
QY 721 IWASALHAAVNFQYIYAGVLPNRPASRRPMPPEGSHDYKKGAGQKEADWVFRTIT 780
Db 731 IWASALHAAVNFQYIYAGVLPNRPASRRPMPPEGSHDYKKGAGQKEADWVFRTIT 790
QY 781 SQFTILGISLIELSKHSSDEVVLGQDEPDRTSDAKALDAFKRFGSLVQIENRIKT 840
Db 791 SQFTILGISLIELSKHSSDEVVLGQDEPDRTSDAKALDAFKRFGSLVQIENRIKT 850
QY 841 MNDSPTLKNRKGVPVEMPMYLLYPNTSDVTGKAEGLTANGIPNSISI 887
Db 851 MNDSPTLKNRKGVPVEMPMYLLYPNTSDVTGKAEGLTANGIPNSISI 897

RESULT 5
US-10-425-114-69756
; Sequence 69756, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69756
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017282G11_FLI.pgp
US-10-425-114-69756

Query Match 95.2%; Score 4498; DB 12; Length 926;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 831; Conservative 33; Mismatches 23; Indels 0; Gaps 0;

QY 1 MFHWGVADRLTGKXKAWSEKGIKGTVRLVKKEVLVDGDFNLSLLDGVHRIILGWDGVAF 60
Db 40 MFHWGVADRLTGKXKAWSEKGIKGTVRLVKKEVLVDGDFNLSLLDGVHRIILGWDGVAF 99
QY 61 QLVYSATAADPSNGRGKVGKAAHLEAVVSLKSTTDGTTVYRVSEFWDGSGQVFGAVLVR 120

Db 100 QLVYSATAADPSNGRGKVGKAAHLEAVVSLKSTTDGTTVYRVSEFWDGSGQVFGAVLVR 159
QY 121 NLOQHAEFFLKSLTLEGVPGKGTGVFVANSWVYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
Db 160 NLOQHAEFFLKSLTLEGVPGKGTGVFVANSWVYVPHKLYSQERIFFANDTYLPSKMPAALVP 219
QY 181 YQDELKILRGDNDPGPIQOEHDRTVRYDYNDLGDPPKGBEHARPILOGSQEHYPHRCR 240
Db 220 YQDELKILRGDNDPGPIQOEHDRTVRYDYNDLGDPPKGBEHARPILOGSQEHYPHRCR 279
QY 241 TGRHPTKDPNSERLFLNLNINIVPRDERFCHLKMDSFLGYSLKTIIEAVLPTLGTFTVD 300
Db 280 TGRHPTKDPNSERLFLNLNINIVPRDERFCHLKMDSFLGYSLKTIIEAVLPTLGTFTVD 339
QY 301 DTPKEFDSEFIDILGYELGPEAPNPLIAEIRKIPSEFRLSRILPNSHSHPLKMPDPNV 360
Db 340 DTPKEFDSEFIDILGYELGPEAPNPLIAEIRKIPSEFRLSRILPNSHSHPLKMPDPNV 399
QY 361 IKSDVLKAPFKFGWRTDEEFARETLAGVNPVLIKELTEFPFAKSTLDPQYGDHTSKIT 420
Db 400 IRSDVLKAPFKFGWRTDEEFARETLAGVNPVLIKELTEFPFAKSTLDPQYGDHTSKIT 459
QY 421 EAHIRHNNGGISVQNALRNKELFLDHDHDFMPVLDINELEGNFYASRTLLFLKDDGT 480
Db 460 EAHIRHNNGGISVQNALRNKELFLDHDHDFMPVLDINELEGNFYASRTLLFLKDDGT 519
QY 481 LKPLAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 540
Db 520 LKPLAIELSLPHDPGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISHWLN 579
QY 541 THAVIEPVIATNQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 600
Db 580 THAVIEPVIATNQLSVVHPVHKLLSPHYRDTLNINALARQTLINAGGVFERTVFPKY 639
QY 601 ALGMSADVKSNNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWMAIE 660
Db 640 ALGMSADVKSNNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVWMAIE 699
QY 661 RWKEYLDIYYPNDGELQRDVELQAWKVEEBAHGLDKORDWMPMDTVQQLARACTTI 720
Db 700 RWKEYLDIYYPNDGELQRDVELQAWKVEEBAHGLDKORDWMPMDTVQQLARACTTI 759
QY 721 IWASALHAAVNFQYIYAGVLPNRPASRRPMPPEGSHDYKKGAGQKEADWVFRTIT 780
Db 760 IWASALHAAVNFQYIYAGVLPNRPASRRPMPPEGSHDYKKGAGQKEADWVFRTIT 819
QY 781 SQFTILGISLIELSKHSSDEVVLGQDEPDRTSDAKALDAFKRFGSLVQIENRIKT 840
Db 820 SQFTILGISLIELSKHSSDEVVLGQDEPDRTSDAKALDAFKRFGSLVQIENRIKT 879
QY 841 MNDSPTLKNRKGVPVEMPMYLLYPNTSDVTGKAEGLTANGIPNSISI 887
Db 880 MNDSPTLKNRKGVPVEMPMYLLYPNTSDVTGKAEGLTANGIPNSISI 926

RESULT 6
US-10-132-350-18
; Sequence 18, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13


```
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-132-350-18

Query Match      95.0%; Score 4487; DB 14; Length 887;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 829; Conservative 34; Mismatches 24; Indels 0; Gaps 0;

QY 1 MFHWGVADRLTGKKNKAESEKIRGTIVLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAF 60
DB 1 MFHWGVADRLTGKKNKAESEKIRGTIVLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAF 60
QY 61 QLVSAADADPSNGRGKGVKAAHLEAAVVSLSKSTADGETTVYRVSEFWDESQIGAVLVR 120
DB 61 QLVSAADADPSNGRGKGVKAAHLEAAVVSLSKSTADGETTVYRVSEFWDESQIGAVLVR 120
QY 121 NLQHAFFELKTLTLEGVPCKGTIVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
DB 121 NLQHAFFELKTLTLEGVPCKGTIVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDGPKGEEHARPIILGSGQEHYPRRCR 240
DB 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDGPKGEEHARPIILGSGQEHYPRRCR 240
QY 241 TGRHPTKDPNSESRLFLNLNIYVPRDEREGHLMKMSDFLGYSLKTIIEAVLPTLGRFVD 300
DB 241 TGRHPTKDPNSESRLFLNLNIYVPRDEREGHLMKMSDFLGYSLKTIIEAVLPTLGRFVD 300
QY 301 DTPKEFDSFEDILGLYEPGPAPNPLIAEIRKIPSEFLRSILPNSHSHDHPKMPLPNV 360
DB 301 DTPKEFDSFEDILGLYEPGPAPNPLIAEIRKIPSEFLRSILPNSHSHDHPKMPLPNI 360
QY 361 IKSDVLKKAPEFKFQWRDEEFARETLAGVNPVILKLTTEPAKSTLDPQYGDHTSKIT 420
DB 361 IKSDVLKKAPEFKFQWRDEEFARETLAGVNPVILKLTTEPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVQNALNKRFLILDHHDHMPVYLDEINELGNFIYASRTLLFLKDDGT 480
DB 421 EAHIRHNMGGLSVQNALNKRFLILDHHDHMPVYLDEINELGNFIYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHDPQOQOQGVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
DB 481 LKPLAIELSLPHDPQOQOQGVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
QY 541 THAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNLNARQTLINAGGVFERTVPPAKY 600
DB 541 THAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNLNARQTLINAGGVFERTVPPAKY 600
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWIAIE 660
DB 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWIAIE 660

; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-132-350-20

Query Match      95.0%; Score 4487; DB 14; Length 887;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 829; Conservative 34; Mismatches 24; Indels 0; Gaps 0;

QY 1 MFHWGVADRLTGKKNKAESEKIRGTIVLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAF 60
DB 1 MFHWGVADRLTGKKNKAESEKIRGTIVLVKKEVLVDGDFNASLLDGVHRIILGWDDGVAF 60
QY 61 QLVSAADADPSNGRGKGVKAAHLEAAVVSLSKSTADGETTVYRVSEFWDESQIGAVLVR 120
DB 61 QLVSAADADPSNGRGKGVKAAHLEAAVVSLSKSTADGETTVYRVSEFWDESQIGAVLVR 120
QY 121 NLQHAFFELKTLTLEGVPCKGTIVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
DB 121 NLQHAFFELKTLTLEGVPCKGTIVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVP 180
QY 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDGPKGEEHARPIILGSGQEHYPRRCR 240
DB 181 YRQDELKILRGDDNPGPYQEHDRVYRYDNDLGDGPKGEEHARPIILGSGQEHYPRRCR 240
QY 241 TGRHPTKDPNSESRLFLNLNIYVPRDEREGHLMKMSDFLGYSLKTIIEAVLPTLGRFVD 300
DB 241 TGRHPTKDPNSESRLFLNLNIYVPRDEREGHLMKMSDFLGYSLKTIIEAVLPTLGRFVD 300
QY 301 DTPKEFDSFEDILGLYEPGPAPNPLIAEIRKIPSEFLRSILPNSHSHDHPKMPLPNV 360
DB 301 DTPKEFDSFEDILGLYEPGPAPNPLIAEIRKIPSEFLRSILPNSHSHDHPKMPLPNI 360
QY 361 IKSDVLKKAPEFKFQWRDEEFARETLAGVNPVILKLTTEPAKSTLDPQYGDHTSKIT 420
DB 361 IKSDVLKKAPEFKFQWRDEEFARETLAGVNPVILKLTTEPAKSTLDPQYGDHTSKIT 420
QY 421 EAHIRHNMGGLSVQNALNKRFLILDHHDHMPVYLDEINELGNFIYASRTLLFLKDDGT 480
DB 421 EAHIRHNMGGLSVQNALNKRFLILDHHDHMPVYLDEINELGNFIYASRTLLFLKDDGT 480
QY 481 LKPLAIELSLPHDPQOQOQGVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
DB 481 LKPLAIELSLPHDPQOQOQGVSKVYTPAHTGVEGHVWQLAKAYACVNDSAWHQLISHWLN 540
QY 541 THAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNLNARQTLINAGGVFERTVPPAKY 600
DB 541 THAVIEPFIATNRQLSVVHPVHKLLSPHYRDTLNLNARQTLINAGGVFERTVPPAKY 600
QY 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWIAIE 660
DB 601 ALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIWIAIE 660
```

QY 661 RWKEYLDIYYPNDGELORDVELQAWKWEVREBAHGDLDKORDWPRMDTVQOOLARACTTI 720
Db 661 RWKEYLDIYYPNDGELORDVELQAWKWEVREBAHGDLDKORDWPRMDTVQOOLARACTTV 720
QY 721 IWASALHAANFQGYPYAGYLPNRPRTASRRPMPPEPGSHDYKKGAGQKADWVFIRIT 780
Db 721 IWASALHAANFQGYPYAGYLPNRPRTASRRPMPPEPGSHDYKKGAGQKADWVFIRIT 780
QY 781 SOFTILGILSILIELSKHSSDEVYLGQDEPRWTSDAKALDAPKRGSLVQIENRIKT 840
Db 781 SOFTILGILSILIELSKHSSDEVYLGQDEPRWTSDAKALDAPKRGSLVQIENRIKT 840
QY 841 MNDSPDLKNRKGPVEMPVMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 841 MNDSPDLKNRKGPVEMPVMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
RESULT 8
US-10-132-350-10
; Sequence 10, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; TYPE: PRT
; LENGTH: 864
; ORGANISM: Zea mays
US-10-132-350-10
Query Match 64.3%; Score 3039; DB 14; Length 864;
Best Local Similarity 66.1%; Pred. No. 4.8e-280;
Matches 584; Conservative 100; Mismatches 176; Indels 24; Gaps 10;
QY 5 GVADRLTGKKEAWSEKIRGTVELVKVEYLDVGDVFNASLLDGVHRLGWDGVAFLVS 64
Db 4 GIIDGLTGANKHA----RLKGTVLMKKNVLDLNDFGATVVDGSISEFLG--KGVTQCLIS 57
QY 65 ATAADPSNGGKGVKGAHLEEAUVSLKSTADGETVYRVSPEND--ESQIGPAGVILRNQ 123
Db 58 STLVDANNNGRVRGAENLEQWLTSLPSLTGSGKGVTFDWEVKLGVPFVAVVKNH 117
QY 124 HAEFFLXTLLEGVPGKGTVFVANSVWVPHKLYSOERIFPANDTYLPKMPAALVPYRQ 183
Db 118 AAEFFLXTLTDVGRGAVTFVANSVWVPHKLYSOERIFPANDTYLPKMPAALVPYRQ 177
QY 184 DELKILGDDNPGYQSDHRYDYNDLGDPKGEBHARPLGSGQEHPPRRCTGR 243
Db 178 DELKILGDDNPGYQSDHRYDYNDLGDPKGEBHARPLGSGQEHPPRRCTGR 235
QY 244 HPTKDDPNSERLFLMLNLYVPRDERFGLKMSDFLGYSKLTIIIEAVLPTGLTFVDDTP 303
Db 236 KPTKDDPNSERLFLMLNLYVPRDERFGLKMSDFLGYSKLTIIIEAVLPTGLTFVDDTP 294
QY 304 KEFSDPDLGLYELGPEAPNPLAIBIRKIPSEFRLSTILPNSGHDHPLKPLPNVKS 363
Db 295 GEFSDPDLGLYELGPEAPNPLAIBIRKIPSEFRLSTILPNSGHDHPLKPLPNVKS 353
QY 364 DVLKKAPEFKGWRDTEFARETLAGVNPVILKRLTEFFPAKSTLDPQYGDHSTKITEAH 423

Db 354 D-----KNARWTDDEFAREVLAGVNPMTITLTPPKSTLDPKSGYGHSTITAEH 405
QY 424 IRRHMGGLSVQNALRNKELFLDHDHDFMPYLDLNELEGNFIYASRLLFLKDDGTLPK 483
Db 406 IEKNLEGLTVQOALDGNELYLIDHEDRPMPLIDVNNLEGNFIYATRLFFLGRGRLAP 465
QY 484 LAIELSLPHPDQOORGAVSKYTPPAHTGVEGVHQLAKAYACVNDSAWHQLISHWLNTA 543
Db 466 LAIEUSEPYIDGLTVAKSKYTPPASSGVAEAWVQAKAYAVVNDSGWHQLVSHWLNTA 525
QY 544 VIEPFIATNRQLSVVHPVHKLLSPHYRDTLINALAQTLINAGGVFERTVFFPAKALG 603
Db 526 VMEPFIATNRQLSVVHPVHKLLSPHYRDTLINALAQTLINAGGVFERTVFFPAKALG 585
QY 604 MSADYKSWNFNEQALPADLVKRGVAVPDQSPGVYRLLIKDYPYADGLVIMWALERV 663
Db 586 MSSVYKSWNFNEQALPADLVKRGVAVPDQSPGVYRLLIKDYPYADGLVIMWALERV 645
QY 664 KEYLDIYYPNDGELORDVELQAWKWEVREBAHGDLDKORDWPRMDTVQOOLARACTTI 723
Db 646 GEYLAIYYPDDGALRGDEELQAWKWEVREBAHGDLDKORDWPRMDTVQOOLARACTTI 705
QY 724 ASALHAANFQGYPYAGYLPNRPRTASRRPMPPEPGSHDYKKGAGQKADWVFIRIT 783
Db 706 ASALHAANFQGYPYAGYLPNRPRTASRRPMPPEPGSHDYKKGAGQKADWVFIRIT 762
QY 784 OTILGILSILIELSKHSSDEVYLGQDEPRWTSDAKALDAPKRGSLVQIENRIKT 843
Db 763 OTILGILSILIELSKHSSDEVYLGQDEPRWTSDAKALDAPKRGSLVQIENRIKT 821
QY 844 SPDLKNRKGPVEMPVMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 822 DPQLNRNGPABFPYMLLYPNTSDHSG--AAAGLTAKGIPNSISI 864
RESULT 9
US-10-132-350-12
; Sequence 12, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; LENGTH: 864
; ORGANISM: Zea mays
US-10-132-350-12
Query Match 64.3%; Score 3039; DB 14; Length 864;
Best Local Similarity 66.1%; Pred. No. 4.8e-280;
Matches 584; Conservative 100; Mismatches 176; Indels 24; Gaps 10;
QY 5 GVADRLTGKKEAWSEKIRGTVELVKVEYLDVGDVFNASLLDGVHRLGWDGVAFLVS 64
Db 4 GIIDGLTGANKHA----RLKGTVLMKKNVLDLNDFGATVVDGSISEFLG--KGVTQCLIS 57
QY 65 ATAADPSNGGKGVKGAHLEEAUVSLKSTADGETVYRVSPEND--ESQIGPAGVILRNQ 123
Db 58 STLVDANNNGRVRGAENLEQWLTSLPSLTGSGKGVTFDWEVKLGVPFVAVVKNH 117

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QY 124 HAEFFLKTLLSGVCKGTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQ 183
Db 118 AAEFFLKTLLDVGFGAVTVANSWVYVPAKYRNRVFNSTYLPSPALPKPYRD 177
QY 184 DELKILRGDNDPGPYQEHDRVYRYDYNDLGDGDRGEEHARDILGSGQEHYPYRRCRTGR 243
Db 178 DELNLRGDDQCGPYQEHDRVYRYDYNDLGDGDRG--NPRFLGSDADHPYPRCRTGR 235
QY 244 HETKDPNSESRLFILNLNIVYPRDERFGLHCKMSDFLGYSUKTIIIEAVLPILGTFVDDTP 303
Db 236 KPTKTDPNSDSRLSIVE-QIYVPRDERFGLHCKMSDFLGYSUKTIIIEAVLPILGTFVDDTP 294
QY 304 KEFDSFEDILGYELGPEAPNPNLAEIRKIKPSEFLRSILPNSGSHDPLKMPILPNVTKS 363
Db 295 GEFDSFQDIINLYEGIKLPKIQALEDEKLPFLQVVKDLAPAGG-DYLLKLPILQIIE 353
QY 364 DVLKKAPEKFWRTDEEFAETLAGVNPVIKRLTEPAPKSTLDLPROYGDHSTKITTAH 423
Db 354 D-----KNAWRTDEEFAETLAGVNPVITRLTEPAPKSTLDLPROYGDHSTKITTAH 405
QY 424 IRHNMGLSVQNALRKRLFILDHDHFMFYLDENELEGNFIVASRTLLFLKODGTLPK 483
Db 406 IEKNLEGLTVQALDGNRLYLIDHDFWPFLLIDVNNLEGNFIYATRLFLRGGGLAP 465
QY 484 LAIELSLPHDPQCGQAGVSKVYTPAHTGVGHWOLAKAYACVNDSAWHQILSHWLNTA 543
Db 466 LAIELSEPYIDGDLTVAKSKVYTPASSGVAEAWVWOLAKAYAVVNDSGWHQILSHWLNTA 525
QY 544 VTEPFVIATNRQLSVYVPHKLLSPHYRDTLNLNARQTLINAGGVFERTVFPKALG 603
Db 526 VNEPFVIATNRQLSVYVPHKLLSHFRDTMNLNARQTLINAGGVFERTVFPKALG 585
QY 604 MSADVKSNNFEQALPADLVKRGVAVPDQSPYGRLLIKDYPYVDGLVWIAERWV 663
Db 586 MSSVYKSNWFTEQGLPADLVKRGVAVADPSLYKVRLLIEDYPYASDGLAIHAIQWV 645
QY 664 KEYLDIYYPNDGELQRDVELQAWKKEVEEAGDLKDRDWMRMDTVQOLARACTIIWV 723
Db 646 GEYLAIPPDDGALGDELOQAWKKEVEGHDHDKDAPWPKMQVASELSACTIIWI 705
QY 724 ASALHAAVNFQGYAGYLPNRPATSRPMPPEGSHDYKKGAGQKADMFVITITSQF 783
Db 706 ASALHAAVNFQGYAGYLPNRPATSRPMPPEGSHDYKKGAGQKADMFVITITSQF 762
QY 784 QTLIGISLIELSKHSSDEVYLGQDEDPDRWTSDAKALDAFKRGSRLVQIENRIKTMND 843
Db 763 QTLIGISLIELSKHSSDEVYLGQDTPDPE-WTSDARALAAFKRGSRLVQIENRIKTMND 821
QY 844 9PDLKXKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 822 DFLKXKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 864
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RESULT 10

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US-10-132-350-2
; Sequence 2, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Kolomietz, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-2
```

```
Query Match
Best Local Similarity 62.6%; Score 2958; DB 14; Length 873;
Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;
```

```
QY 10 LTGNKKEAWSEGKIRGTVRLVKKVEV--LDVGDENASLLDGVHRIILGMDGVAFQQLVSATA 67
Db 14 LTGNKNA-----HLKGNVVLVRKTVLGLDVTSTAGSLLDGIGEFGLG--RGVTCQLISSTV 67
QY 68 ADSNGGRGKVGKAAHLEEAVALSKTADGETVYRVSFEWD--ESQIIPGAVLVRNLCHAE 126
Db 68 VDPNNGNRGKLGAEASLEQWLLNPLPPLLSSENOFRVTFDWEVEKQIGPAIIKNNHASE 127
QY 127 FFLKTLTLEGPCKGTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQDEL 186
Db 128 FFLKTLTNDVPCHGTVFVANSWYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQDEL 187
QY 187 KIIRGDDNPGPYQEHDRVYRYDYNDLGDGDRGEEHARDILGSGQEHYPYRRCRTGRHPT 246
Db 188 RNLRGDDQCGPYQEHDRVYRYDYNDLGDGDRG--NPRFLGSGTKELPYRRCRTGRKPT 245
QY 247 KDPNSESRLFILNLNIVYPRDERFGLHCKMSDFLGYSUKTIIIEAVLPILGTFVDDTPKEF 306
Db 246 KSPNSESRLTVLGDVYVPRDERFGLHCKMSDFYGAIKALVNAVIPAIRTYVDSLSPGEF 305
QY 307 DSPEDILGYELGPEAPNPNLAEIRKIKPSEFLRSILPNSGSHDPLKMPILPNVTKSVDL 366
Db 306 DSPEDIMKLYEGGIQPKIPALEDLKQFPLELVKDVLPVGG--DYLLKLPMPQIIXED-- 362
QY 367 KKAPEKFWRTDEEFAETLAGVNPVIKRLTEPAPKSTLDLPROYGDHSTKITTEAHRH 426
Db 363 -----KTGMWDEEFGRIILAGVNPMLVRLTEPAPKSTLDLPROYGDHSTKITTEAHRH 416
QY 427 NMGLSVQNALNRKRLFILDHDHFMFYLDENELEGNFIVASRTLLFLKODGTLPKALAI 486
Db 417 KLEGLTVQALHGNRLYLIDHDFWPFLLIDVNNLEGNFIYATRLFLRGGGLTPVPAI 476
QY 487 ELSLPHDPDQCGQAGVSKVYTP--AHTGVGHWOLAKAYACVNDSAWHQILSHWLNTAHTV 545
Db 477 ELSLPELRDGLTTAKSTVTPKSTTGAEAWVWHLAKAYAVVNDYCMHQILSHWLNTAHTV 536
QY 546 EPPVIATNRQLSVYVPHKLLSPHYRDTLNLNARQTLINAGGVFERTVFPKALGMS 605
Db 537 EPPVIATNRQLSVYVPHKLLSPHYRDTMNLNARQMLVNAVAGGIFETTVFPQYAFWS 596
QY 606 ADVYKSNWNEQALPADLVKRGVAVPDQSPYGRLLIKDYPYVDGLVWIAERWVKE 665
Db 597 SVIYKDNWNTFQALPDLLIKRGMAVADPSSPKYKVRLLVEDYPYASDGLAIHAIQWVTE 656
QY 666 YLDIYYPNDGELQRDVELQAWKKEVEEAGDLKDRDWMRMDTVQOLARACTIIWVAS 725
Db 657 YLAVIYYPNDGVLRAVDELQAWKKEAEVGHADLKADAPWPKMQVTAELVKACTIIWIAS 716
QY 726 ALHAAVNFQGYAGYLPNRPATSRPMPPEGSHDYKKGAGQKADMFVITITSQFOT 785
Db 717 ALHAAVNFQGYAGYLPNRPATSRPMPPEGSHDYKKGAGQKADMFVITITSQFQA 773
QY 786 ILGISLIELSKHSSDEVYLGQDEDPDRWTSDAKALDAFKRGSRLVQIENRIKTMNDSP 845
Db 774 LVGISLIELSKHSSDEVYLGQDTPKE-WTSDAKAQAEAFKRGALTEIEKRVWVNDAP 832
QY 846 DLKXKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
Db 833 RLKXKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 873
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RESULT 11

US-10-132-350-4
; Sequence 4, Application US/10132350
; Publication No. US20030166855A1
; GENERAL INFORMATION:
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Kolomiets, Mikhailo V.
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Lipoxigenase Polynucleotides and Methods
; FILE REFERENCE: 35718/246439
; CURRENT APPLICATION NUMBER: US/10/132,350
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/286,889
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/305,366
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Zea mays
US-10-132-350-4

Query Match 62.6%; Score 2958; DB 14; Length 873;
Best Local Similarity 63.6%; Pred. No. 2.6e-272;
Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;

QY 10 LTGKNKEAWSEKIRGTVRLVKKEV--LDVGDFNASLLDGVHRLGWDGVAFLVSATA 67
DB 14 LTGSNKA---HLKGNVVLVRKTVGLDVTISIAGSLDGIQFLG--RGVTCQLISSTV 67

QY 68 ADPSNGRGKVGKAAHLEAAVLSKSTADGTVTYRVSPFDW--ESQIGPGAVLVRNLQHA 126
DB 68 VDPNNGNRKGLGAEASLEQWLNPPPLLSSENQPRVTFDMEVEKQIGPGLAIKVNHA 127

QY 127 FFLKTLTLLEGVPGKTVFVANSWVYVPHKLYSQRIEFPANDTYLPSKMPAALVPYRDEL 186
DB 128 FFLKTIITLNDVPGHGTIVFVANSWVYVPHKLYSQRIEFPANDTYLPSKMPAALVPYRDEL 187

QY 187 KILRGDDNPGYQEHDRVYRDYNDLGDPPDKGHEARPIILGSGQEHPPRRCTGRHPT 246
DB 188 RNLRGDDQGGPYQEHDRVYRDYNDLGLPDSG--NRPVLGGTKELPYRRCTGRKPT 245

QY 247 KKDPSNRSRLFLNINIVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTFFVDDTPKEF 306
DB 246 KSDPNSESRLLTVDGVVVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTFFVDDTPKEF 305

QY 307 DSFEDILGLYELGPEAFNNPLIARIRKIPSEFLRSILPNSGSHDHPKMPNPKVSDVL 366
DB 306 DSFKDLMKLYEGGIQLPKIPALEDLRKQFPLELVKQVLPVGG--DYLKLPMPQIIRKED-- 362

QY 367 KKAPEFKGWTDEFEARETLAGVNPVILKLTTFPPAKSTLDPQYGDHSTKITEAHIRH 426
DB 363 -----KTGWMTDEFEARETLAGVNPVILKLTTFPPAKSTLDPQYGDHSTKITEADLEN 416

QY 427 NMGGLSVQNALRNKRLFLDHDHFMVPLDEINLEGNFIYASRTLLFLKDDGTLKPLAI 486
DB 417 KLEGLTVQALHGNRLIILDHDFMPLFVYRNSLEGNFIYATVTLFLSGDGTLPVVAI 476

QY 487 ELSLPHDPDQQRGAVSKYTP--AHTGVEGHVQWLAKAYACVNSAMHQLISHWLNTHAVI 545
DB 477 ELSLPELRDGLTTAKSTYTFKSTTGAEAWWHLAKAYANNVNDYCMHQLISHWLNTHAVM 536

QY 546 EPPVIATNRQLSVVHPVHKLISPHYRDTLNLAROTLNLNAGVPERVTFPAKVALGMS 605
DB 537 EPPVIATNRQLSVTHPVHKLISPHYRDTLNLNAGVPERVTFPAKVALGMS 596

QY 606 ADVTKSWNFEQALPADLVKGVAVPQSSPYGVRLLIKDYYPVAVDGLVITWIAERWYKE 665
DB 597 SVIYKDNWTFEQALPDLIRKGNVAVDSSPYKVRLLVEDYPVAVSDGLAIWHAIEQWTE 656

666 YLDIYYPNDGELQDORVLOAWKVEYREAHGDLKORDWPRMDTVQQLARACTTIWVAS 725
DB 657 YLAVYYPNDGVLRADVLEQAWKVEYREAHGDLKORDWPRMDTVQQLARACTTIWVAS 716

QY 726 ALHAAVNFQYFAGYVLPNRPASRRPMPPEPSGSHDYKXKLGAGCKEADWVFRTITISQFOT 785
DB 717 ALHAAVNFQYFAGYVLPNRPASRRPMPPEPSGSHDYKXKLGAGCKEADWVFRTITISQFOT 773

QY 786 ILGISLIEILSKHSSDEVYLGORDPDRWTSDAKALDAFKPFGSLVQIENRIKTMNDSP 845
DB 774 LVGISLIEILSKHSSDEVYLGORDPDRWTSDAKALDAFKPFGSLVQIENRIKTMNDSP 832

QY 846 DLKNRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
DB 833 RLKNRNGPAEFYTYLLYPNTSDVTGKAEGLTAMGIPNSISI 873

RESULT 12
US-10-425-114-62915
; Sequence 62915, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62915
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: L1B3068-041-F8_FLI.pap
US-10-425-114-62915

Query Match 62.6%; Score 2958; DB 12; Length 891;
Best Local Similarity 63.6%; Pred. No. 2.7e-272;
Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;

QY 10 LTGKNKEAWSEKIRGTVRLVKKEV--LDVGDFNASLLDGVHRLGWDGVAFLVSATA 67
DB 32 LTGSNKA---HLKGNVVLVRKTVGLDVTISIAGSLDGIQFLG--RGVTCQLISSTV 85

QY 68 ADPSNGRGKVGKAAHLEAAVLSKSTADGTVTYRVSPFDW--ESQIGPGAVLVRNLQHA 126
DB 86 VDPNNGNRKGLGAEASLEQWLNPPPLLSSENQPRVTFDMEVEKQIGPGLAIKVNHA 145

QY 127 FFLKTLTLLEGVPGKTVFVANSWVYVPHKLYSQRIEFPANDTYLPSKMPAALVPYRDEL 186
DB 146 FFLKTIITLNDVPGHGTIVFVANSWVYVPHKLYSQRIEFPANDTYLPSKMPAALVPYRDEL 205

QY 187 KILRGDDNPGYQEHDRVYRDYNDLGDPPDKGHEARPIILGSGQEHPPRRCTGRHPT 246
DB 206 RNLRGDDQGGPYQEHDRVYRDYNDLGLPDSG--NRPVLGGTKELPYRRCTGRKPT 263

QY 247 KKDPSNRSRLFLNINIVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTFFVDDTPKEF 306
DB 264 KSDPNSESRLLTVDGVVVPRDERFGLKMSDFLGSYLKTIIEAVLPTLGTFFVDDTPKEF 323

QY 307 DSFEDILGLYELGPEAFNNPLIARIRKIPSEFLRSILPNSGSHDHPKMPNPKVSDVL 366
DB 324 DSFKDLMKLYEGGIQLPKIPALEDLRKQFPLELVKQVLPVGG--DYLKLPMPQIIRKED-- 380

QY 367 KKAPEFKGWTDEFEARETLAGVNPVILKLTTFPPAKSTLDPQYGDHSTKITEAHIRH 426
DB 381 -----KTGWMTDEFEARETLAGVNPVILKLTTFPPAKSTLDPQYGDHSTKITEADLEN 434

Query Match	62.0%	Score 2929.5	DB 10	Length 862
Best Local Similarity	63.0%	Pred. No. 1.3e-269		
Matches 561	Conservative 110	Mismatches 188	Indels 31	Gaps 12
Qy	1	MFHGVGADRLTGKKNKAWSEKRGITGRLVKEVLDVGDENASLLDGVHRLGWDGVAF	60	
Db	1	MLLGLLDTLTGANKSA-----RLAGTVVLMKRWLDLNDFGATIIDGIGBEFLG--KGWTC	54	
Qy	61	QLVVSATAADPSNGRGKVGKAAHLEBAVSVLSKSTADGETVYRVSPFWD--ESQGITPGAVLV	119	
Db	55	QLIESTAVDQNGRGKVGAAELEQWVTSLPSTTGESKFLGTFDWEVKLVGVEGAIVV	114	
Qy	120	RNLQHAZFFELKTLLEGVPGK-GTVFVANSWVPHKLYSOERIFFANDTILPSKMPAAL	178	
Db	115	NYVHSSBFLKTIILHDVPGSGNLTTFVANSWITPAANYRYSRVFFANDTILPSQMPAAL	174	
Qy	179	VYPRQDELKILRGDNPFGPYQEHDRVRYDYINDLGDPPDKGEEHARPILGSOQHYPYRR	238	
Db	175	KPYRDDLENLRGDQQQPGYQEHDRIVRYDYNDLGE-----GRPILGNSDHPYPRR	227	
Qy	239	CRIGRHETKKDPNSESRLFLNLNLNIVYPRDERFGHLKMSDFGLYSLXTIIEAVLPTLGTP	298	
Db	228	GRTERKENADSPSLESLSLE-QIYVPRDESKFGLKTSDFGLYSIKAITQGLPAVRTY	286	
Qy	299	VDDTFKEFDSPEDILGILYELGPEAPNNPLAIEIRKKIPSEFLRILPNSGHDHPLKMLPL	358	
Db	287	VDDTFGEFDSFDIINLYEGGIKLPKVAALEELRKQFLQIKDLLPVGG-DLSLLKLPVP	345	
Qy	359	NVIKSDVLKAPKPFQWRDDEEFARETLAGNVPIIKRUTTEPPAKTLDPRQVGDHTSK	418	
Db	346	HIIQ-----ENKQAWRTDEEFAREYLAAXNPFVMITRLTEPPKSSLPSPKFGDHTST	397	
Qy	419	ITEAHIRHNMGGISVQNALNKRFLILDHHDHNPYLDEINELSGNFIYASRTLFLKDD	478	
Db	398	ITEAHIEKNLEGLTVQQALESNRLYLIDHHDHFMFPLIDVNNLPGNFIYATRTLFFURGD	457	
Qy	479	GTIKPLAIELSLPHPDQQRGAWSKVYTPAHTG-VEGHVMQLAKAYACVNDSAWHQLISH	537	
Db	458	GRUTPLAIELSEPIIQGLLTAKSKVYTPVPSGVEGVWVWELAKAYAVVNDSGHWQLVSH	517	
Qy	538	WLNTHAVIEPVIATNRQLSVVHPVHKLSPHYRDTLINALARQTILINAGGVFERTVFP	597	
Db	518	WLNTHAVMEPFVISTNRHLSVTHPVHKLSPHYRDTWTINALARQTILINAGGIFEMTVFP	577	
Qy	598	AKYALGMSADVYKSNFNEQALPADLVKRGVAVDPDQSSPYGVRLLIKDYVPVADVGLVW	657	
Db	578	GKPAFGMSAVVYKDWKTEQGLPDLLIKRGAVEDPSPYKVRLLVSDYPIAADGLAIWH	637	
Qy	658	AIERWKEYLDIYYPNDGELQDVELQAMWKEVREEAHGLKORDWHPRMDTVQQLARAC	717	
Db	638	AIEQYVSEYLAIYYPNDGLVQGDTEVQAMWKETREVGHGLKDAWPKMQSPVELAKAC	697	
Qy	718	TTIIWVASALHAAVNFGQYPVAGVLPNRPATASRRPMEPGSHDYKKLGACQKQKADVMVPIR	777	
Db	698	TTIIWGSALHAAVNFGQYPAGVLPNRPVTSRRRMEPGTETAEEL---ERDPERAFIH	754	
Qy	778	TITSQFTQITLIGISLIETLSKSHSDDEVYLGORDSPDRWTSDAKADAPKRFSGSLVQIENR	837	
Db	755	TITSQITLIGVSLLEVLKSHSDLEYLGORDTPE-WTSDPKALEVFKRESDLRVLIESK	813	
Qy	838	IKTWNSDPDLNKRKGPVEMPMYMLLYPNWTSVDTGKAEGLTAMGIPNSISI	887	
Db	814	VGMNHDPDLNKRNGAKFPYMLLYPNWTSHPKG-AAAGLTAKGIPNSISI	862	

RESULT 15	
US-09-751-687-18	
; Sequence 18, Application US/09751687	
; Publication No. US20030167544A1	
; GENERAL INFORMATION:	
; APPLICANT: Douda, Anneke	
; APPLICANT: Doderer, Albert	

```

; APPLICANT: Cameron-Mills, Verona
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-09-751-687-18

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Query Match	60.6%	Score 2860	DB 10	Length 864
Best Local Similarity	62.2%	Pred. No. 5.7e-263		
Matches 551	Conservative 117	Mismatches 188	Indels 30	Gaps 11
QY	5	GVADRLTGKKEAWSSEKRGTVRLVKKEVLVGVGDFNANSLDGVHRIILGWDGVAFLVLS	64	
Db	6	GIVSDLTGGIRGA-----HLKGSVLMRKNALDNDFGAHVMDGVTELLG--RGVTCQLIS	59	
QY	65	ATAADPNNGRGKGVKAAHLEBAV--SLKSTADGETVYRVVSFEWD--ESQIGPAVLVRN	121	
Db	60	STNYDHNNGRGKGVGAANLEQWLLPTNLFFITIGENKFAVTFDSVSKLGVPGCAIIVKN	119	
QY	122	LQHAFFLKLTLLEGVPGKTVFVANSWVYVPHKLYSQERIFFANDTVLPKMKPAALVPY	181	
Db	120	NHASEFFLKTLTLDNVPGRGTVFVANSWVYQAKYRNVRFVANDTVLPQMPAALXPY	179	
QY	182	QODEKILRGDDNPGPYQYBHRVYRVYNDLGDGDPKGBEHARPLGGSQEHYPVRRORT	241	
Db	180	RDDBLRWLRGDQGGPYLDHDRVYRVYVNDLGD-----SRDLVGSKDLPYRRORT	232	
QY	242	GRHPTKDPNSBSRLFLNLTNVPRDEFHGLKMSDFELGYSLKTIIEAVLPTLTGTVDD	301	
Db	233	GRKESDKPHEBSRLLLVQNVTVLRDELFGHLKQSDLLGLTKGNLGDIIAIRTVDL	292	
QY	302	TPKEFDSFDILGYELGPEAPNPLIAIRKIPSEFLRSILPNGSHDHPKMLPENVI	361	
Db	293	SPGEBDSFADILKYEGLGKLPNIPALEBVRKRFPLQVLKQIG--DFLLKLPKPEII	351	
QY	362	KSDVLKKAPEFKGWTDEEFARETLAGVNPVYIKELTEFFPAKSTLDPROYGDHTSKITE	421	
Db	352	KVD--QKA-----WMTDEEFAREMLAGVNPVMIKRLTEFFPKSTLDSKYGDMTSWTE	403	
QY	422	AHTRHNMGSLVQNALRNKRLFILDHDHFMFYLDEINELEGNTFYASRTLLFLFKDGGTL	481	
Db	404	EHVAKSLEGLTVQQAAGNRLYTVQHDNLMPFLDINNLDASFVYATRTLLFLRGDGTLL	463	
QY	482	KPLAIELSLPHDPQORGAVSKVYTPAHTGVGEHTWQAKAYACVNDSAKHLLSHLWNT	541	
Db	464	APVAIEUSSPLIGELTTAKSAVYTPQHAGVGEHTWQAKAYASVNDYGHQLLSHWNT	523	
QY	542	HAVIEPPVIATNRQLSVVPHVKLSPHRYDPTNLNALARQTLINAGGVFERTVFPKYA	601	
Db	524	HAVMEPPVIATNRQLSVTHPVYKLLPHRYDPTMNINARAGLLINAGGVEMTVFPKHKA	583	
QY	602	LGHSAADYKSWNNEQALPADLVKGVAVPODSSPYGVRLLIKDYPANVDGLVNWAIER	661	
Db	584	MPMSVMYKHNWNPTEQALPADLVKGVAVPODSSPYGVRLLIKDYPATDGLVNDIAEQ	643	
QY	662	WVKEYLDIYPNDGELQRLVDELQAWKEVREEAHGDLDKDRDWPFRMDTVQQLARACTII	721	
Db	644	WVSDYLTIYPNDGVLGQDVELQAWKEVREVGHGDLDKDAAWPKWQTVABELIKACATII	703	
QY	722	WVASALHAANVGOYFAGYLYLNNRTASRRPMPEPGSHDYKLLGNGKEADWVIRITTS	781	
Db	704	WTGSALHAANVGOYFAGYLYLNNRTASRRPMPEPGSHDYKLLGNGKEADWVIRITTS	760	
QY	782	QFQTLIGLSILETILSHSSDEVYLQORDEPQRTWSDAKALDAFKRFGRSLVQIENIKTW	841	

Db 761 QFHALVGISLMEILSKHSSEVYLGQHDTP-IWTSDAKALEAFKRFGAKLEGIEKQVVAM 819

Oy 842 NDSPDLKNRKGPEMPYMLLYENTSDVTGEKAEGLTAMGIPNSISI 887

Db 820 NSDPOLKNRTGPAKFPYMLLYENTSDHTGQ-AEGLTARGIPNSISI 864

Search completed: March 23, 2004, 07:11:45
Job time : 336 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 06:36:23 ; Search time 30 seconds
(without alignments)
2844.063 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFHWGVADRLTGKNEAWSE.....VTGKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	3369.5	71.3	876	2 T05943	probable lipoxigenase
2	2936.5	62.2	862	2 T05941	lipoxigenase (EC 1
3	2860	60.6	864	2 T05945	lipoxigenase (EC 1
4	2829.5	59.9	865	1 S23454	lipoxigenase (EC 1
5	2724.5	57.7	862	2 S57964	lipoxigenase (EC 1
6	2695.5	57.1	862	2 T07775	lipoxigenase (EC 1
7	2626.5	55.6	859	1 JQ2267	lipoxigenase (EC 1
8	2597	55.0	861	2 S44940	lipoxigenase (EC 1
9	2511	53.2	859	2 T06332	lipoxigenase (EC 1
10	2510	53.1	859	2 T06339	lipoxigenase (EC 1
11	2498.5	52.9	876	2 T07101	lipoxigenase (EC 1
12	2486	52.6	865	1 DASYL1	lipoxigenase (EC 1
13	2480.5	52.5	857	2 S01864	lipoxigenase (EC 1
14	2458.5	52.1	864	1 S07075	lipoxigenase (EC 1
15	2437	51.6	861	1 S01142	lipoxigenase (EC 1
16	2433	51.5	877	2 T10085	lipoxigenase (EC 1
17	2423.5	51.3	878	2 S74207	lipoxigenase (EC 1
18	2420	51.2	865	2 T11852	lipoxigenase (EC 1
19	2405.5	50.9	862	2 S22153	lipoxigenase (EC 1
20	2394	50.7	853	2 T07036	lipoxigenase (EC 1
21	2393.5	50.7	856	2 T06596	lipoxigenase (EC 1
22	2393.5	50.7	868	2 T06827	lipoxigenase (EC 1
23	2389	50.6	859	2 T06429	lipoxigenase (EC 1
24	2385.5	50.5	858	2 T12442	lipoxigenase (EC 1
25	2375	50.3	853	2 T07662	lipoxigenase (EC 1
26	2370.5	50.2	864	2 S13381	lipoxigenase (EC 1
27	2355.5	49.9	839	1 DASYL2	lipoxigenase (EC 1
28	2353	49.8	839	2 T06354	lipoxigenase (EC 1
29	2329.5	49.3	866	2 T06454	probable lipoxigenase

30	2295.5	48.6	868	2 S56655	lipoxigenase (EC 1
31	2231	47.2	741	2 S18906	lipoxigenase (EC 1
32	1827.5	38.7	517	2 T06274	probable lipoxigenase
33	1823	38.6	908	2 T07409	lipoxigenase (EC 1
34	1823	38.6	914	2 T07065	probable lipoxigenase
35	1794.5	38.0	599	2 S18612	lipoxigenase (EC 1
36	1721	36.4	926	2 E96749	probable lipoxigenase
37	1667.5	35.3	896	2 JQ2391	lipoxigenase (EC 1
38	1648	34.9	899	2 T07062	probable lipoxigenase
39	1630	34.5	896	2 T07408	lipoxigenase (EC 1
40	1606.5	34.0	899	2 T11578	probable lipoxigenase
41	1586.5	33.6	923	2 A53054	lipoxigenase (EC 1
42	1569.5	33.2	917	2 B96699	probable lipoxigenase
43	1559	33.0	936	2 T06190	lipoxigenase (EC 1
44	1552.5	32.9	870	2 T47454	lipoxigenase AtLOX
45	1478	31.3	823	2 T07664	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

T05943

Probable lipoxigenase (EC 1.13.11.12) - barley

C;Species: Hordeum vulgare (barley)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999

C;Accession: T05943

R;van Mechelen, J.R.; Smits, M.; Graner, A.; Douma, A.C.; Schuurink, R.C.; Heidekamp, F.

submitted to the EMBL Data Library, June 1997

A;Description: Barley grain lipoxigenase isoenzymes: cDNA cloning, characterization and

A;Reference number: Z15464

A;Accession: T05943

A;Status: preliminary; translated from GB/EMBL/DBSJ

A;Molecule type: mRNA

A;Residues: 1-876 <VAN>

A;Cross-references: EMBL:L37359; NID:g2182266; PIDN:AAB60715.1; PID:g2182267

A;Experimental source: cv. Triumph

C;Genetics:

A;Gene: LoxB

A;Map position: 4

C;Superfamily: lipoxigenase

C;Keywords: oxidoreductase

Query Match 71.3%; Score 3369.5; DB 2; Length 876;

Best Local Similarity 72.5%; Pred. No. 7.5e-235;

Matches 648; Conservative 87; Mismatches 134; Indels 25; Gaps 9;

QY	1	MFHWGVADRLTGKNEAWSE	KGIRGTVRLVKVLDVGDVFNASLDGVHRIIGWDGVAF	60
DB	1	MLLHGLVDRLTGKNEAWSE	KGIRGTVRLVKVLDVGDVFNASLDGVHRIIGWDGVAF	60
QY	61	QLVSTATAADPSNGGRKVGKAAHLE	EAIVSLKSTADGETVYRVSEWDESGQIPGAVLR	120
DB	61	RLVSTATAADPSNGGRKVGKAAHLE	EAIVSLKSTADGETVYRVSEWDESGQIPGAVLR	120
QY	121	NLQHAFFKLTLLTGVPKGVVFNANS	WVPHKLYSOERIFFANDYTLSPKPAALVP	180
DB	121	NTYRSEYLLKLTLLTGVPKGVVFNANS	WVPHKLYSOERIFFANDYTLSPKPAALVP	176
QY	181	YRQDELKILRGDNDPGPYQEHDRV	RYDYNDLGDPPDKGEBHARPILGSGSEHPYRRCR	240
DB	177	YRQDELNLRLGDDTTGKEYKADRV	RYDYNDLGEPPD--NDNRPVLGGTQELPYRRCR	234
QY	241	TGRHPTKDPNSERL-----	FLNINIVPRDERFGHLKMSDFLGYSKLTIEAVLPTLG	296
DB	235	TGRPTETDPNSERIPKYIKKAL	NIYVPRDERFGHLKMSDFLGYSKLTIEAVLPTLR	294
QY	297	TFVDDTPKPEPSFEDILGLYELG	PEAPNPLIARIKKIPSEFLRILPNSGSHDPLKMP	356
DB	295	TYVDSPTKPEPSFQDIYNLYDGL	LKVPDNOHLKELKNK-SLQFIKSLAVAGDSDS--KLA	351
QY	357	LPNVLKSDVLKGAPEFKGWTDE	FARETLAGVNPVILKELTBPAKSTLDPRQYGDHT	416

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Db      352 LPHVKS-----QYAMRSDEEFARMLAAVDPCIRRLTKFVKKYLDPSVYDQS 403
QY      417 SKITEAHRHNM--GGLSQNALRNKRLFIIDHHDHMFYLDNEINELEGNFIYASRTLLF 475
Db      404 STIIEQIQNLNLEGLTVRQAMDKRLFIIDHHDHMFYLDNEINELEGNFIYASRTLLF 463
QY      476 KDDGLTLPALIELSLPHDPDQOORGAVSKVYTPA--HTGVGSHVWQLAKAYACVNDGSAHQ 533
Db      464 KADGTLKPLALIELSQPHDPDGIQHGAKSTVYLPADINSVGDQIWLQAKAYASVDDGSAHQ 523
QY      534 LISHLWLNTHAVTEFPVATNRQLSVVHPVHKLLSPHYRDTLNLNALAROTLINAGGVFER 593
Db      524 LISHLWLNTHAVTEFPVATNRQLSVVHPVHKLLSPHYRDTLNLNALAROTLINAGGVFER 583
QY      594 TVFPKALGMSADYKSWNPNFNEQALPADLVKRGAVVPDQSSPYGVRLLIKDYPAVDGL 653
Db      584 TVFPQYALEMSAVVYKWKLTQGLPDDLKRGMAVPDESSPYGIRLLIKDYPAVDGL 643
QY      654 VIMWAIERWVKEYLDIYYPNDGELQDVLOAWKVEVEEAHGDLDKRDWPMWMDTVQQL 713
Db      644 VIMWAIERWVKEYLDIYYPNDGVLRADKELEWKEVREVGHDLDKRDWPMWMDTVQQL 703
QY      714 ARACTTIWASALHAAVNFQGYPYAGYLPNRPRTASRRPMPGSHDYKKLGAGQKAD 773
Db      704 AKTCTTIWASALHAAVNFQGYPYAGYLPNRPRTASRRPMPGSHDYKKLGAGQKAD 763
QY      774 VFIRTTISQOTILIGISLIEILSKHSSDEVYLGORDEPDEWTSADKALDAFRKFSRLVQ 833
Db      764 VFIRTTISQOTILIGISLIEILSKHSSDEVYLGORDEPDEWTSADKALDAFRKFSRLV 822
QY      834 IENRIKTMNDPSDLKRNKRGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db      823 IEXRILDMNDKDPALKNRGNPVQVPMYMLLYPNTSDANGKALGITANGIPNSVSI 876

RESULT 2
T05941
lipoxigenase [EC 1.13.11.12] 1 - barley
C:Species: Hordeum vulgare (barley)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T05941
R:van Mechelen, J.R.; Smits, M.; Douma, A.C.; Rouster, J.; Cameron-Mills, V.; Heidekamp,
Biochim. Biophys. Acta 1254, 221-225, 1995
A:Title: Primary structure of a lipoxigenase from barley grain as deduced from its cDNA
A:Reference number: Z15463; MUID: 95127754; PMID: 7827128
A:Accession: T05941
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-862 <VAN>
A:Cross-references: EMBL:L35931; NID:9532571; PIDN:AAA64893.1; PID:9532572
C:Genetics:
A:Gene: LoxA
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match      62.2%; Score 2936.5; DB 2; Length 862;
Best Local Similarity 63.1%; Pred. No. 1.3e-203;
Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY      1 MFVHGVADELTKGNKEAWSSEKIRGTVRLVKKEVLDVGDNFASLLDGVHRIILGWDDGVAF 60
Db      1 MLLGGLIDTLTGANKSA---RLKGTWLMKRNKVLNDLDFGATIIDIGIEFLG--KGYTC 54
QY      61 QLVSAATAADPSNGRGKVGKAAHLEAVVSLKSTADGETVYRVSPFWD--ESQIGQAVLV 119
Db      55 QLSISSTAVDQDNGRGKVGKAAHLEAVVSLKSTADGETVYRVSPFWD--ESQIGQAVLV 114
QY      120 RNLCHAEFFLTKLTLEGPQK--GTVVVFVANSWYVPHKLYSQRIFFPANDTYLPSKMPAL 178
Db      115 NVVHSSEFLTKLTLDVPCRSNLTAFVANSWYVPHKLYSQRIFFPANDTYLPSKMPAL 174
QY      179 VPRQBELKILRGDNPQVQEHDRVYRDYNDLGDPKGBEHARPIILGSGQEHYPFR 238

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Db      175 KEYRDELNLRLGDDQCGPYQEHDRYRYDYVNDLGE-----GRPILGNSDHPYPRR 227
QY      239 CETGHRPKKDPNSRSRLFLNLNLYYVDRDERFGLKMSDFLGYSLKTIIEAVLPTLTGF 298
Db      228 GRTKRPNASPSPLESRLSLE-QIYVPRDEKFGHLKTSDFLGYSIKAITGILPAVRTY 286
QY      299 VDDTKPEFDSPEIILGLYELGPEAPNPNLIAIRKIKPSBEFLRSILPNSGSHDHPKMLP 358
Db      287 VDDTKPEFDSFDIILNLYEGGKLPKVAALBELRKQFPQLIKDLLPVGG--DSLILKLPVP 345
QY      359 NVIKSDVLKAPKPEFGHRTDEEFARETLAGNVPVVKRLTEPPAKSTLDRQVGDHTSK 418
Db      346 HIIQ-----ENKQAWRTDEEFARETLAGNVPVVKRLTEPPAKSTLDRQVGDHTST 397
QY      419 ITEAHIRENMGSLSYQNALRNKRLFIIDHHDHMFYLDNEINELEGNFIYASRTLLF 478
Db      398 ITEAHIRENMGSLTVQQALESNRLYILDHHDHMFYLDNEINELEGNFIYASRTLLF 457
QY      479 GTLKELATELSLPHDPDQOORGAVSKVYTPAHTG--VEGHVWOLAKAYACVNDGSAHQ 537
Db      458 ORLTPLATELSEPTIQGGLTTAKSKVYTPVPSGSGVGVWVWELAKAYACVNDGSAHQ 517
QY      538 WLNTHAVTEFPVATNRQLSVVHPVHKLLSPHYRDTLNLNALAROTLINAGGVFERVFP 597
Db      518 WLNTHAVTEFPVATNRQLSVVHPVHKLLSPHYRDTLNLNALAROTLINAGGVFERVFP 577
QY      598 AKYALGMSADYKSWNPNFNEQALPADLVKRGAVVPDQSSPYGVRLLIKDYPAVDGLVW 657
Db      578 GKFGALMSAVVYKWKLTQGLPDDLKRGMAVPDESSPYKVRLLVSDYPYAADGLAIWH 637
QY      658 AIERWVKEYLDIYYPNDGELQDVLOAWKVEVEEAHGDLDKRDWPMWMDTVQQLARAC 717
Db      638 AIEQVSEYLAIIYYPNDGVLQDTEVQAWKETEVEVGHDLDKAPWPKQSVPELAKAC 697
QY      718 TTIWASALHAAVNFQGYPYAGYLPNRPRTASRRPMPGSHDYKKLGAGQKADWVFIR 777
Db      698 TTIWIGSALHAAVNFQGYPYAGYLPNRPRTASRRPMPGSHDYKKLGAGQKADWVFIR 754
QY      778 TITSOFTILIGISLIEILSKHSSDEVYLGORDEPDEWTSADKALDAFRKFSRLVQ 837
Db      755 TITSOFTILIGISLIEILSKHSSDEVYLGORDEPDEWTSADKALDAFRKFSRLVQ 813
QY      838 IKTWNDSPLKRNKRGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db      814 VVGWMDHPELKNRGNPAKFPYMLLYPNTSDHKG--AAAGLTAKGIPNSISI 862

RESULT 3
T05945
lipoxigenase [EC 1.13.11.12] 2 - barley
C:Species: Hordeum vulgare (barley)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C:Accession: T05945
R:van Mechelen, J.R.; Smits, M.; Graner, A.; Douma, A.C.; Schuurink, R.C.; Heidekamp, F
submitted to the EMBL Data Library, September 1997
A:Description: Barley grain lipoxigenase isoenzymes: cDNA cloning, characterization and
A:Reference number: Z15465
A:Accession: T05945
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-864 <VAN>
A:Cross-references: EMBL:L37358; NID:G2429086; PIDN:AAE70865.1; PID:G2429087
A:Experimental source: cv. Triumph
C:Genetics:
A:Gene: LoxC
A:Map position: 7
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match      60.6%; Score 2860; DB 2; Length 864;
Best Local Similarity 62.2%; Pred. No. 4.5e-198;
Matches 551; Conservative 117; Mismatches 188; Indels 30; Gaps 11;

```


RESULT 5

S57964
 lipoxigenase (EC 1.13.11.12) - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jun-1999
 C:Accession: S57964
 R:Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.
 submitted to the EMBL Data Library, January 1995
 A:Description: Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA.
 A:Reference number: S57964
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-862 <VER>
 A:Cross-references: EMBL:X84040; NID:g899343; PIDN:CA58859.1; PID:g899344
 C:Superfamily: lipoxigenase
 C:Keywords: oxidoreductase

Query Match 57.7%; Score 2724.5; DB 2; Length 862;
 Best Local Similarity 59.9%; Pred. No. 2.7e-188;
 Matches 533; Conservative 111; Mismatches 215; Indels 31; Gaps 11;

QY 1 MFHGVADRLTGKKNKANSWG-KIRGTVRLVKKVLDVGFNASLIDGVHRLIGWDDGVA 59
 DB 1 MFEKIVDAITGKD-----DGKKVKGTVLKKKRVLDFTDINASVLDGVLEFLG--RRVVS 53
 QY 60 FQLVSATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSPFWDSEQ-GIPGAVL 118
 DB 54 LELISSVNADPANGLOGKRSKAAYLENWLNTSPIAAGESAFRTVDWDDEEGFVGAFI 113
 QY 119 VRNIQHAFFLKTILLEGVPGKGTVVVANSWYVPHLYSQERIFPANDTYLPSKPPAAL 178
 DB 114 IKNLHFSEFFLKSITLEDVFNHGVFCVNSWYVPAKYSKDSRIFFANQAYLPSETPDL 173
 QY 179 VPRQDELKILRGDNDPGPYQEHDRVRYDYNDLGDPPDKGEGHARPIILGSGSEHYPRR 238
 DB 174 RYRENELVTLRG-DGFGKLEEDRWVDYAYNDLGDPPDKGQDLSRPLVGSSEHYPRR 232
 QY 239 CRTGRHTKDPNSERL-FLNLNITYPRDERFGLHKMSDFLGYSKTIIEAVLPTLGT 297
 DB 233 GRTGRKPTKDPNSERLPIILMSLDIYPRDERFGLHKMSDFLTALKSIQVLLPEFKA 292
 QY 298 FVDDTPKEFSDFDILGVLGELGPEAPNPLIAIRKKIPSEFLRSILPNSGHDHPKMP 357
 DB 293 LFDSTHNEFSDFDVLKLYEGGKLPQGPLLKAITDSIPLILKEIL-RSDGEGLEKYPT 351
 QY 358 PNWIKSVLKKAPKFKGWRDSEFARBTLAGVNPVILKLTBPFAKSTLDPQYGDHTS 417
 DB 352 PQVIQED-----KTAWRDTEFGREMLAGVNPVILSLQEFPPKSKLDPKIYGNQS 403
 QY 418 KITEAHTRHNMGLSVQNALRNKELFTLDHHDHFMVYLDLNELEGNFIYASFTLLFLKD 477
 DB 404 TITREQIEDKLDGUTIDEAIKTNKLFILNHDHILMPYLRINTSTDTKYVASFTLLFLQD 463
 QY 478 DGTLPKLAIELSLPHDPQDQGVAVSKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISH 537
 DB 464 NGTLKPSAIELSLPHDPDQDQGVAVSKYVTPADQGVGSIWQLAKAYAAVNDSSGVHQLISH 523
 QY 538 WLNTHAVIEPVIATNQLSVVPHVKLSPHYRDTLNALARQTLINAGGVFEFTVFP 597
 DB 524 WLNTHAAIEPVIATNQLSALHPYKLLPHFRFTNINALARQTLINAGGVFEFTVFP 583
 QY 598 AKYALGMSADYKSWNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIW 657
 DB 584 AKYSWMSAVVYKDWVFEQALPTDLLKRGVAVEDSSSPGIRLLIQDYPYAVDGLKWS 643
 QY 658 AIERWVVEYLDIYYPNDGELQDVELQAWKVEEHAHGLKDRDWRPMDTVOQLARAC 717
 DB 644 AIKSWVTEYCNYYKSDAVQKDTQLQAWKELREBEGHGDKDEPWWPKMVTQVELIDSC 703
 QY 718 TTIITWASALHAAVNFQYYPVAGYLPNRPATASRRPMPGSHDYKKLGAQKQKADWVFIR 777
 DB 704 TTIITWASALHAAVNFQYYPVAGYLPNRPPTLSRNFMPEPGSPYEEL---KTNPKVFLK 760

QY 778 TITTOFQFQILGISILSKHSDEVYLGQDEDPRTWSTAKALDAPKRGSRVLQIENR 837
 DB 761 TITPOLQTLGLISILSKHSDEVYLGQDEDPRTWSTAKALDAPKRGSRVLQIENR 819
 QY 838 IKTWNDSDDLKNRKGPEVMPYMLLYPNTSDVTGKAEGLTAMGIPNSIS 887
 DB 820 IMQNVNDEKKNRSGPVKVPYLLFPFSEG-----GLTGKGIPIPNVSI 862

RESULT 6

T07775
 lipoxigenase (EC 1.13.11.12) LX-3 - potato
 C:Species: Solanum tuberosum (potato)
 C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
 C:Accession: T07775
 R:Kolomietz, M.V.; Hannapel, D.J.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z16124
 A:Accession: T07775
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-862 <COL>
 A:Cross-references: EMBL:U60202; NID:gl407704; PIDN:AAB67865.1; PID:gl407705
 A:Experimental source: cv. Berolina
 C:Genetics:
 A:Gene: LX-3
 C:Function:
 A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pe
 C:Superfamily: lipoxigenase
 C:Keywords: fatty acid oxidation; oxidoreductase

Query Match 57.1%; Score 2695.5; DB 2; Length 862;
 Best Local Similarity 59.2%; Pred. No. 3.4e-186;
 Matches 526; Conservative 119; Mismatches 216; Indels 27; Gaps 11;

QY 1 MFHGVADRLTGKKNKANSWG-KIRGTVRLVKKVLDVGFNASLIDGVHRLIGWDDGVA 60
 DB 1 MLEKIVDAITGKD-----NGKKVKGTVLKKKRVLDFTDINASVLDGVLEFLG--KRVS 56
 QY 61 QLVSATAADPSNGGRGKVGKAAHLEAVVSLKSTADGETVYRVSPFWDSEQIGIPGAVL 120
 DB 57 QLVSVHADPNSLQGRKSNPAYLEKWLTTGTSLVAGESAPDVTDFWDEIDGVPQARTIN 116
 QY 121 NLQHAFFLKTILLEGVPGKGTVVVANSWYVPHLYSQERIFPANDTYLPSKPPAALVP 180
 DB 117 NFHNEFYLKSLTLEDVFNHGVFCVNSWYVPAKYSKDSRIFFANQAYLPSETPDLRN 176
 QY 181 YRQDELKILRGDNDPGPYQEHDRVRYDYNDLGDPPDKGEGHARPIILGSGSEHYPRR 240
 DB 177 YREKELVNLRGNGN-GKLEEDRWVDYAYNDLGDPEKQYARTILGSGSAEYPPRRGR 235
 QY 241 TGRHTKDPNSERL-FLNLNITYPRDERFGLHKMSDFLGYSKTIIEAVLPTLGT 299
 DB 236 TGRKPTKDPNSERLPIILMSLDIYPRDERFGLHKMSDFLTALKSIQVLLPEFKA 295
 QY 300 DDTPEFSDFDILGVLGELGPEAPNPLIAIRKKIPSEFLRSILPNSGHDHPKMP 359
 DB 296 DSTPEFSDFDVLKLYEGGKLPQGPLLKAITDSIPLILKEILRTDG-EGKFKFTPQ 354
 QY 360 VIKSVLKKAPKFKGWRDSEFARBTLAGVNPVILKLTBPFAKSTLDPQYGDHTSKI 419
 DB 355 VIQED-----KSSWRDTEFGREMLAGVNPVILSLQEFPPKSKLDPKIYGNQSTI 406
 QY 420 TEAHTRHNMGLSVQNALRNKELFTLDHHDHFMVYLDLNELEGNFIYASFTLLFLKDDG 479
 DB 407 TKEHNTLDGTLTDDAIKTNKLFILNHDHILMPYLRINTNTK-LYASFTLLFLQDDG 465
 QY 480 TLKPLAIELSLPHDPQDQGVAVSKYVTPAHTGVEGHVWQLAKAYACVNDSSAWHQLISH 539
 DB 466 TWKPVAILSLPHDPDGLGAVSKYVTPADQGVGSIWQLAKAYAAVNDSSGVHQLISH 525
 QY 540 NTHAVIEPVIATNQLSVVPHVKLSPHYRDTLNALARQTLINAGGVFEFTVFP 599

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Db 526 NTHAAIEFVATNRQLSVLPHIHKLLHPHPRDTMNALARQLINAGGVLEWTFPAK 585
Qy 600 YALGHSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIMWAI 659
Db 566 YAMESAIVYKSWFPEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIMWAI 645
Qy 660 ERWKEYLIDYIPNDGELQRDVELQAWKKEVREBAHGDLDKRDWPRMDTVQQLARACTT 719
Db 646 KSWTEVCNFFYKSDLVKNEIQAWKKEVREBAHGDLDKRDWPRMDTVQQLARACTT 705
Qy 720 IIVWASALHAHVNFQGYPIYAGYLNPRPTASRRPMPPEGSHDYKKGAGQKEADWVFRTI 779
Db 706 IIVWASALHAHVNFQGYPIYAGYLNPRPTASRRPMPPEGSHDYKKGAGQKEADWVFRTI 762
Qy 780 TSQQTLLIGLSIILSKHSDVYLGORDEPDRTSDAKALDAFKRFGSLVQIENRIK 839
Db 763 TPQLQTLIGLSIILSKHSDVYLGORDEPDRTSDAKALDAFKRFGSLVQIENRIK 821
Qy 840 TMNDSPDLKRNKGVEMPYMLLYPNTSDVTEKAEGLTAMGIPNSISI 887
Db 822 QMNGDKKRNKGVEMPYMLLYPNTSDVTEKAEGLTAMGIPNSISI 862

RESULT 7
JQ2267
lipoxigenase (EC 1.13.11.12) Lox1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JQ2267
R:Melan, M.A.; Dong, X.; Endara, M.E.; Davis, K.R.; Ausubel, F.M.; Peterman, T.K.
Plant Physiol. 101, 441-450, 1993
A:Title: An Arabidopsis thaliana lipoxigenase gene can be induced by pathogens, abscisic
A:Reference number: JQ2267; MUID:94105302; PMID:7506426
A:Accession: JQ2267
A:Molecule type: mRNA
A:Residues: 1-859 <MEL>
A:Cross-references: GB:L04637; NID:g289202; PIDN:AAA32827.1; PID:g289203
C:Comment: This enzyme catalyzes the hydroperoxidation of polyunsaturated fatty acids co
C:Superfamily: lipoxigenase
C:Keywords: fatty acid oxidation; oxidoreductase

Query Match 55.6%; Score 2626.5; DB 1; Length 859;
Best Local Similarity 58.0%; Pred. No. 3.2e-181;
Matches 512; Conservative 128; Mismatches 211; Indels 31; Gaps 13;

Qy 8 DRLTGKNEANSEKIGITVRLVKKVLDVGDNFASLLDGVHRLGWDGVAFLYSATA 67
Db 7 DLLTGGGNETTK-KVXGTVMKKNVLDNFDFNASFLDLHBEFLG--NKITLRLVSSDV 63

Qy 68 ADPSNGGRGVKGAHLEEAIVSLKSTADGETVYRVSEFWEDESQGIPIGAVLVRLQHAFF 127
Db 64 TDSNGSKGLGKAHLEDWITITSLTAGESAPKVTFTDYETDFGYGAPLIENSHFSEF 123

Qy 128 FLKTLTLEGVPGKTVVFNANSVYPHKLSQERIFPANDTYLPSKMPAALVYRQDEUK 187
Db 124 LLKSLTLEDVPGHGRVHYICNSWIYPAKHVTTDRVFESNKTYPHETPATLLKYREEELV 183

Qy 188 ILRGDDNPGVQYQHDVRYDYNDLGDPKGEEHARPILGSGOEHPYRRCRTGRHPK 247
Db 184 SLRG-TGEGELKEDWRYDYAYNDLGVPPK--NRPVLGGTQEQYEPYRGRGTGRKPK 239

Qy 248 KDPNSRL-FLNLNIVPRDERFGLKMSDFLGYSKLTIIIEAVLPTGTFVDDTPKPEF 306
Db 240 EDPOTESRLPITSSLDIYVPRDERFGLKMSDFLAVAKAIAQIOPALEAVPDDTPKPEF 299

Qy 307 DSPEDILGLVGLGPEANPNLIAIRKIPSEFLRSLTPNGSHDPLKMPNPKVSDVL 366
Db 300 DSFEDLVKIYEEGLDLPQALISIVKNIPEMLKEIFRTDQGF-LKFPVPOVKEK-- 356

Qy 367 KKAPEFKGWRTEBEFARETAGNVPVHIIKRLTEPPAKSTLDPQYGDHSTKIIEAHIR 426
Db 357 -----KTAWRTDEEFAREMLAGNVPVHIIKRLTEPPAKSTLDPQYGDHSTKIIEAHIR 410
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Qy 427 NMGGLSVQNALRNKBLFILDHHDHWPYLDINELEGNFIYASRTLLFLKODGTLLKPLAI 486
Db 411 NLDGLTVSEALEKERLFILDHHDHWPYLDINELEGNFIYASRTLLFLKODGTLLKPLAI 469
Qy 487 ELSLPHDPGQQRGAYSKVYTPAHTGVEGHVWQLAKAYACVNDASAWHQLISHWLNTHAVIE 546
Db 470 ELSLPHDPGQQRGAYSKVYTPAHTGVEGHVWQLAKAYACVNDASAWHQLISHWLNTHAVIE 528
Qy 547 PVIATNRLSVVHVHKLSPHVEDTININALAROTLINAGGVFEERTVFPKALGNSA 606
Db 529 PVIATNRLSVVHVHKLSPHVEDTININALAROTLINAGGVFEERTVFPKALGNSA 588
Qy 607 DVIYS-WMFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIMWAIERWYKE 665
Db 589 FIYKHNWTFPDQALPAELKRGMAVEDPEAPHGLRLIKDYPIYAVDGLVIMWAIERWYKE 648
Qy 666 YLDIYVNDGELQRDVELQAWKKEVREBAHGDLDKRDWPRMDTVQQLARACTTIIWVAS 725
Db 649 YIFLYKIEEDIQDTLQAWKKEVREBAHGDLDKRDWPRMDTVQQLARACTTIIWVAS 708
Qy 726 ALHAAVNFQGYPIYAGYLNPRPTASRRPMPPEGSHDYKKGAGQKEADWVFRTITISQPT 785
Db 709 ALHAAVNFQGYPIYAGYLNPRPTASRRPMPPEGSHDYKKGAGQKEADWVFRTITISQPT 765
Qy 786 ILGISLILSKHSDVYLGORDEPDRTSDAKALDAFKRFGSLVQIENRIKTMNDSP 845
Db 766 LLGISLILSKHSDVYLGORDEPDRTSDAKALDAFKRFGSLVQIENRIKTMNDSP 824
Qy 846 DLKRNKGVEMPYMLLYPNTSDVTEKAEGLTAMGIPNSISI 887
Db 825 TLKNTGLVKVPTLLFFSSSG-----GVTRGIPNSVSI 859

RESULT 8
S44940
lipoxigenase (EC 1.13.11.12) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C:Accession: S44940
R:Casey, R.
submitted to the EMBL Data Library, May 1994
A:Reference number: S44940
A:Accession: S44940
A:Molecule type: mRNA
A:Residues: 1-861 <CAS>
A:Cross-references: EMBL:X79107; NID:g486618; PIDN:CAA55724.1; PID:g486619
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 55.0%; Score 2597; DB 2; Length 861;
Best Local Similarity 58.5%; Pred. No. 4.4e-179;
Matches 508; Conservative 112; Mismatches 222; Indels 26; Gaps 10;

Qy 22 KIRGTVRLVKKVEILDVGDNFASLLDGVHRLGWDGVAFLYSATAADPSNGGRGVKGA 81
Db 18 KVXGTVMKKNVLDNFDFNASFLDLHBEFLG--QKVSFQLISSVQGDFTNGLQGHNSP 75

Qy 82 AHLREAVVSLKS-TADGETVYRVSEFWEDESQGIPIGAVLVRLQHAERFLKLTLEGVPGK 140
Db 76 AYLENSLFTLPTAGSETAFGVTFDWNBEFVGPAGIINKWHINEFLKSLTLEDVFNH 135

Qy 141 GTVVFVANSWYPHKLSQERIFPANDTYLPSKMPAALVYRQDEUKILRGDDNPGVQY 200
Db 136 GKWHFVNCNSWYVPSINYSKSDRIFPANDTYLPSKMPAALVYRQDEUKILRGDDNPGVQY 194

Qy 201 HDRVYDYNDLGDPKGEEHARPILGSGOEHPYRRCRTGRHPKTPKPEF 259
Db 195 WDRYDYNDLGDPKGEEHARPILGSGOEHPYRRCRTGRHPKTPKPEF 254

Qy 260 NLNIVPRDERFGLKMSDFLGYSKLTIIIEAVLPTGTFVDDTPKPEFSDILGLYELG 319
Db 255 SLDIYVPRDERFGLKMSDFLGYSKLTIIIEAVLPTGTFVDDTPKPEFSDILGLYELG 314
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C:Superfamily: lipoygenase
C:Keywords: oxidoreductase

Query Match 53.1%; Score 2510; DB 2; Length 859;
Best Local Similarity 56.7%; Pred. No. 8.3e-173;
Matches 502; Conservative 111; Mismatches 240; Indels 32; Gaps 13;

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QY 5 GVADRLTGKNEANSEGIKRVLRVAVKEVLVDGDFNASLLDGVHRILGWDGVAFOVLS 64
DB 5 GIVDAILEGD-----DRPKVKERVILMKQVLDNFINGASVVDGIDSLDG--QRVSIQILS 58
QY 65 ATAADPSNGRGKVGKAAHLEAAVSLKSTADGETVYRVSEFWEDESQ-GIPGAVLVANLQ 123
DB 59 GSV--NYDGLGKLSNPALTESLWLTIDIPITAGESFTSVTDWDRDFGVPGAFIKNLH 116
QY 124 HAERFLKTLTLEGVPGKGVTVFVANSVYVPHKLYSQERIIFANDTYLPSKMPAALVYRQ 183
DB 117 LNEFFLKSLTLEDVNYKIHFVNCNSVYPAFRYKSRIFPANOAYLPSETPQRLRYRE 176
QY 184 DELKILRGDDNPGPYQEHDRVYDYNDLGDGPKGEHARPIILGSGQEHPPYRRCRTGR 243
DB 177 NELVALRG-DGTGKLEEDRWVVDYACVNDLGECPKGEYARPIILGSGSEYPPYRGRGTGR 235
QY 244 HPTKDPNSERLFL-LNLTIVPRDERFHLKMSDFLGYSKTYIIIEAVPLTGLTFVDDT 302
DB 236 EPTKADPNCEARNPLPMSLDIYVPRDERFHVKSDSLTSSKSLQTLPLPAFKALCDNT 295
QY 303 PKEPDSFDIILGVLGPEAPNPLIABIRKIPSEFLRSILPNSHDPHPLKPLNVIK 362
DB 296 PNEFNSFADVLNVEGGIKLPEGWLKAITNISEILKQILDQDGG-LLKYPTPOVIQ 354
QY 363 SDVLKKAPEFKFGRWTDDEFPARETAGVNPVILKLTFFPAKSTLDPQYGDHFTSKITEA 422
DB 355 GD-----KTAWRTDEFGREMLAGSNPVLISRLQEFPPKSLDPTIYGNQNSTITTE 406
QY 423 HIRNMGLSVQNALRNKRLFIILHDDHFMFVLDSEINELEGNFYASRTLLFLKDDGTLK 482
DB 407 HVQDKINGLTWNEAKSKNRLFIILHDDHFMFVLDSEINELEGNFYASRTLLFLKDDGTLK 466
QY 483 PLATLSLPHPDGQORGAVSKYTPAHTGVGHHVWQLAKAYACVNSAWHQLISHWLNTH 542
DB 467 PLATLSLPHPDGQDQGVTVSKYTPADQGVGSIWQFAKAYAVAVNDMGHQLISHWLNTH 536
QY 543 AVIEFPVATNRQLSVHVPKLLSPHYRDTLNINALAROTLINAGGVPERFTVPKAYAL 602
DB 527 AVIEFPVATNRHLSVLPIHKLPHFRNTMNLALARETLTDVGG-FETSLPPAKYSM 585
QY 603 GMSADVYKSNFNEQALPADLVYKRGVAVPDQSSPYGVRLATIKOYPYAVDGLVWIAERW 662
DB 586 EMSAAAYKDWVFPQALPADLLKRGVAVEDLSSPHGIRLLILDYPAVDGLIWAALKSW 645
QY 663 VKEILDITYPNDGELORVELQAWKVEBEAHGDLKDRDWPMDTVQOLARACTIIV 722
DB 646 VTEYCKFYKDETVKEDTELQAWKELREHGDGKDEAWMPKLQTRQELRDCCTIIV 705
QY 723 VASALHAAVNFGQPYAGYLPNRTASRRPMPGSHDYKKGAGQKEADWVFRTITSQ 782
DB 706 LASALHAALHGLSYAGYLPNRTLSCLNMPGSEVEYEL---KTNPKVLFKTFVPQ 762
QY 783 FQTLIGISLIEILKSHSDEYVLGOREPDRWTSDAKALDAFKRFGSRLVQIENRKTMM 842
DB 763 LQSLLEISIFVSSRHASDEYVLGORDSIE-WTKDKEPLVAFAFERFGMLSDIENRIMN 821
QY 843 DSPDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887
DB 822 SHKSKWRSGPVNFTYLLFP-TSE-----EGLTGKIPNSVSI 859
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RESULT 11

T07101

lipoygenase (EC 1.13.11.12) - potato
C:Species: Solanum tuberosum (potato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999

C:Accession: T07101
R:Basso, B.; Giribaldi, G.; Sironi, G.; Mizzi, L.M.; Righi, M.
submitted to the EMBL Data Library, April 1995

A:Reference number: Z15920

A:Accession: T07101

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-876 <BAS>

A:Cross-references: EMBL:U24232; NID:g1117792; PIDN:AAD09202.1; PID:g1117793

C:Genetics:

A:Introns: 79/1; 173/3; 254/1; 368/3; 397/3; 433/3; 535/2; 623/1

C:Function:

A:Description: catalyzes the peroxidation of polyunsaturated fatty acids to their corres

C:Superfamily: lipoygenase

C:Keywords: fatty acid oxidation; iron; oxidoreductase

Query Match 52.9%; Score 2498.5; DB 2; Length 876;

Best Local Similarity 56.6%; Pred. No. 5.8e-172;

Matches 493; Conservative 130; Mismatches 217; Indels 31; Gaps 15;

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QY 22 KIRGTVRLVKEVLVDGDFNASLLDGVHRILGWDGVAFOVLSATAADPSNGRGKVGKA 81
DB 32 KRGTVVLMEECLDUTNVGASLLDRFHEVIG--KGVSLQLISADHAEF--GCTGRLGP 87
QY 82 AHLEAAVSLKSTADGETVYRVSEFWEDESQ-GIPGAVLVANLQAHFFLKTLLLEGVPGK 141
DB 88 AFLEKWISSLTISAGDATFNTFDWDESMGVGPAFIKNVHHSQFYLRVTVLEDPVGHG 147
QY 142 TVFVANSVYVPHKLYSQERIIFANDTYLPSKMPAALVYRQDELKILRGDDNPGYQEH 201
DB 148 ELHFVNCNSVYPAFRYKXYDRVFFANKTYLPSNTPBPLPYRQELLSSRGSGS-GKLKEW 206
QY 202 DRVRYDYNDLGDGPKGEHARPIILGSGQEHPPYRRCRTGRHPTK--KDPNSSRLFL 258
DB 207 DRVYDYRFDLGFDPKDPYVYRVLGSGSEYPPYRGRGTSTRATKTGFADPMSSSLPP 266
QY 259 LNLNIVPRDERFHLKMSDFLGYSKTYIIIEAVPLTGLTFVDDTPEKPSFDILGLTEL 318
DB 267 LGLDIYAPDERFTPVKLSDFLAYAKSLGQVLIPEIAALFDKTIENFDNFDVLKLEG 326
QY 319 GPEAPNPLIABIRKIPSEFLRSILPNSHDPH-LKMPLPNVIKSDVLKKAPEKFGWR 377
DB 327 GIKLPDHL-KKLQCIPEMLKELV--RSDGEPFLKPMFDPVVKV-----RSAR 375
QY 378 TDEFPARETAGVNPVILKLTFFPAKSTLDPQYGDHFTSKITEAHIRNMGLSVQNAL 437
DB 376 TDEFGREMLAGVNPVIRRLQEFPPASKLDPDEVYGNQTSIIKREHIEKNMDGLTVDEAI 435
QY 438 RNKRLFIILHDDHFMFVLDSEINELEGNFYASRTLLFLKDDGTLKPLAIELSLPHDQO 497
DB 436 EGNRLFIILHDDHALLPYLRINTTKT-TYATRTLLYLQDNGTLRPLAIELSLPHDQDX 494
QY 498 RGAVKSVYTPAHTGVGHHVWQLAKAYACVNSAWHQLISHWLNTHAVIEPVPVIATNROLS 557
DB 495 HGATSLVFTPADEGVGTVWQLAKAYAVAVNDMGHQLISHWLNTHATIEPFIATIRLS 554
QY 558 VVHPVHKLSPHYRDTLNINALAROTLINAGGVPERFTVPKAYALGMSADVYKSNFNEQ 617
DB 555 VLHPFKLQPHFRDITMNLALAGILALTVPKRYAMEMSSIVKKNVWVFTEQ 614
QY 618 ALPADLVKRGVAVPDQSSPYGVRLATIKOYPYAVDGLVWIAERWVVKGYLDIYFNDGEL 677
DB 615 GLLL-LFLRGVAVLDSQSPYALKLLIEDYPPAVDGLVWIAEALEAVDDVY-FYISTDDMI 672
QY 678 QRDVELQAWKVEBEAHGDLKDRDWPMDTVQOLARACTIIVVASALHAAVNFGQYP 737
DB 673 RDTTELQSWMEVRNEHGDGKDEPWNFQMOQTRAEVACTIIIVVASALHAAVNFGQYP 732
QY 738 YAGYLPNRTASRRPMPGSHDYKKGAGQKEADWVFRTITSQFQTLIGISLIEILSK 797
DB 733 YSGLTSNRTVSRRFMPGEPYAEAL---ESNPVAVLKTIITAFQTLIGVSLIEILSR 789
QY 798 HSDSEVYLQORDEPDRWTSDAKALDAFKRFGSRLVQIENRKTMMDSPLKNRKGFVEMP 857
```

790 TASDEIYLQRENPE-WTSDVEPQSFQRPHDKLVDYENKIVERNNDNRKNGRNGFVKVP 848
QY 858 YMLLYPNTSDVTGEKAE-GLTAMGIPNSISI 887
Db 849 YMLLYPNAS---GDNSESLTGKGIPIINSVSI 876

RESULT 12
DASYLI
lipoxigenase (EC 1.13.11.12) 2 - soybean
N:Alternate names: carotene oxidase 2; lipoxidase 2
C:Species: Glycine max (soybean)
C>Date: 31-Mar-1989 #sequence revision 30-Jun-1991 #text_change 19-Jan-2001
C:Accession: A28161; A30831; A37160; S13536
R:Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.
J. Biol. Chem. 263, 6816-6821, 1988
A:Title: Primary structure of soybean lipoxigenase L-2.
A:Reference number: A28161; MUID:88198254; PMID:2834391
A:Accession: A28161
A:Molecule type: mRNA
A:Residues: 1-865 <SH>
A:Cross-references: GB:J03211; NID:G170013; PIDN:AAA33987.1; PID:G170014
A:Note: there are no disulfide bonds
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
Plant Mol. Biol. 7, 11-23, 1986
A:Title: Two soybean seed lipoxigenase nulls accumulate reduced levels of lipoxigenase
A:Reference number: A30831
A:Accession: A30831
A:Molecule type: mRNA
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-362, 'E', 364-399, 'P', 401-427, 'H', 429-485, 'G', 487
A:Cross-references: GB:M16876
A:Note: due to a frameshift error, residues in the region 691-865 do not correspond to
A:Experimental source: clone pLX-65
R:Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.
unpublished results, cited by Yenofsky, R.L.; Fine, M., and Liu, C., in Mol. Genet.
A:Reference number: A37160
A:Accession: A37160
A:Molecule type: mRNA
A:Residues: 232-262, 'NL', 265-312, 'Y', 314-399, 'PK', 402-427, 'H', 429-485, 'G', 487-501, 'G', 50
A:Note: this is a revision to the sequence from reference A30831
R:Shibata, D.; Kato, T.; Tanaka, K.
Plant Mol. Biol. 16, 353-359, 1991
A:Title: Nucleotide sequences of a soybean lipoxigenase gene and the short intergenic re
A:Reference number: S13381; MUID:91370880; PMID:1909908
A:Accession: S13536
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 859-865 <SH2>
A:Cross-references: EMBL:X56139; NID:G18745; PIDN:CAA339605.1; PID:9829267
C:Comment: In soybean, four isozymes are found with distinct electrophoretic properties.
C:Function:
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per
C:Superfamily: lipoxigenase
C:Keywords: fatty acid oxidation; iron; metalloprotein; oxidoreductase
P:527,532,718,722,865/Binding site: iron (His, His, His, Asn, Ile) #status predicted

Query Match 52.6%; Score 2486; DB 1; Length 865;
Best Local Similarity 54.5%; Pred. No. 4.5e-171;
Matches 487; Conservative 137; Mismatches 196; Indels 74; Gaps 15;

QY 22 KIRGTVRLVKKEVD---VGDFN-----ASLLDGVHRIIGWDGVAFLV 63
Db 18 KIRGTVRLVKKEVD---VGDFN-----ASLLDGVHRIIGWDGVAFLV 63

QY 64 SATAAPDSNGRKGKVAHLEBAVSLKSTADGETVTVVSVFEDWSQIGPAGAVRLNQ 123
Db 76 SAT--KPLANGKGVKGTFTLEGIIVSLPTLAGESAFNIQFEWDSMGIPGAFYKKNY 133

QY 124 HAEFFLKTLEGVGKGTGVFVANSWYPHKLYSQERIFFEANDTVLPKMPAALVPYRQ 183
Db 134 QVEFYLSLTLEDVFNQGTIRFCVNSWVNTKLYKSVRIFPANHVTVPSETPAALVGIRE 193

QY 184 DELKILRGDNPQYQEHDRVVRVYDNDLGDPOKGEHARPILGGSOEHPPRRCTGR 243
Db 194 BELNLRG-DGGERKEHRIYDYVDYNDLGNPDHGENFARPIILGSSSTHEYPARGTR 252
QY 244 HPTKDPNSERLFLNLNINIVPRDRFGHLKMSDFLYGSLKTIIEAVLPLGTFTVD--D 301
Db 253 YPTRKQNSEK-----PGEVYPRDENFGHLKSDFLAYGKISQVYLPAPFESVFDLNF 307
QY 302 TPKEFDSPELILGLYELGPEAPNPLIAEIRKKTPSEFLRSILP-----NGSHDHL 353
Db 308 TENEDFSQDVRDLHEGG-----IKLPTVISTIMPLPVVKELFRDGGQVL 354
QY 354 KMLPLNWTKSVDLKKAPKFKGWRTDEFARETLAGNPVILKRLTFFPAKSTLDPRQYG 413
Db 355 KFPPEHVIVQS-----KSAMNTDEFAFEMVAGVNPVIRGLQELFFPKNSLDPTIYG 406
QY 414 DHTSKITEAHRHNMGGSLVQNALRNKRLFTLDHHDHFMYPYLDINLEGNFIYASRTLL 473
Db 407 EQTSKITADAL--DLDDGYTDEALASRLFLMVDHDFVMPYIRINTQYAK-AIATRTIL 463
QY 474 FLKDDGTTLKPLAIELSLPHPDGQQRGAVSKVYTPAHTGVGHHVWQLAKAYACVNDSAHQ 533
Db 464 FLRENGTLKPVAIELSLPHPDGDLGSAVSQVILPAKEGVVESTIMLLAKAYVYVNDSCVHQ 523
QY 534 LISHWLNTHAVIEPEFVATNQLSVVHPVHKLSPHYRDTLNINALAROTLINAGGVFER 593
Db 524 LMSWLNTHAVIEPFITATNHLHSAHPYKLLTPHYRDTLNINALARQSLINADGHIK 583
QY 594 TVFPKALGMSADYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKQYPAVDGL 653
Db 584 SFLPSKHSVSSAVYKXNVFTDQALPADLVKRGVAVPDQSSPYGVRLLIKQYPAVDGL 643
QY 654 VIWAIEHWKEYLDIYYPNDELQORVLOQAWKEVEEAAHGLDKDRDMPMDTVOQL 713
Db 644 EIIWAIKTWQVYVSLIYARDDDVPQSELOQWKEAVEKGHGLDKDRDMPMDTVOQL 703
QY 714 ARACITTIWASALHAAVFNQYPIYAGYLPNRPPTASRRPMPPEGSHDYKKGAGQKAD 773
Db 704 VEICITTIWASALHAAVFNQYPIYAGYLPNRPPTASRRPMPPEGSHDYKKGAGQKAD 761
QY 774 VFITITSQFOTILIGISLITLSKHSDEYVIGORDEPDWTSDAKALDAFKFGSLVQ 833
Db 762 -ILATITSKFTLVLDLSVIELSHASDEVVLGQDNP-HWTSKALQAFQKFGNKLKE 819
QY 834 IENRKTMDSPDLNKRKGPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 820 IEEKLARKMNDQSLNRLGPVQLPYTLHFN-----SEGTCRGIPNSISI 865

RESULT 13
S01864
lipoxigenase (EC 1.13.11.12) 3 - soybean
C:Species: Glycine max (soybean)
C>Date: 18-Oct-1989 #sequence revision 18-Oct-1989 #text_change 28-Apr-1993
C:Accession: S01864
R:Yenofsky, R.L.; Fine, M.; Liu, C.
Mol. Gen. Genet. 211, 215-222, 1988
A:Title: Isolation and characterization of a soybean (Glycine max) lipoxigenase-3 gene.
A:Reference number: S01864
A:Accession: S01864
A:Molecule type: mRNA
A:Residues: 1-857 <YEN>
A:Cross-references: EMBL:X06928
C:Genetics:
A:Gene: lox-3
A:introns: 70/1; 165/3; 246/1; 353/1; 381/3; 417/3; 519/2; 607/2
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 52.5%; Score 2480.5; DB 2; Length 857;
Best Local Similarity 55.4%; Pred. No. 1.1e-170;
Matches 488; Conservative 133; Mismatches 211; Indels 49; Gaps 14;

lipoxigenase (EC 1.13.11.12) 3 [similarity] - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
A:Accession: S01142
B:Ealing, P.M.; Casey, R.
Biochem. J. 253, 915-918, 1988
A:Title: The complete amino acid sequence of a pea (Pisum sativum) seed lipoxigenase pre-
A:Reference number: S01142; MUID:89025643; PMID:3140791
A:Accession: S01142
A:Molecule type: mRNA
A:Residues: 1-861 <EAL>
A:Cross-references: EMBL:X07807; NID:g20799; PIDN:CAA30666.1; PID:g20800
C:Superfamily: lipoxigenase
C:Keywords: oxidoreductase

Query Match 51.6%; Score 2437; DB 1; Length 861;
Best Local Similarity 53.4%; Pred. No. 1.6e-167;
Matches 471; Conservative 148; Mismatches 213; Indels 50; Gaps 14;

QY	22	KIRGTIVRLVKEVLDVG-----DFNASLLDGVHRIILGDDGVAFOVLVSATAA	68
DB	14	KIRGTIVRLVKEVLDVG-----DFNASLLDGVHRIILGDDGVAFOVLVSATAA	71
QY	69	DPSNGRGKGVKAHLEAVVSLKSTADGETVYRVSEFDESGQIPGAVLVRNLQAEFF	128
DB	72	DAT--GKGLKATFLEGLISLPTLGAGQAPKIHFEWDDMGIPGAFYIKNFQTEFF	129
QY	129	LKTLTEGVPGKGVVFWANSWVPHKLYSQERIFPANDTYLPSKMPAALVPRQDELKI	188
DB	130	LVSUTLDDIPNHSIYFCNSWIYNAKHKIDRIFFANQYLPSETPAPLVHYREBELNN	189
QY	189	LRGDDNPGFYQEHDRVRYDYNDLGDPPDKEEHARPIILGSGDEHPYPRCRTGREPTKK	248
DB	190	LRG-DGTGERKEWRIYDYNDLGNPDSENHARFVLGSETPYPRGRTRGRKPTRK	248
QY	249	DPNSESRLFLNLNIYPRDRPQHLKMSDPLGLSLKTIIEAVLPTLGTFTVDD---TPKE	305
DB	249	DPNSESRLFLNLNIYPRDRPQHLKMSDPLGLSLKTIIEAVLPTLGTFTVDD---TPKE	304
QY	306	FDSFEDILGLYELGPEAPNPLIARIRKIPSEFLRSLPNSGSHDHPKPLNVIKSDV	365
DB	305	FDSFEDILGLYELGPEAPNPLIARIRKIPSEFLRSLPNSGSHDHPKPLNVIKSDV	358
QY	366	LKKAPEFKGKRTDEEFARETLAGNVPIIKRLTEPPAKSTLDPQYGDHSTSKIETAH	425
DB	359	-----RSGWMTDEEFARETLAGNVPIIKRLTEPPAKSTLDPQYGDHSTSKIETAH	411
QY	426	HNMGSLVONALRNKRLFILDHDHFMFYLDEINELSGNFIYASRTLLFLKDDGTLKPLA	485
DB	412	PNLEGLTVEEAIQNKKFLLDHDSINPYLRINSTTK-AYATRTILFLNNQNLKPLA	470
QY	486	IELSLPHPDGQORGAISKVYTPAHTGVGHVWQLAKAYACVNDSAMHQLISHWLNTHAV	545
DB	471	IELSLPHPDGQORGAISKVYTPAHTGVGHVWQLAKAYACVNDSAMHQLISHWLNTHAV	530
QY	546	EPFVIATNRQLSVVPHVHLLSPHYRTLTNALAROTLINAGGVPERTVFPKAYALGMS	605
DB	531	EPFVIATNRHLSCHHPYIKLYPHYRTMTNLSRLSLVNDGGIIEKTLFWGRISWEMS	590
QY	606	ADVYKSMNFNEQALPADLVKRGVAVPQSSPYGVRLLIKDYPYAVDGLVIWIAERWYKE	665
DB	591	SKVYKNWVFTQALPADLVKRGVAVPQSSPYGVRLLIKDYPYAVDGLVIWIAERWYKE	650
QY	666	YLDIYYPNDGLQORVLEQAWKEVBEAHCDDLKDRDWRMDTVOQLAACAIIHWAS	725
DB	651	YVLSYIYTSDEKRLQDSELQAWKELVEVGHGDKNEPWPMPQMTREDLIEVCSIVITAS	710
QY	726	ALHAAVNFGQYYPAGYLPNRPETASRRMPFSGSHDYKKLGAGQKEADMFVIRITISQFQ	785
DB	711	ALHAAVNFGQYYPAGYLPNRPETASRRMPFSGSHDYKKLGAGQKEADMFVIRITISQFQ	767
QY	786	ILGISLLEILSKSHSDEVIYLGORDEPDRWTSDAKALDAFKRFGSRLVQIENRIKTNDSP	845

Db 768 LIDLVSVEILSRHASDELYLGERDNPN-WTSDKRALEAFKFGNKLAEIEKKLTORNNDE 826
QY 846 DLKNRKGVPVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSIS 887
Db 827 KLNRHGGPVEMPYTLLYPSSK-----EGLTFRGIPNSIS 861

Search completed: March 23, 2004, 07:01:33
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 03:49:23 ; Search time 20 Seconds
(without alignments)
2309.311 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFHGVADRLTGKKEANSE.....VTGEKAEGLTANGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2936.5	62.2	862	1 LOX1_HORVU	P29114 hordeum vul
2	2829.5	59.9	865	1 LOX2_ORYSA	P29250 lycza sativ
3	2627.5	55.6	860	1 LOXA_LYCES	P38415 lycopersico
4	2626.5	55.6	860	1 LOX1_ARATH	Q06327 arabidopsis
5	2597	55.0	861	1 LOX1_SOLTU	P37831 solanum tub
6	2510	53.1	859	1 LOXB_LYCES	P38416 lycopersico
7	2486	52.6	865	1 LOX2_SOYBN	P09439 glycine max
8	2473.5	52.4	857	1 LOX3_SOYBN	P09186 glycine max
9	2458.5	52.1	864	1 LOX2_PEA	P14856 pisum sativ
10	2437	51.6	861	1 LOX3_PEA	P09918 pisum sativ
11	2405.5	50.9	862	1 LOXA_PHAVU	P27480 phaseolus v
12	2375	50.3	853	1 LOXA_SOYBN	P38417 glycine max
13	2370.5	50.2	864	1 LOXX_SOYBN	P24095 glycine max
14	2355.5	49.9	839	1 LOX1_SOYBN	P08170 glycine max
15	2309	48.9	866	1 LOX1_LENCU	P38414 lens culina
16	2231	47.2	741	1 LOXB_PHAVU	P27481 phaseolus v
17	1667.5	35.3	896	1 LOXC_ARATH	P38418 arabidopsis
18	1650	34.9	896	1 LOX2_HORVU	Q89sm2 hordeum vul
19	1587.5	33.6	923	1 LOXC_ORYSA	Q89sm2 hordeum vul
20	1559	33.0	936	1 LX21_HORVU	P38419 oryza sativ
21	1455	30.8	932	1 LX22_HORVU	P38419 hordeum vul
22	601	12.7	1066	1 AGL3_PLEHU	Q16025 plexaura ho
23	538	11.4	711	1 LXE3_MOUSE	Q9wv07 mus musculu
24	513.5	10.9	676	1 LX1B_HUMAN	Q15296 homo sapien
25	513	10.9	711	1 LXE3_HUMAN	Q95y71 homo sapien
26	511.5	10.8	701	1 LOXR_MOUSE	Q70582 mus musculu
27	507	10.7	677	1 LX1B_MOUSE	Q35936 mus musculu
28	504	10.7	662	1 LOXE_MOUSE	P55249 mus musculu
29	503.5	10.7	662	1 LOXL_MOUSE	P39654 mus musculu
30	503	10.7	701	1 LOXE_HUMAN	Q75342 homo sapien
31	486.5	10.3	662	1 LOX2_RAT	Q02759 rattus norv
32	485.5	10.3	673	1 LOX5_MOUSE	P48999 mus musculu
33	480	10.2	672	1 LOX5_MESAU	P51399 mesocricetu

ALIGNMENTS

RESULT 1

ID	LOX1_HORVU	STANDARD;	PRT;	862 AA.
AC	P29114; Q42845;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Lipoxygenase 1 (EC 1.13.11.12).			
GN	LOX1.1 OR LOXA.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Triumph;			
RX	MEDLINE=95127754; PubMed=7827128;			
RA	van Mecheelen J.R., Smits M., Douma A.C., Rouster J., Cameron-Mills V.,			
RA	Heidekamp F., Valk B.E.;			
RT	"Primary structure of a lipoxygenase from barley grain as deduced			
RT	from its cDNA sequence."			
RL	Biochim. Biophys. Acta 1254:221-225(1995).			
RN	[2]			
RP	SEQUENCE OF 274-294 AND 832-845.			
RC	STRAIN=cv. Triumph; TISSUE=Embryo;			
RX	MEDLINE=92207997; PubMed=1554746;			
RA	Doderer A., Kokkelink I., van der Veen S., Valk B.E., Schram A.W.,			
RA	Douma A.C.;			
RT	"Purification and characterization of two lipoxygenase isoenzymes			
RT	from germinating barley."			
RL	Biochim. Biophys. Acta 1120:97-104(1992).			
CC	-1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF			
CC	DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND			
CC	DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO			
CC	WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING			
CC	A CIS, CIS-1,4-PENTADIENE STRUCTURE.			
CC	-1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-			
CC	hydroperoxyoctadeca-9,11-dienoate.			
CC	-1- COFACTOR: Iron, one atom tightly bound per molecule.			
CC	-1- SUBUNIT: Monomer.			
CC	-1- DEVELOPMENTAL STAGE: IN BOTH QUIESCENT AND GERMINATING SEEDS.			
CC	-1- MISCELLANEOUS: WITH LINOLEATE AS SUBSTRATE, LIPOXYGENASE 1 SHOWS A			
CC	SPECIFICITY FOR CARBON 9 AS THE SITE FOR HYDROPEROXIDATION (IN			
CC	CONTRAST TO LIPOXYGENASE 2, WHICH SHOWS A PREFERENCE FOR CARBON			
CC	13).			
CC	-1- SIMILARITY: Belongs to the lipoxygenase family.			
CC	-1- SIMILARITY: Contains 1 PLAT domain.			
CC	-----			
CC	This SWISS-PROT entry is copy-right. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

P09917 homo sapien
P12527 rattus norv
P39555 mus musculu
P18054 homo sapien
P27479 bos taurus
P16050 homo sapien
P16469 sus scrofa
P12530 oryctolagus
O19043 oryctolagus
Q9uug0 s fatty aci
P06313 homo sapien
P58281 mus musculu

```

CC EMBL; L35931; AAA64893.1; --
DR PIR; T05941; T05941.
DR HSP; P09186; ILNH.
DR InterPro; IPR000907; Lipoxxygenase.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; lipoxxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE 2; FALSE_NEG.
DR OXIDOREDUCTASE; DIOXYGENASE; Iron; Multigene family.
KW DOMAIN 34 161
FT METAL 517 IRON (BY SIMILARITY).
FT METAL 522 IRON (BY SIMILARITY).
FT METAL 708 IRON (BY SIMILARITY).
FT METAL 862 IRON (BY SIMILARITY).
SQ SEQUENCE 862 AA; 96393 MW; F55954473467BEAA CRC64;

Query Match 62.2%; Score 2936.5; DB 1; Length 862;
Best Local Similarity 63.1%; Pred. No. 2.4e-204;
Matches 562; Conservative 110; Mismatches 187; Indels 31; Gaps 12;

QY 1 MFHWGVADRLTKGNKEAWSEKIGRTVRLVKKEVLDVGFNFASLLDGVHRLGWDDGVAF 60
DB 1 MLLGLGLDITLTCANKSA-----RLKGTIVLMKKNVLDLDFGATIIDGIFLGG--KGVTC 54

QY 61 QLVSATADPSNGRGKVGKAAHEAAVSLKSTADGETVYRVVSFEWD--ESQIGPGAVLV 119
DB 55 QLIISTAVDQNGRGKVGKAAHEAAVSLKSTADGETVYRVVSFEWD--ESQIGPGAVLV 114

QY 120 RNLOHAEFFLTKLLEGVPGK-GTVFVANSVWVPHKLYSQERIFFANDTYLPSKMPAAL 178
DB 115 NNVHSEFFLTKLTHDVPGRGNLTFFVANSWIYPAANYRSYRVFFANDTYLPSQMPAAL 174

QY 179 VPYQDELKILRGDNPQYQEHDRVYRVYDNDLGPDPKGEHARPILOGSQQEHPYPR 238
DB 175 KPYRDDLELRNGDDQQQYQEHDRVYRVYDNDLGE-----GRPLGNSDHPYPR 227

QY 239 CRTGRHPTKDPNSERLFLNLNLIYVPRDFGHLKQVSDFLGYSLXTIIEAVLPTIGTF 298
DB 228 GRTERKPNASDPSLESLSLE-QIVYPRDEKFGHLKTSDFLGYSIKAITQGIPLPAVRY 286

QY 299 VDDTPKEDSFEDILGILYELGPEAPNPLIAEIRKTPSEFLSILPNSGSHDPLKMLP 358
DB 287 VDTTPGEFDSQDINLYEGGIGLKPVALEELKQFPLOLQIDLLPVGG-DSLLKLPVP 345

QY 359 NVIKSDVLKAPKPFKGRTRTDEEFARETLAGVNPVIRKLTFFPAKSTLDPQVQDHTSK 418
DB 346 HIQ-----ENKQAWRTUDEEFAREVLAVGNVPMITRTEPPKSSLDPSKFGDHTST 397

QY 419 ITEAHIRNMWGLSVQNALNKRILFDLHDHDFPYPDNEINEGNFIYASRTLLFLKDD 478
DB 398 ITAEHIEKNEGLTVQQALESNRLYILHDHDFPYPDNEINEGNFIYATRTLLFLRGD 457

QY 479 GTLKPLALELSPHDPGQORCAVSKVTPAHTG-VEGHVWQLAKAYACVNDSSAWHOLISH 537
DB 458 GELTFLALELSEPIIOGLLTAKSKVTPVPSPGSGVEGWVWELAKAYAVNDSSGHWQLVSH 517

QY 538 WLNTHAVIEPTVIATNRQLSVVPHKLLSPHYRDTLNINALARQTILINAGGVFERTVFP 597
DB 518 WLNTHAVMEPFIATNRHLSVTHPVHKLSPHYRDTLTINALARQTILINAGGIFEMTVFP 577

QY 598 AKYALGMSADVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVIW 657
DB 578 KCFALGMSAVVYKWKFTQGLPDLLIKRGMAVEDPSPKVRLVLLSDYPIYADGLAIWH 637

QY 658 AIERWYKELYDIYPNDGELQDVELQAWKVEEAEAGDLKORDWPRMDTVQQLARAC 717
DB 638 AIEQVVSLEYLAITYYPNDGVLQDTEVQAWWKETREVGHGDLKQAPWPKQSVPELAKAC 697

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QY 718 TTIIVASALHAANVFGQYVAGYLPNPTASRRPMPEPGSHDYKLCAGQKEADWVEIR 777
DB 698 TTIIWIGSALHAANVFGQYVAGYLPNPTASRRPMPEPGTEEYAEAL---BRDPERAFIH 754

QY 778 TITTSQFQILGISLIEILSKHSSDEVYLGQRDEPRMTSDAKALDAFRRFGSRLVQIENR 837
DB 755 TITTSQIITIGVSLLEVLVSKHSSDELYLGQRDTPE-WTSDPKALEVFRFRFDRLEIIESK 813

QY 838 IKTWNDSPLKNRKGVPVPMYMLYPNTSDVTGEKAEGLTAMGIPNSISI 887
DB 814 VVGMNHDPELKNRNGPAKPPYMLLYPNTSDHKG-AAAGLTAKGIPNSISI 862

RESULT 2
ID LOX2 ORYSA STANDARD; PRT; 865 AA.
AC P29250;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxxygenase L-2 (EC 1.13.11.12).
GN LOX1.1
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
ON NCBI_TaxID=4530;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN:cv. Nipponbare;
RX MEDLINE=92283256; PubMed=1597177;
RT "cDNA cloning of rice lipoxxygenase L-2 and characterization using an
active enzyme expressed from the cDNA in Escherichia coli.";
RL Eur. J. Biochem. 206:331-336(1992).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X64396; CAA45738.1; -.
DR PIR; S23454; S23454.
DR HSP; P08170; 2SBL.
DR Gramene; P29250; -.
DR InterPro; IPR000907; Lipoxxygenase.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR008976; PLAT LH2.
DR Pfam; PF00305; lipoxxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE 2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Oxidoreductase; Dioxxygenase; Iron; Multigene family.
KW DOMAIN 38 158
FT DOMAIN 38 158

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Db 76 AYLENFLLTLPLAAGATAGVTFDWNBEFGVGFVFKNMHNEFFLKSLTLESDVPHG 135
QY 142 TVFVANSWVPHKLYSCERIFENDTVLPKMPAAALVPVRODELKILRGDDNPGPYQEH 201
Db 136 KVHFVCSNVVPSFRYKIDRIFANQPLPSETPELLKRYENELVIRG-DGFGKKEAW 194
QY 202 DRVRYDYNDLGDPPDKGEHARPLFGSQBHPYPRKCRGTGRHPTKDPNSESRL-FLN 260
Db 195 DRIVDYNDVNDLGNPDQGNVUTLGGSDADYPYPRGRTGRPTRTDPKSESRIPLLS 254
QY 261 LNIYVPRDERGHLKMSDFLCYSKTLIEAVLPLTGTFVDDTPKPFDSFEDILGLYLP 320
Db 255 LDIVYPRDERGHLKMSDFLTALKSVQFLLPELHAFDGTNPFDNFSDVRLYEGGI 314
QY 321 EAPNPLIAEIRKIPSEFLRSIILPNSGSHDHPKMPLEFNVIKSDVLKKAPEFFKGMRTDE 380
Db 315 KLPOQLFKALTDALPELWIRELLRTDG-EGILRFPPLVIX-----DSKTAWRTDE 365
QY 381 EFARETLAGVNPVILKLTETEPKASTLDPROYGHSTKITEAHIRHNWGLSVONALRNK 440
Db 366 EFAREMLAGVNPVILSRLLEFPFKSKDPELYGNQNSTITAEHIEGKLDGLTIDEAINS 425
QY 441 RLFLDHDHFMFVDEINELEGNFIYASRTLLFLKDDGTLKPLAIELSLPHPDGQORGA 500
Db 436 KLFILNHEDVLIPLYLRINTWTTK-TYASRTLLFLQDNGSLKPLAIELSLPHPDGQFGV 484
QY 501 VSKVYTPAHTGVGHVWQOLAKAYACVNSAHQILISHNLNTHAVIEPFIATNRQLSVH 560
Db 485 TSKVYTPSDQGVGSINQOLAKAYAVNDSGVHQLISHNLNTHAVIEPFIATNRQLSVLH 544
QY 561 PVHKLSSPHYRDLINALARQTLINAGGVFERTVPKAYALGMSADVYKSWNFNEQALP 620
Db 545 PIHKLLYPHFDTNWINALARQILINAGGVLESTVFPKAMENSAYVYKDWFPDQALP 604
QY 621 ADLVKRGVAVDPQSPGVRLIKDYPYAVDGLVIMWAIERWYKEYLDIYPNDGELQRD 680
Db 605 ADLVKRGVAVDSSPHGVRLIDDPYAVDGLVIMWAIERWYKEYLDIYPNDGELQRD 664
QY 681 VELOAWKVEVEEAHGLDKDRMDWPRMDTVQOLARACTTIWASALHAAVNRQGPYAG 740
Db 665 NELQAWKVEVEVGHGKXKPNWAEWETPGLDSDCTTIWASALHAAVNRQGPYAG 724
QY 741 YLPNRPASRRMPPEPSHDYKYLKAGQKADMYFIFITTSQPTLIGLSILBILSKHS 800
Db 725 YLPNRPVSRKFMPEPGTPEEEL---KQNPDKAFLKTIQAQLQTLGLVSLBILSRHTT 781
QY 801 DEVYLGORDEPDRWTSKALDAFKRGLVQIENRIKTMWDSPLDKNKGVPMPYML 860
Db 782 DEIVLQGRESE-WTKQKEPLAERFGNKLTIDIEQIMORNGNLIITNRTGPNAPYTL 840
QY 861 LYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 841 LFPTSEG-----GLTQKGIPINSVSI 860

RESULT 4
LOC1_ARATH
ID LOC1_ARATH STANDARD; PRT; 859 AA.
AC Q06327;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase 1 (EC 1.13.11.12).
GN LOC1 OR AtIGS5020 OR F14C21.3 OR F14C21.54.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Root;
RX MEDLINE=94105302; PubMed=7506426;

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RA Melan M.A., Dong X., Endara M.E., Davis K.R., Ausubel F.M.,
RA Peterman T.X.;
RA "An Arabidopsis thaliana lipoxygenase gene can be induced by
RT pathogens, abscisic acid, and methyl jasmonate.";
RL Plant Physiol. 101:441-450(1993).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Landsberg erecta;
RC MEDLINE=94137782; PubMed=8305494;
RA Melan M.A., Nemhauser J.M., Peterman T.X.;
RA "Structure and sequence of the Arabidopsis thaliana lipoxygenase 1
RT gene.";
RL Biochim. Biophys. Acta 1210:377-380(1994).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White C., Alonso J., Alcáfi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Krenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Ienz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: BY WOUNDING, ABSISIC ACID (ABA) AND METHYL JASMONATE.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAR domain.
CC -----
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CC -----
CC EMBL; L04637; AAA32827.1; -
CC EMBL; U01843; AAA17036.1; -
CC EMBL; AC069144; AAG51123.1; -
CC F01; JQ2267; JQ2267.
CC HSP; F08170; 2SBL.
CC InterPro; IPR000907; Lipoxygenase.
CC InterPro; IPR001024; Lipoxygenase_LH2.
CC InterPro; IPR008976; PLAT_LH2.
CC Pfam; PF00305; lipoxygenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS50095; PLAT; 1.

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KW Oxidoreductase; Dioxigenase; Iron; Multigene family.
FT DOMAIN 21 161 PLAT.
FT METAL 519 519 IRON (BY SIMILARITY).
FT METAL 524 524 IRON (BY SIMILARITY).
FT METAL 711 711 IRON (BY SIMILARITY).
FT METAL 859 859 IRON (BY SIMILARITY).
SQ SEQUENCE 859 AA; 98045 MW; 493788BACD5FF579 CRC64;

Query Match
Best Local Similarity 55.6%; Score 2626.5; DB 1; Length 859;
Matches 512; Conservative 128; Mismatches 211; Indels 31; Gaps 13;

QY 8 DLTGKKNKAESEKIRGTVRLVKEVLDVGFNLSLDGVHRIILGWDGVAFOLVSATA 67
DB 7 DLTGCGNETTK-KVKGTVVLMKKNVLDNFDFNLSLDGVHRIILGWDGVAFOLVSATA 63

QY 68 ADPSNGCRKGVKAHLEAVVSLKSTADGETVYRVSVFEDWSQIGPAGVLRNQLQAEF 127
DB 64 TSENGSKGLKGAHLEADWITITSLTAGESAPKVTDYEDTDFYGPAGFLIRSHFSEF 123

QY 128 FLKTLTLEGVPOKGVTVFVANSWYTHKLYSRIFFANDTYLPKMPAAALVYRQDELK 187
DB 124 LLKSLTLEDPVGHGRVHVCNSWYPAKHYYTDRVFFSNKTYLPHETATLLKYREELV 183

QY 188 ILRGDNDPGYOEHRVRYDYNDLGDGDKEEHARPLGGSQSHYPRECRTRGHPK 247
DB 184 SLRG-TGSELKENDRVYDIAYINDLVPPK---NPRPVLGQTYPPRRGRTGRKPTK 239

QY 248 KDPNSESRL-FLNLNLYVPRDERFGLKMSDFLGYSKTTIEAVLPTLGTFFVDDTPKEF 306
DB 240 EDPQTESRLPITSLDIYVPRDERFGLKMSDFLAYALKATQIOPALEAVFDDTPKEF 299

QY 307 DSFEDILGILGPGAPNPLAEATKIPSEFLASILPNSHSHDPLKMP;PNVKSVDL 366
DB 300 DSFEDVLKLYERGIDLPQALIDSIVKNLPLEMLKEIFRTDQKPF-LKFPVPQIKED-- 356

QY 367 KKAPFKFGWRDEEFARETLAGVNPVITKRTEPPAKSTLDPDROGHTSKITEAHIRH 426
DB 357 -----KTAWRTDEEFARETLAGVNPVITKRTEPPAKSTLDPDROGHTSKITEAHIRH 410

QY 427 NMGSLVQNALNKFLFILDHHDHMPVLDDEINELEGNFTVASRTLLFKDDGTLKPLAI 486
DB 411 NLDGTLTVEALEKEFLFILDHHDHMPVLDDEINELEGNFTVASRTLLFKDDGTLKPLAI 469

QY 487 ELSLPHDPQQRGAGVSKVYTPAHTGVEGHVWOLAKAYACVNDASWHQLISHLANTHAVIE 546
DB 470 ELSLPHDPNGDKFAGVSEVYTPGE-GVYDSLWQLAKAFVGVNDSGNHQLISHWQTHASIE 528

QY 547 PVIATNRQLSVVPHKLLSPHYRDTLNINALARQTLINAGGVFERTVFFPAKVALGNSA 606
DB 529 PVIATNRQLSVLHPVFKLEPHFRDTWNINALARQTLINAGGVFERTVFFPAKVALGNSA 588

QY 607 DVYKS-WNFNEQALPADLVKRGVAVPDOSSPGVVELLIKDYPAVDGLVIVWATERWYKE 665
DB 589 FIYKHWTFPDQALPAELKRGMAVEDPEAPGLRLKIDPYAVDGLVIVWATERWYKE 648

QY 666 YLDIYVNDGELQDRVLOQAWKVEYREAHGDLKDRDWRMDTVQQLARACTIIVWAS 725
DB 649 YIFLFYKIEEDIQTDTLQAWKVEYREAHGDLKDRDWRMDTVQQLARACTIIVWAS 708

QY 726 ALHAAVNFQGYVAGVLRNPATSPRPMPEFGSHDYKLGAGQKQADWVFTITTSQFOT 785
DB 709 ALHAAVNFQGYVAGVLRNPATSPRPMPEFGSHDYKLGAGQKQADWVFTITTSQFOT 765

QY 786 ILGISLILSKSHSDEVYLGQRDPRDWTSDAKALDAFKRFGSLVQIENRIKTMNDSP 845
DB 766 ILGISLILSKSHSDEVYLGQRDPRDWTSDAKALDAFKRFGSLVQIENRIKTMNDSP 824

QY 846 DLKRRKGPVEMPMYLLYNTSDVTGKAEGLTAMGIPNSISI 887
DB 825 TLKRRKGPVEMPMYLLYNTSDVTGKAEGLTAMGIPNSISI 859

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RESULT 5
LOXI_SOLUTU STANDARD; PRT; 861 AA.
AC P37831;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Lipoxigenase 1 (EC 1.13.11.12).
GN LOX1-1 OR LOX1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Tuber;
RX MEDLINE=95175602; PubMed=7870815;
RA Casey R.;
RT "Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber
  lipoxigenase."
RL Plant Physiol. 107:265-266(1995).
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
  DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
  DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
  WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
  A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
  hydroperoxyoctadeca-9,11-dienoate.
CC -1- COFACTOR: Iron, one atom tightly bound per molecule.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
EMBL; X79107; CAA55724.1; -
PIR; S44940; S44940.
HSP; P09186; ILNH.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR KEGG; K01000; Lipoxigenase; Iron; Multigene family.
FT DOMAIN 29 160 PLAT.
FT METAL 522 522 IRON (BY SIMILARITY).
FT METAL 527 527 IRON (BY SIMILARITY).
FT METAL 713 713 IRON (BY SIMILARITY).
FT METAL 861 861 IRON (BY SIMILARITY).
SQ SEQUENCE 861 AA; 96966 MW; 09732AG751DEE20D CRC64;

Query Match
Best Local Similarity 55.0%; Score 2597; DB 1; Length 861;
Matches 508; Conservative 112; Mismatches 222; Indels 26; Gaps 10;

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QY 22 KIRGTVRLVKEVLDVGFNLSLDGVHRIILGWDGVAFOLVSATAADPSNGCRKGVKA 81
DB 18 KVKGTVVLMKKNVLDNFDFNLSLDGVHRIILGWDGVAFOLVSATAADPSNGCRKGNP 75
QY 82 AHLEAVVSLKS-TADGETVYRVSVFEDWSQIGPAGVLRNQLQAEFFLTKLTLEGVPGK 140

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Db 76 AYLENSLTFLTAGSTAFGVTFDWNNEEGVPCATIIKMHINEFFLSLTLEDVPHN 135
QY 141 GTVVVANSWYVPHKLYSQEIRIFANDTYLPKSKMAALVPYRDELKILRGDNDPGVQE 200
Db 136 KGVHVCNSWYVPSLNYKSDRIIFANQVPLESEVPELLKRYRENELLTLRG-DGTGREA 194
QY 201 HDRVRYDNDLGDGPKGEHARPILOGSOEHYPYRCRTGRHPTKKDNSSRL-FL 259
Db 195 WDRYDYDNDLGNPDGKENVTTLGGSAEYYPYRGRGTGRPTTDPKSESRIPL 254
QY 260 NLNIVPRDERFGLKNSDPLGYSKTIIBAVLTGLTGFVDDTKPEFSDILGLYELG 319
Db 255 SLDIYVDERFGLKNSDFTYALKSVIQLPELHALDGTNPEDSFEDVRLYEGG 314
QY 320 PEAPNPLIABIRKIPSEFLRSILPNSGHDHPLKMLPNVYKSVLKAPEKFGWRD 379
Db 315 IKLQGPLFKALTAAPLEMRRELTG-EGILRFPPLVIK-----DSKTAWRTD 365
QY 380 EEFARETLAGVNPVILKELTEFFAKSLDPRQYGDHTSKITEAHIRHNVGSLVQNALRN 439
Db 366 EEFAREMLAGVNPVILSRQLQFPKSLDPAFAYGNQNSTTAEHIEDKLDGLTVDEAMN 425
QY 440 KRLFILDHHDHMPYLPDEINELEGNFYASRTLLFLKDDGTLKPLAIELSLPHDPGQRG 499
Db 426 NKLFLANHHVIIIPYLRINTTITK-AYASRTLLFLQDNGSLKPLAIELSPHPDQFG 484
QY 500 AVSKVYTPAHRFVGEHGWOLAKACVNDNSAHQOLISHMLNTHAVIEPFIATNQLSVV 559
Db 485 VTSKYVTPSDQGVSSIWOLAKAVAVNDGVHQLISHMLNTHAVIEPFIATNQLSVL 544
QY 560 HPVHKLASPHYRDLINALAROTLINAGVFERTVFPKAYALGMSADVYKSNFNEQAL 619
Db 545 HPIHKLLYPHPTDMNINASARQLLVNAGVLESTVFSKFAMEMSAVVYKDWVFPDQAL 604
QY 620 PADLVKGVAVPDOSSPYGRVLLIKDYPIYAVDGLVIMWAIERWVKEVLDIYPNDGELQ 679
Db 605 PADLVKGVAVDESSPHGRVLLIEDYPIYAVDGLVIMWAIERWVKEVLDIYPNDGELQ 664
QY 680 DVELQAWWKEVREAHGDLKORDWPRMDTVQQLARACTIIIVASALHAANVFGVPYA 739
Db 665 DNEIQAAMWKEVREAHGDLKORDWPRMDTVQQLARACTIIIVASALHAANVFGVPYA 724
QY 740 GYLNRPTASRRPMPGSHDYKKGAGQKADWVFRTTSQFTILGSLIEILSKGS 799
Db 725 GYLNRPTASRRPMPGSHDYKKGAGQKADWVFRTTSQFTILGSLIEILSKGS 781
QY 800 SDEVYLGQRDPDRWTSADAKALDAFRRGSLVVOENRIKTMNDSPLKVRKGPVEMPYM 859
Db 782 TDEIYLGQRESPE-WTKDKEFLAAPDRFGKLTIDIEKQIIQRNGDNLTTRSGFVAPYT 840
QY 860 LLYPNTSDVTGEKAEGLTAMGIPNSIS 887
Db 841 LLFPTSEG-----GLTKGIPNSVSI 861

RESULT 5
LOCB_LYCES
ID LOCB_LYCES STANDARD; PRT; 859 AA.
AC P38416;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase B (EC 1.13.11.12).
GN LOX1.2 OR LOXB.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Caruso; TISSUE=Pericarp;

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RX MEDLINE=95062736; PubMed=7972514;
RA Ferrie B.J., Beaudoin N., Burkhart W., Bowsher C.G., Rothstein S.J.;
RT "The cloning of two tomato lipoxigenase genes and their differential
RL Plant Physiol. 106:109-118(1994).";
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Fruit specific.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; U09025; AAA53183.1; -
DR FIR; T06339; T06339.
DR HSP; P09186; L1NH.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR01024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT_1.
DR SMART; PRO0087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR OXidoreductase; Dioxygenase; Iron; Multigene family.
KW DOMAIN 34 158
FT METAL 521
FT METAL 526
FT METAL 711
FT METAL 859
SQ SEQUENCE 859 AA; 97122 MW; DAD79B10AE627434 CRC64;
Query Match 53.1%; Score 2510; DB 1; Length 859;
Best Local Similarity 56.7%; Pred. No. 1.7e-173; Indels 32; Gaps 13;
Matches 502; Conservative 111; Mismatches 240;
QY 5 GVADRLTGKKEAMSEKIRGTVRLVKEVLDVGDVFNASLLDGVHRILGMDGVAFLVLS 64
Db 5 GIVDAILGKD---DRPKVGRVILMKKNVLDNFNIGASVVDGISDLIG--QKVSILQLS 58
QY 65 ATAADPSNGRGKVKCAHLEAEVSLKSTADGETVYRVSVSEWDESQ-GICAVLVRNLQ 123
Db 59 GSV--NYDGLGKLSNPAYLSWLTDTITTAGSTSTFVTDWRDREDFGVGFATIKNLH 116
QY 124 HAEFFLTKLTLEGVPGKGVVFNANSWYVPHKLYSQEIRIFANDTYLPKSKMAALVPYRQ 183
Db 117 LNEFFLKSILTLEDVNYKIHFCVNSWYVPAFYKSDRIIFANQVPLESEVPELLKRYRE 176
QY 184 DELKILRGDNDPGPYQEHDRVRYDYNDLGDGPKGEHARPILOGSOEHYPYRCRTGR 243
Db 177 NELVALRG-DGTGKLEEDWDRYDYACVNDLGEDEPKGEYARPILOGSEYYPYRGRGTGR 235
QY 244 HPTKDPNPSERLFL-LNLIYVPRDERFGLKNSDPLGYSKTIIBAVLTGLTGFVDDT 302
Db 236 EPTKADPNCESRNPJPMSLDIYVPRDERFGLKNSDPLGYSKTIIBAVLTGLTGFVDDT 295
QY 303 PKEFOSFEDILGLVELGPEAPNNPLIAIRKKIPSEFLRSILPNSGHDHPLKMLPNV 362

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Db 296 PNEFNSFADVLNLYEGIKLPGPMLKAITDNISSEILKDIILQTDQG-LLKYPTFPQVIQ 354
Qy 363 SDVLKKAPEFKGWRDEEFARETLAGVNPVILKLTREPAKSTLDPQYGDHSTKITEA 422
Db 355 GD-----KTAWRITDEEFGREMLAGSNPVLISRLQBPFPKSKLDPTIYGNQNSTITTE 406
Qy 423 HIRHNMGGLSVQNALRNKELFILDHHDHMPYLDINELEGNFIVASRTLLFLKDDGTLK 482
Db 407 HVQDKLNGLTVEAIKSNELFILNHDIWPLLRKINMSANTKAYASRTLLFLQDDRLK 466
Qy 483 PLAIELSLPHDQOQBGAVSKYTPAHTGVGHVQOLAKAYACVNDSSAWHQLISHWLNTH 542
Db 467 PLAIELSLPHDQDQGTYSKYTPADQGVESIQWQAKAYAVNDMGIHQHLSHLNTH 526
Qy 543 AVIEPVIATNRQLSVVHVHKLSPHYRDTLINALAROTLINAGGVFERTVFPKAYAL 602
Db 527 AVIEPVIATNRHLSVLHPIHKLHPHFENTWINALAREILTYDGG-FETSLFPKYSM 585
Qy 603 GMSADVYKSWNFNEQALPADLVKRGVAVDPQSPYGVRLLIKDYPIYAVDGLVWIAIRW 662
Db 586 EMSAAAYKDWVPEQALPADLVKRGVAVEDLSPHGIRLLILDYPIYAVDGLVWIAIRW 645
Qy 663 VKEYLDIYVNDGELORDVLOQWKEVREAHGDKORDWPRMDTVQOLARACTTIW 722
Db 645 VKEYCKFYKSDTEVEKOTELQAWKELREZEGHGDKEAWPKLQTRQELADCCITIIW 705
Qy 723 VASALHAANVFGQYVAGVLPNRPASRRPMPPEPGSHDYKLGAGQKADVMVFTINTPSQ 782
Db 706 IASALHAALHFLGYSYAGVLPNRPASRRPMPPEPGSHDYKLGAGQKADVMVFTINTPSQ 762
Qy 783 FOTILGISLIELTSLKSHSDEVVLGORDPDRWTSDAKALDAPKRGSLVOIENRIKTMN 842
Db 763 LAGLLEISIFVSSRHASDEVVLGORDSIE-WTKDEFLVAFERPGKMLSDIENRIMNMN 821
Qy 843 DSPDLNKRKGPVEMPYMLLPNTSDVTGKAEGLTAMGIPNSISI 887
Db 822 SHKSWKNSRGPVNPVYTLFF-TSE-----EGLGKGIPIVSVSI 859

RESULT 7
LOX2_SOYBN STANDARD; PRT; 865 AA.
AC P09439;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase-2 (EC 1.13.11.12) (L-2).
GN LOX1.2 OR LOX2.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88198254; PubMed=2834391;
RA Shibata D., Steczko J., Dixon J.E., Andrews P.C., Hermodson M.,
RA Axelrod B.;
RT "Primary structure of soybean lipoxigenase L-2.";
RL J. Biol. Chem. 263:6816-6821(1988).
RN
SEQUENCE OF 231-865 FROM N.A.
RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,
RA Altschuler M.;
RT "Two soybean seed lipoxigenase nulls accumulate reduced levels of
RT lipoxigenase transcripts.";
RL Plant Mol. Biol. 7:11-23(1986).
CC
-!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.

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CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 691
CC TO 865 DUE TO A FRAMESHIFT.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; J03211; AAA33987.1; -.
CC PIR; A28161; DASYL1.
CC HSP; P08170; 2SBL.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR001024; Lipoxigenase_LH2.
CC InterPro; IPR008976; PLAT LH2.
CC Pfam; PF00305; lipoxigenase; 1.
CC Pfam; PF01477; PLAT; 1.
CC PRINTS; PR00087; LIPOXYGENASE.
CC SMART; SM00308; LH2; 1.
CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
CC PROSITE; PS00095; PLAT; 1.
CC Oxidoreductase; Dioxygenase; Iron; Multigene family.
KW DOMAIN 50 175
FT METAL 527 527 IRON (BY SIMILARITY).
FT METAL 532 532 IRON (BY SIMILARITY).
FT METAL 718 718 IRON (BY SIMILARITY).
FT METAL 865 865 IRON (BY SIMILARITY).
FT CONFLICT 263 264 KP -> NL (IN REF. 2).
FT CONFLICT 313 313 D -> Y (IN REF. 2).
FT CONFLICT 400 400 L -> P (IN REF. 2).
FT CONFLICT 428 428 L -> H (IN REF. 2).
FT CONFLICT 486 486 D -> G (IN REF. 2).
FT CONFLICT 502 502 V -> G (IN REF. 2).
FT CONFLICT 534 534 V -> L (IN REF. 2).
SQ SEQUENCE 865 AA; 97145 MW; 74CDD32E3E4A0C85 CRC64;

Query Match 52.6%; Score 2486; DB 1; Length 865;
Best Local Similarity 54.5%; Pred. No. 9.4e-172;
Matches 487; Conservative 137; Mismatches 196; Indels 74; Gaps 15;

Qy 22 KIRGTVLVKKEVLD---VGDFN-----ASLLDGVHRIIGWDGVAFLV 63
Db 18 KIRGTVLVKRNKVLDPNSVADLTGKNGVGLITGLNVVGTSLDNLTAFLG--RSVALQI 75

Qy 64 SATADFPNSGKRGKVGKAAHLEAEVVSLSKSTADGETVYRVSEFWEDESQIGAVLVRNLQ 123
Db 76 SAT--KPLANGKGVKGVKDTFLEGLIVSLPTLGAGESAFNIQFEWDESMGIPGAFYIKNYM 133

Qy 124 HAEFFLKTITLGVPGKGVTFVANSWYVPHKLYQSERIFFANDTYLPSKMAALVPIRQ 183
Db 134 QVEFYLSLUTLEDVFNQGTIRFCVNSWVYNTKLYKSVRIFFANHTYVPSTPAALVGYKE 193

Qy 184 DELKILRGDNDPGPYQEHDRVYRYDNDLGPDPDKEEHARPTLGSGQSHYPYRRCTGR 243
Db 194 EELKNLR-DGKERKEHRIYDYVDYNDLGNPDHGENFARPLTGGSTHYPYRRGTR 252

Qy 244 HPTKDPNSESRLFLNLNINIVPRPERFHLKMSDFLGLSKLTITTEAVLPTLTGTFVD--D 301
Db 253 YPTRKDQNSEK-----PGEVYVPRDENFGLKSSDFLAYGIKLSQYVLPAPESVFDLNF 307

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QY 667 LDIYYPNDGELQDVQLQAWKEVREAEHGDLDKDRDMPMDTVQOLARACTTIWVASA 726
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
648 VELYKSDDTLREDPELQACWELVEVGHGDKKNEPWPQWQTRLEVEACALIWTASA 707
QY 727 LHAANFGQYPYAGVLPNRPASRRPMPPEPGSHDYKKGAGOKEDMWFIPTISQFOTI 786
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
708 LHAANFGQYPYGGILNRPPTLSRRPMPPEKGAEEEL---RKNPQKAYLTKITPKFTL 764
QY 787 LGISLIEILSKSHSDEVILQORDEPRMTSDAKALDAFKRFSRLVQIENRIKTMNDSPD 846
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
765 IDLSVIELSRHASDEVILGERDNP-WTSDTRALEAFKRGKLAQIENKLSERNDK 823
QY 847 LKNRKGVPMPYMLYPNTSDVTGKABGLTAMGTPNSISI 887
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
824 LNRRCGPVMPYTLPLPSK-----EGLTFRGIPNSISI 857

RESULT 9
LOX2_PEA STANDARD; PRT; 864 AA.
AC F14856;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seed lipoxigenase-2 (EC 1.13.11.12).
GN LOX1.2
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Birte;
RX MEDLINE=90147555; PubMed=2515855;
RA Ealing P.M., Casey R.;
RT "The cDNA cloning of a pea (Pisum sativum) seed lipoxigenase.
RT Sequence comparisons of the two major pea seed lipoxigenase
RT isoforms.";
RL Biochem. J. 264:929-932 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Birte;
RA Casey R.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE AND SENESCENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
DR EMBL; X17061; CAA34906.1; -
DR EMBL; X78580; CAA55318.1; -
DR PIR; S07075; S07075.
DR HSSP; P08170; 2SBL.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.

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DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase; Dioxigenase; Iron; Multigene family.
KW DOMAIN 46 171
FT METAL 524 524 IRON (BY SIMILARITY).
FT METAL 529 529 IRON (BY SIMILARITY).
FT METAL 716 716 IRON (BY SIMILARITY).
FT METAL 864 864 IRON (BY SIMILARITY).
FT CONFLICT 333 333 L -> I (IN REF. 2).
FT CONFLICT 562 562 MISSING (IN REF. 2).
FT CONFLICT 578 578 L -> I (IN REF. 2).
SQ SEQUENCE 864 AA; 97133 MW; 2919AF5FA272CDF CRC64;

Query Match 52.1%; Score 2458.5; DB 1; Length 864;
Best Local Similarity 54.8%; Pred. No. 9.1e-170;
Matches 486; Conservative 128; Mismatches 216; Indels 57; Gaps 15;

QY 22 KIRGTVRLVKEVLD-----VGDFN-----ASLLDGVHRIILGWDGVAFLV 63
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 KIRGTVLVRKKNVLDFTNTIVSIGGVHGVDSINIGTIDGLTAFLG--RSVSLQLI 71
QY 64 SATADPSNGRGKVGKAAHLEAVVSLKSTADGTVTVRVSEWDESGQIPGAVLRNLQ 123
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
72 SATKSDAN--GKGVGKDTFLEGLASPTLGAGESAPNHFWDHEMGIPGAFYKKNY 129
QY 124 HAEFFLTKLTLEGVPGKGVVAVNSVYVPHKLYSQERIFFANDTYLPSKMPAALVPYRQ 183
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
130 QVEFFLKSITLEDVPHNGTIRFVCSWYNSKLYSPRIFFANKSVLSETPSLVKYRE 189
QY 184 DELKILRGDNDPGPQEHDRVTRYNDLGDPPDGEHARHILGSGSEHPYRRCRGR 243
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
190 BELQTLRG-DGTGERKLEHRIYDYNDLGNPDGHEHARILGSGSTHYPYRRCRGR 248
QY 244 HPTKDPNSESRLFLNLNIVYPRDERFGLHQLKWSDFLGYSLKTIIEAVLTGLTFVD--D 301
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
249 YPTRKDPNSEKPA---TETVYPRDENFGLKSSFLAYGKSVQCVVPAPESAFDLNF 304
QY 302 TPKEFDSFEDILGLVELGPEAPNPLIAIRKIPSEFLRSLPNSGSHDHPMLPNVI 361
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 TPNEFDSFQVRLNLEGGIKLPDVI STLSPVVKEIFRT-----DGEVLKFTPPHVI 359
QY 362 KSDVLKKAPEFFKGRWTEEFARETELAVGNVPIIKRLTEFFPAKSTLDRQYGDHNSKITE 421
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
360 RVS-----KSAMWTEEFAREWLAGVNPQWIRGLQEFPPKSNLDPAEYGDHNSKISV 411
QY 422 AHIRENMGSLVQNALRNKRLFILDHDFHFMPLYDEINELEGNFTYASRTLLFLKDDGTL 481
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
412 DVL--NLDGCTIDEALASGRLLFDYDHTFPFLRRINETSARAYATRTILFKENGT 468
QY 482 KPLAIELSLPHDPDGOORGNAVSKVYTPAHTVEGHVWQLAKAYACVNSAHQLISHWLT 541
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
469 KPAVIELSLPHDPDGOORGNAVSKVILLPADEGVESTIWLAKAYVNVVWVSCYQLMSHWLT 528
QY 542 HAVIEFFVIATNRQLSVVHPVHKLSPHYRDT-LAINALARQTLINAGVFERTVFPARY 600
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
529 HAVIEFFVIATNRQLSVVHPINKLAPHYRDTMWINALARDSLINANGLIERSPLSKY 588
QY 601 ALGMSADVYKSNWNEQALPADLVTRGVAVPDQSSPYGVRLLIKDYPAVNDGLVWIAIE 660
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
589 AVEMSSAVYKWWFTDQALPNDLIKRNNAVVDSSPYGLRLIEDIYPYAVDGLIEIWTAK 648
QY 661 RWVKEYLDIYYPDCELOQDVLEQAWKEVREAEHGDLDKDRDMPMDTVQOLARACTTI 720
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
649 TWVQYVSLYATDNDIKNDSELQHWKEVVEKGHGDLDKDPWPKLQTFPDELVEVCTII 708
QY 721 IWSALHAANVFGQYPYAGVLPNRPASRRPMPPEPGSHDYKKGAGOKEDMWFIPTIT 780
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
709 IWSALHAANVFGQYPYAGVLPNRPASRRPMPPEPGSHDYKKGAGOKEDMWFIPTIT 765

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QY 781 SOFTTILGILBILKSHSDEVYLGQRPDWTSDAKADAFKRFGRSLVQIENRIKT 840
Db 766 PKFTLIDLVSILSRHASDEVYLGQRENPHWTSKALQAFKFGKLAIEIAKLTN 824
QY 841 MNDSPDLKRGKGVEMPYMLLYENTSDVTGKAEGLTAMGIPNSISI 887
Db 825 KNNDPSLYHRVGPVQLPYTLHPSSK-----EGLTFRGIPNSISI 864

RESULT 10
ID LOX3_PEA STANDARD; PRT; 861 AA.
AC P0918;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
GN Seed lipoxigenase-3 (EC 1.13.11.12).
OS LOX1.3.
ON Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3886;
RN [1]
RN NCBI_TaxID=3886;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Birte;
RX MEDLINE=89025643; PubMed=3140791;
RA Baling P.M., Casey R.;
RT "The complete amino acid sequence of a pea (Pisum sativum) seed
RT lipoxigenase predicted from a near full-length cDNA.";
RL Biochem. J. 253:915-918(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Birte;
RA Casey R.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENSATION OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -1- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienol + H2O.
CC -1- COFACTOR: Iron.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the lipoxigenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07807; CAA30666.1; -
DR EMBL; X78581; CAA55319.1; -
DR PIR; S01142; S01142.
DR HSP; P09186; 1LNH.
DR InterPro; IPR00907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE 2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase; Dioxygenase; Iron; Multigene family.
FT DOMAIN 41 166
FT METAL 522 522 IRON (BY SIMILARITY).

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FT METAL 527 527 IRON (BY SIMILARITY).
FT METAL 713 713 IRON (BY SIMILARITY).
FT METAL 861 861 IRON (BY SIMILARITY).
SQ SEQUENCE 861 AA; 97628 MW; 442510278225D750 CRC64;

Query Match 51.6%; Score 2437; DB 1; Length 861;
Best Local Similarity 53.4%; Pred. No. 3.3e-168;
Matches 471; Conservative 148; Mismatches 213; Indels 50; Gaps 14;

QY 22 KIRGTVRLVKKEVLVVG-----DFNASLLDGVHRLGWDGVAFLVSTAA 68
Db 14 KIRGTVLMRKQVLDINSLLTVGVIGQFDILGSTVDNLTAFLG--RSVSLQLISATKP 71
QY 69 DPSNGGRGKVGKAAHLEAEVAVVSLKSTADGETVVRVSPFVDESDQIGPAVLVRLQHAFF 128
Db 72 DAT--GKGLGKATFLGSIUPTLGCAGSAFKIHFEDDDMGIGPAFYIKFMQTEFF 129
QY 129 LKTLTLGVPKGVTVFVANSWVPHKLYSQERIFFANDTYLPSKMPAALVPRQDLKI 188
Db 130 LVSLTLDIPNHGSIYFVNCNWIYNAKHKIDIFFANQTYLPSFETPAFLVHYREEELNN 189
QY 189 LRGDNDPGVQEHDRVRYVDYNDLGDPDGGEHARPILGSOEHPYPRCRRGHPHKK 248
Db 190 LRG--DGTGERKEWERIYDYVDYNDLGNPDGENHARFVLSGSETYPYPRGRTGRKTRK 248
QY 249 DPNSERLFLNLNIVYPRDERFGLHLMQSDFLGYSKLTIEAVLPTLGTTFVD--TPKE 305
Db 249 DPNSER--SDYVYLFDRDEAFGLKSSDFTLYGLKAVSQNVVPALESVFFDLNFTPE 304
QY 306 FDSFEDILGLYELGPEAPNPPLIAETIRKTPSEFLRSILPNSGSHDHPKPLPNIKSDV 365
Db 305 FDSFDEVHGLYEGGIKLPTN--ILSQIS---PLPVLEIFRTDG--ENTLKYPKPVQVVS- 358
QY 366 LKAPPEKFGWRITDEEPARETLAGVNPVILIKRTEPPAKSLDPRQVGDHSTKITEAHIR 425
Db 359 -----RSGWMTDEEPAREMLAGVNPVILCCLQEPFRSKLDSQIYGDHSTKISKHELE 411
QY 426 HNMGLSVQNALNRKFLILDHHDHMPYLDENELGEGFIYASRTLLFLKDDGTGKPLA 485
Db 412 PNEGLTVEAIGKQLFLDHDHDSIMPYLRINSTGK--AYATRTLLFLNNQNLKPLA 470
QY 486 IELSLPHDPGQQRGAHSVYTPAHTGVGHVWOLAKAYACVNDSAWHQLTSHWLNTHAVI 545
Db 471 IELSLPHDPGQDEGAVSVYTPALEGVSSILWLAAYVINDSCYHQLVSHWLNTHAVV 530
QY 546 EPPVIATNRQISLVHPVHKLLSHYRDTLNINARQTLINAGGVFERTVFPKAYALGMS 605
Db 531 EPPVIATNRHLSCLHPYIKLLYPHYRDTWNINSLARLSLVNDGGIIEKTFMGYSNEMS 590
QY 606 ADVYKSNFNEQALPADLVKRGVAVPDQSPYGVRLIKDYPYAVDGLVWMAIERWVKE 665
Db 591 SKVYKNWVTEQALPADLILKRGMAIEDPSPFCGVKLWVEDYPYAVDGLVWMAIERWVKE 650
QY 666 YLDIYYPNDELQDVELQAWWKEVEEAHGDLDKORDWPRMDTVOQLARACTTIIWVAS 725
Db 651 YVSLYITSDEKLQDSELQAWWKEVEVEHGDKKNEFPMPQMTREDLIEVCISIVWTAS 710
QY 726 ALHAAVNVFGQYVAGYLPNRPTASRPMPEPGSHDYKLGAGKEADMFVIRITTSQFOT 785
Db 711 ALHAAVNVFGQYVAGYLPNRPTASRPMPEPGSHDYKLGAGKEADMFVIRITTSQFOT 767
QY 786 ILGISILIELSKHSDEVYLGQRPDWTSDAKADAFKRFGRSLVQIENRIKTWNSDP 845
Db 768 LIDLVSILSRHASDEVYLGQRENPHWTSKALQAFKFGKLAIEIAKLTN 826
QY 846 DLKNRKGPVEMPYMLLYENTSDVTGKAEGLTAMGIPNSISI 887
Db 827 KLRNRGVPVEMPYMLLYENTSDVTGKAEGLTAMGIPNSISI 861

RESULT 11
LOXA_PHAVU
ID LOXA_PHAVU STANDARD; PRT; 862 AA.

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AC P27480;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipoxigenase 1 (EC 1.13.11.12).
 GN LOXA OR LOX1.
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eursoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Red Mexican; TISSUE=Leaf;
 RX MEDLINE=9417173; PubMed=8130796;
 RA Biben H.G., Siuarenko A.J.;
 RT "Complex spatial and temporal expression of lipoxigenase genes during
 RL Plant J. 5:123-135 (1994).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X63525; CAA45088.1; -
 CC PIR; S22153; S22153.
 CC HSP; P08170; 2SBL.
 CC InterPro; IPR000907; Lipoxigenase.
 CC InterPro; IPR01024; Lipoxigenase_LH2.
 CC InterPro; IPR008976; PLAT_LH2.
 CC Pfam; PF03005; lipoxigenase; 1.
 CC Pfam; PF01477; PLAT; 1.
 CC PRINTS; PR00087; LIPOXYGENASE.
 CC SMART; SM00308; LH2; 1.
 CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
 CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
 CC PROSITE; PS50095; PLAT; 1.
 CC Oxidoreductase; Dioxigenase; Iron; Multigene family.
 FT DOMAIN 44..171
 FT METAL 522
 FT METAL 527
 FT METAL 713
 FT METAL 862
 FT METAL 862
 SEQUENCE 862 AA; 97154 MW; 24D56D1CE3C191E CRC64;
 Query Match 50.9%; Score 2405.5; DB 1; Length 862;
 Best Local Similarity 53.8%; Pred. No. 6.2e-156;
 Matches 477; Conservative 132; Mismatches 224; Indels 53; Gaps 13;
 QY 22 KIRGVTVLVKKEVLVDGDFNASLLDGVHRIIG-----WDDGVAFO 61
 DB 10 KIKGVTVLVKTVDFNFVEFVSTTGGIVGAGGLFGAATDVGIVDGAIFSRNIAQ 69
 QY 62 LVSTADAPDSGKGVKGAHLEBAVSLKSTADGTVYRVGFPEWDSQGFCAVLVRN 121
 DB 70 LISATKTD--GLGKGVKGVKQTFLEKHLPSLNLGDRQDAFNVYFWEWDFEIPAFYIKN 127

122 LQHAFFFLKTLLEGVPGKGVVVFVANSWVYPHKLYSQERIIPFANDTYLPSKMPAALVPY 181
 DB 128 FMOSEFFLSLTLEDIFNEGTHFVCSWVTAASYKRDRIIFANKTYLPNETPASLVKY 187
 QY 182 RODELKILRGDDNPGPVQSHDRVYRVDYNDLGDGPKGEHARPILGGSOEHYPERCET 241
 DB 188 KKELENLRG-DGTGERKEYDRIYAVYVNDLGNPKXNKLARTILGSSDDFPYPRGRT 246
 QY 242 GRHPTKDDNSRSLFLNLNIYVPRDERFGLHKMSDFGLGYSLKTIIEAVLPTLGFVDD 301
 DB 247 GRKSTRDKPCE-----IPTSDTYIPRDNFGLKSGDFLTAYKSLTQNVLPFTQKAFG 302
 QY 302 TPKEFDSFEDILGLVELGPEADNNPLIAIRKIPSEFLRSILPNSGSHDHPKMLPNVI 361
 DB 303 N-NEFTTFEDVRGLFEGGLYLPD-----VISKISPIPVULKEILRTDG-QQVULKFPFPHVI 356
 QY 362 KSDVLKKAPEFKGMRDEEFARETLAGVNPVIIKELTEFPFAKSTLDPQYGDHTSKITE 421
 DB 357 R-VTKSA-----WMTDEFGREMLAGVNPCLIQRLQEFPPKSKLDVTVYGDQSTMTK 408
 QY 422 AHIRHNMGLSVQNALRNKELFTLDHHDHMPVLDINELEGNFIYASLTLLFLKDDGTL 481
 DB 409 EHLNINLGGTLVEEALHGNRLFILDHDAFIPYLERINDLPFAKCYATATITLFLKDDNTL 468
 QY 482 KPLAIELSLPHFDGQQRGAVSKVYTPAHTGVEGHVWQLAKAYACVNDNSAWHOLISHWLT 541
 DB 469 KPLAIELSLPNPG--KGANSRVILPADGGAESTIWLAKAYVWVNDSCYHQLMHWLNT 526
 QY 542 HAVIEPVIATNRQLSVHPVKLLSPHYRDTLINNALAROTLINAGGVFEFTVPKAYA 601
 DB 527 HAVMEPVIATNRHLSVLHPITYKLLPHYRDTMNLARQLINAGGVFIERSFLPGEFA 586
 QY 602 LGMSADVYKSMFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPIYAVDGLVIMWAIER 661
 DB 587 VEMSSAVYKSWFTDQALPADLIRKGMVDEDFSSPYGLRLVVEDYPIYAVDGLVIMWTQT 646
 QY 662 WKVEYLDIYVNDGELQORVLOAWKVEYREAHGDLKDRDWPMDTVQQLARACTII 721
 DB 647 WKVDYVSLYPIYNDVAVKDTQLQAWKKEAVKGGHGLDKPKWPKLNTPDQDIHTCSII 706
 QY 722 WVASALHAAVNFQGYPIYAGYLEPNRPTASRPMPEPGSHDYKKGAGQKEADMVFRTITS 781
 DB 707 WIASALHAAVNFQGYPIYGGFILNRRPTITRLLPEPGTKEYGELTSNYQKA---YLRTITG 763
 QY 782 QFQTILGISLILSKHSDDEVILQORDEPDWTSADALDAKDFKFGRLVQIENRIKTM 841
 DB 764 KVEAIVDLSEVILSRHASDEVILQORDNPN-WTNNIKALQAFKFGQKLEIERKIMGR 822
 QY 842 NDSPDLKRRKGPVEMPYMLLYENTSDVTGKAEGLTAMGIPNSISI 887
 DB 823 NKDSSLNENGVKMPYTVLLPTCED-----EGLTFRGIPNSISI 862

RESULT 12
 LOX4_SOYBN
 ID LOX4 SOYBN STANDARD; PRT; 853 AA.
 AC P38417;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipoxigenase-4 (EC 1.13.11.12) (L-4) (VSP94).
 GN LOX1.5 OR LOX4.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eursoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Enrei;
 RC Kato T., Shirano Y., Iwamoto H., Shibata D.;
 RT "Soybean lipoxigenase L-4, a major component of the 94-kilodalton
 RT storage protein in vegetative tissues: expression and accumulation in

SEQUENCE FROM N.A.
 RC STRAIN=cv, Williams 82; Tissue=Radicle;
 RA Park T., Holland M.A., Laskey J.G., Polacco J.C.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
 CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
 CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
 CC !- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC !- COFACTOR: Iron, one atom tightly bound per molecule.
 CC !- SUBUNIT: Monomer.
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.
 CC !- TISSUE SPECIFICITY: GERMINATED COTYLEDONS.
 CC !- INDUCTION: By jasmonate.
 CC !- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
 CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
 CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
 CC !- SIMILARITY: Belongs to the lipoxigenase family.
 CC !- SIMILARITY: Contains 1 PLAT domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X56139; CAA39604.1; -
 CC EMBL; U04526; AAA03728.1; -
 CC F01; S13381; S13381.
 CC HSP; P08170; 2SBL.
 CC InterPro; IPR000807; Lipoxigenase.
 CC InterPro; IPR001024; Lipoxigenase_LH2.
 CC InterPro; IPR008976; PLAT_LH2.
 CC Pfam; PF00305; lipoxigenase; 1.
 CC Pfam; PF01477; PLAT; 1.
 CC PRINTS; PR00087; LIPOXYGENASE.
 CC SMART; SM00308; LH2; 1.
 CC PROSITE; PS00711; LIPOXYGENASE_1; 1.
 CC PROSITE; PS00081; LIPOXYGENASE_2; 1.
 CC PROSITE; PS00095; PLAT; 1.
 CC Oxidoreductase; Dioxxygenase; Iron; Multigene family.
 KW OXIDOREDUCTASE; DIOXYGENASE; IRON; MULTIGENE FAMILY.
 FT DOMAIN 44 171
 FT METAL 525 525 IRON (BY SIMILARITY).
 FT METAL 530 530 IRON (BY SIMILARITY).
 FT METAL 716 716 IRON (BY SIMILARITY).
 FT METAL 864 864 IRON (BY SIMILARITY).
 FT CONFLICT 233 233 S -> C (IN REF. 2).
 FT CONFLICT 240 240 R -> L (IN REF. 2).
 FT CONFLICT 604 604 D -> H (IN REF. 2).
 FT CONFLICT 695 695 M -> K (IN REF. 2).
 SQ SEQUENCE 864 AA; 96816 MW; 66F31PB1FA5F3B60 CRC64;
 Query Match 50.2%; Score 2370.5; DB 1; Length 864;
 Best Local Similarity 52.1%; Pred. No. 2,1e-163;
 Matches 469; Conservative 134; Mismatches 215; Indels 79; Gaps 15;
 QY 22 KIRGTVLVKKVLDVGFNA-----SLDGVHRIILGW-----DDGVAF----- 60
 DB 10 KIKGTVLVMPKNVL--DFNAITSGKGGVIDTATGILGQGVSLVGGVIDTATSGFLGNI 66
 QY 61 --OLVSATAADNSGGRGVKGAHLEAVVSLKSTADGETVYRVSWFDESGQIRGAVL 118
 DB 67 SMQLISATQTDGS--GNGKGVKEVLEKHLPTLPTLGARQDAFSIFFEWDSFSGIPGAFY 124
 QY 119 VRLNQHAFFLKTLLEGVPGKGVTVFVANSVWYEHKLYSGERIFFANDYLPKMPAAL 178
 DB 125 IKNFWTDEFFLVSKLEIDIPNHGTIEFCVNSWVNFYSYKKNRIFVNDYTLPSATAPL 184
 QY 179 VPIRQDELKILGDDNPGPYQEHDRVYDYNDLGDGPKGEHARPLGGSQEHPIPRR 238

DB 185 LKYRKEEVLVRG-DGTGKRKDFDIYDVYNDLGNPDGGD--PRPILGGSSIVPYPRR 241
 QY 239 CRTGREPTKDDNSERLFLNLINIVPERDERFGLKMSDFLGYSKLTIIIEAVLPLGTF 298
 DB 242 VRTGRETRTDNSEK-----PGEVYVPADENFGLKMSDFLTGYIKLSHVDVILFKSA 296
 QY 299 VDD---TPKEFSPFEDILGLYELGPEAPNPLIABIRKIPSEFLRSILP-----NG 347
 DB 297 IFQLRVTSSEFSEFSDVRSLYEGG-----IKLPTDILSQISPLPALKEIFRT 343
 QY 348 SHDHLKMLPNVKSVDLKKAPKFGWRTDEEFARETLAGVNPVVIKRLTEFFAKSTL 407
 DB 344 DGENVLQFPFPHVAKVS-----KSGWUTDEEFAREVIAGVNPVIRRLQEFPPKSTL 395
 QY 408 DPRQYGDHSTKITEAHIRNMGGLSVQNALRNKRILFDHHDHFPYLDIENELGNFTY 467
 DB 396 DPTLYGQDSTITKEQLEINMGVTVVEALSTQRLFDLYQDAFIPYLTRINSLPTAKAY 455
 QY 468 ASRTLLFLKDDGTLKPLATELSLPHPDGQORGAVSKVYTPAHTGVGHVWQLAKAVCVN 527
 DB 456 ARTIILFLKDDGTLKPLATELSLPHPDGQNLGSPESIVLPATEGVDSTIWLAKARVIVN 515
 QY 528 DSAHOLISHMLNTHAVIEFFVIATNRQLSVVHPVHKLSPHYRDTLNINALAROTLINA 587
 DB 516 DSGYHQLVSHMLNTHAVMEFFAIATNRHLSVLHPYKLLYPHYRDTININGLAROSLINA 575
 QY 588 GGVFERIVTPAKVALGMSADVYSKWNFNQALPADLYKGVAVPOSSPYGVRLAIKQYP 647
 DB 576 DGIIEKSFPGKYSIEMSSSVYVNWVFTDQALPADLVKRLGLAIEDPSAPHGURLVIEDYP 635
 QY 648 YAVDGLVIVWAIERWVKEYLDIYYPNDGELQDLVQLQAWKKEVREBEAHDGLKDRDWPWM 707
 DB 636 YAVDGLVINDAIKTWVHEVVSIVYPTDAAVQDQLQAWKKEVREBEAHDGLKDRDWPWM 695
 QY 708 DTVOQLARACTIIVASALHAAVNFQYPIAGYLPNRTASRRPMPPEPESHDKYKLGAG 767
 DB 696 QTTEDLIQSCSIIVMTASALHAAVNFQYPIAGYLPNRTASRRPMPPEPESHDKYKLGAG 752
 QY 768 QKEADWVFRTITTSQFTILGISLIEILSKHSDEVILGQRPDPRDWTSDAKALDAFKRF 827
 DB 753 VKNPQKAYLRTITPKETLIDLSVIELSRHASDEILGERETPN-WTTDKKALEAFKRF 811
 QY 828 GSRLOIENRIKTMNDSPDLKVRKGVEVMPYMLLPNTSDVTGKAEGLTANGIENSISI 887
 DB 812 GSKLTGIEGKINARNSDPSLRNRTGVPQLPYTLHRSS-----EGLTFKGIENSISI 864
 RESULT 14
 ID LOX1 SOYBN STANDARD; PRT; 839 AA.
 AC P08170;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Seed lipoxigenase-1 (EC 1.13.11.12) (L-1).
 GN LOX1.1 OR LOX1
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87280024; PubMed=3112136;
 RA Shibata D., Steczko J., Dixon J.E., Hermodson M., Yazdanparast R.,
 RA Axelrod B.;
 RT "Primary structure of soybean lipoxigenase-1.";
 RL J. Biol. Chem. 262:10080-10085 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Bominori; TISSUE=Cotyledon;
 RA Fukazawa C., Masayoshi M., Chikafusa F.;

RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 426-752 FROM N.A.
 RA Start W.G., Ma Y., Polacco J.C., Hildebrand D.F., Freyer G.A.,
 RA Altschuler M.;
 RT "Two soybean seed lipoxigenase nulls accumulate reduced levels of
 RT lipoxigenase transcripts";
 RL Plant Mol. Biol. 7:11-23(1986).
 RN [4]
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES, AND REVISIONS TO 479-482.
 RX MEDLINE=92232702; PubMed=1567851;
 RA Steczko J., Doncho G.P., Clemens J.C., Dixon J.E., Axelrod B.;
 RT "Conserved histidine residues in soybean lipoxigenase: functional
 RT consequences of their replacement";
 RL Biochemistry 31:4053-4057(1992).
 RN [5]
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES.
 RX MEDLINE=92360013; PubMed=1497657;
 RA Steczko J., Axelrod B.;
 RT "Identification of the iron-binding histidine residues in soybean
 RT lipoxigenase L-1";
 RL Biochem. Biophys. Res. Commun. 186:686-689(1992).
 RN [6]
 RP ACTIVE SITE, AND IRON LIGANDS.
 RX MEDLINE=93298753; PubMed=8518276;
 RA Minor W., Steczko J., Bolin J.T., Otwinowski Z., Axelrod B.;
 RT "Crystallographic determination of the active site iron and its
 RT ligands in soybean lipoxigenase L-1";
 RL Biochemistry 32:6320-6323(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=93276267; PubMed=8502991;
 RA Boyington J.C., Gaffney B.J., Amzel L.M.;
 RT "The three-dimensional structure of an arachidonic acid
 RT 15-lipoxygenase";
 RL Science 260:1482-1486(1993).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RX MEDLINE=96346062; PubMed=8718858;
 RA Minor W., Steczko J., Stec B., Otwinowski Z., Bolin J.T., Walter R.,
 RA Axelrod B.;
 RT "Crystal structure of soybean lipoxigenase L-1 at 1.4-A resolution";
 RL Biochemistry 35:10687-10701(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RX MEDLINE=21305677; PubMed=11421204;
 RA Tomchick D.R., Phan P., Cymborowski M., Minor W., Holman T.R.;
 RT "Structural and functional characterization of second-coordination
 RT sphere mutants of soybean lipoxigenase-1";
 RL Biochemistry 40:7509-7517(2001).
 CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
 CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
 CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
 CC WOUNDING. WITH LINOLEATE AS SUBSTRATE, L-1 SHOWS A PREFERENCE FOR
 CC CARBON 13 AS THE SITE FOR HYDROPEROXIDATION (IN CONTRAST TO L-2
 CC AND L-3, WHICH UTILIZE EITHER CARBON 9 OR 13).
 CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
 CC hydroperoxyoctadeca-9,11-dienoate.
 CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: THE HYDROPEROXIDE PRODUCT SERVES TO ACTIVATE THE
 CC RESTING ENZYME. THE ACTIVATION IS ACCOMPANIED BY THE OXIDATION
 CC OF FE(2+)ENTADIENE STRUCTURE. L-1 PREFERENCES ANIONIC SUBSTRATE.
 CC -!- MISCELLANEOUS: SOYBEAN CONTAINS AT LEAST 4 DISTINCT ISOENZYMES,
 CC L-1, L-2, L-3A AND L-3B IN DRY SEEDS, AND AT LEAST TWO DISTINCT
 CC ISOZYMES IN THE HYPOCOTYL/RADICLE REGION OF THE SEEDLING STEM.
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.
 CC -!- SIMILARITY: Contains 1 PLAT domain.
 CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN AT POSITIONS 663
 CC TO 697 DUE TO A FRAMESHIFT.
 CC -----

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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J02795; AAA33986.1; -;
 DR EMBL; X67304; CAA47717.1; ALT_FRAME.
 DR PIR; S25064; DASYL2.
 DR PDB; 1F8N; 04-JUL-01.
 DR PDB; 1FGM; 24-OCT-01.
 DR PDB; 1FGO; 04-JUL-01.
 DR PDB; 1FGQ; 04-JUL-01.
 DR PDB; 1FGR; 18-JUL-01.
 DR PDB; 1FGI; 04-JUL-01.
 DR PDB; 1YGE; 23-JUL-97.
 DR PDB; 2SBL; 27-FEB-95.
 DR InterPro; IPR000907; Lipoxigenase.
 DR InterPro; IPR001024; Lipoxigenase_LH2.
 DR InterPro; IPR008976; PLAT_LH2.
 DR Pfam; PF00305; lipoxigenase; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR SMART; SMC0308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS50095; PLAT; 1.
 DR Oxidoreductase; Dioxigenase; Iron; Multigene family; 3D-structure.
 KW DOMAIN 16 145
 FT METAL 499 499
 FT METAL 504 504
 FT METAL 690 690
 FT METAL 839 839
 FT METAL 494 494
 FT METAL 494 494
 FT METAL 499 499
 FT METAL 504 504
 FT METAL 517 517
 FT METAL 522 522
 FT METAL 531 531
 FT METAL 690 690
 FT CONFLICT 426 427
 FT CONFLICT 558 560
 FT CONFLICT 572 574
 FT CONFLICT 641 641
 FT CONFLICT 741 748
 FT STRAND 16 16
 FT HELIX 17 19
 FT TURN 20 20
 FT HELIX 24 26
 FT HELIX 32 35
 FT TURN 37 38
 FT STRAND 40 50
 FT TURN 52 53
 FT STRAND 56 58
 FT STRAND 62 63
 FT STRAND 66 68
 FT TURN 76 77
 FT STRAND 79 86
 FT HELIX 89 91
 FT STRAND 94 101
 FT STRAND 107 114
 FT TURN 117 120
 FT STRAND 123 131
 FT STRAND 133 133
 FT HELIX 134 136
 FT STRAND 141 144
 FT HELIX 151 153
 FT HELIX 156 158
 FT HELIX 159 170
 FT TURN 173 180
 FT STRAND 186 187

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FT STRAND 189 189 49.9%; Score 2355.5; DB 1; Length 839;
FT TURN 195 197 Beat Local Similarity 53.4%; Pred. No. 2.5e-162;
FT STRAND 199 201 Matches 465; Conservative 140; Mismatches 223; Indels 43; Gaps 14;
FT STRAND 206 206
FT STRAND 217 218
FT STRAND 224 224
FT TURN 229 230
FT STRAND 232 232
FT HELIX 242 244
FT HELIX 251 253
FT HELIX 255 257
FT HELIX 258 264
FT TURN 265 265
FT HELIX 266 275
FT TURN 276 277
FT HELIX 286 290
FT HELIX 291 293
FT TURN 294 295
FT STRAND 297 298
FT HELIX 301 307
FT TURN 308 309
FT TURN 311 312
FT HELIX 313 316
FT STRAND 318 319
FT STRAND 324 326
FT HELIX 331 333
FT HELIX 339 341
FT HELIX 343 352
FT TURN 356 357
FT TURN 360 361
FT STRAND 363 373
FT HELIX 373 376

Query Match 49.9%; Score 2355.5; DB 1; Length 839;
Beat Local Similarity 53.4%; Pred. No. 2.5e-162;
Matches 465; Conservative 140; Mismatches 223; Indels 43; Gaps 14;

QY 22 KIRGVRLVKEVLVDGDFNASLLDGVHRIIGWDDGVAFQVLSATAADPSNGRGKVGKA 81
DB 7 KIKGVVLPKNELVNP-DGSAVDNLNFAIG--RSVSLQLISATKADAH--GKRGVKD 61

QY 82 AHLEBAVYLSKTADGTVYRVSVFESQIGPQAVLVNQLQHAEPFLKTLTLEGVPGK 141
DB 62 TFLGINTSLPTLGAESAFNIHFWDGSMGIPGAFYIKNTVMQVEFFLKSLTLEAISNQ 121

QY 142 TVVFVANSVVPKLYSOERIFENDTVLPSKMPAALVPYQDELKILRGDDNPGPQEH 201
DB 122 TIRFCNSVNTKDKSVRIFFANHTVVPSETPAPLVSVREELKSLRG-NGTGERKEY 180

QY 202 DRVYDYNDLGDGKGEHARPLIGSQEHYPRRCRTGRHTPKDPSSESR--LFL 259
DB 181 DRIYDYVNDLGNPDKSEKLARPLVGGSTFPYPRRGRTGRGFTVTDNTEKQGEV 238

QY 260 NLNIYVPRDERFGLKMSDFLYGSLKTLIEAVLPLTGLTFVD--DTPKEFDSFEDILG 317
DB 239 ----VVPDENLGHUKSDALEIGTKLSQIVQAFESAFDLKSTPIEFHSFQDVHDL 294

QY 318 LQPEAPNPPLIAEIRKIPSPFLRSILPNSGSHDHPKMPNVIKSDVLKKAPEKFGWR 377
DB 295 GGKLPDVIPTIIPLVIKELYRI-----DQHLKFPQPHVQVS-----QSAWM 341

QY 378 TDEEFARETLAGNVPVIRKITEPPAKSTLDPQYDHTSKITTAHTRHNGLSVQNAL 437
DB 342 TDEEFAREMAGNVPVIRGEEFPPKSNLDPATYGGQSSKITADSL--DLDGVTMD 399

QY 438 RNKRLFIIDHDFHMFYDEINELEGNFIYASRTLLFLKDDGTLKPLAELSLPHPDQ 497
DB 400 GSRRLFMLDYHDFMFPYVQNLNSAKTYATRIILFREDGTLPKVAELSLPHSAG 459

QY 498 RGAUSKVTPAHTGVGHVQWQAKAYACVNSAHLQISHWINTHAVIEPFIATNRQL 557
DB 460 SAAVQVVLPAKEGVESTIWLKAYVIVNDSYHQLMSHNLNTHAAMEPFIATNRH 519

QY 558 VVHPVHKLLSPHYRDTLNALARQTLINAGGVFERTVFPKAYALGMSADVYKSWNF 617

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DB 520 VLHPYIKLTPHYRNNMNLARQSLNANGLITTTLPFSYVMSGSAVYKNNVFTDQ 579
QY 618 ALPADLVKRGVAVPQSSPYGVRLLIKDYFYAVDGLVIMWAIERWVWKEYLDIYYPNDGEL 677
DB 580 ALPADLVKRGVAVPQSSPYGVRLLIKDYFYAVDGLVIMWAIERWVWKEYLDIYYPNDGEL 639
QY 678 QRDVELQANWKEVREAHGDLKORDWPRMDTVQOLARACTTIIIVASALHAANFGQYP 737
DB 640 KNDSELQHWKKEAVKSGHGLKDKPWPVKLQLEDVLCVLIIVIASALHAANFGQYP 699
QY 738 YAGYLFENRPTASRRPMPPEGSHDYKKGAGQKQKADWVIRITTSOFOTILGISLIEILSK 797
DB 700 YGGLINRPTASRRLLPEKGTPEYBEMINNEKA--YLRITTSKLPILSLSVIEILST 756
QY 798 HSDDEVYLGORDEPDRWTSKADALDAFKRFGSRIVQIENRIKTNWDSPLK-NRKGPEM 856
DB 757 HASDEVYLGORDNP-HWTSDSKALQAFQKFGNKLKEIBEKLVRRNNDPSLQNLGVPQL 815
QY 857 PYMLYPNTSDVTGKAEGLTANGIPNSISI 887
DB 816 PYTLVPSSE-----EGLTFRGIPNSISI 839

RESULT 15
LOX1 LENCU
ID AC P38414; STANDARD; PRT; 866 AA.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX1.1.
OS Lens culinaris (Lentil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Lens.
OX NCBI_TaxID=3864;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seedling shoot;
RX MEDLINE=94162308; PubMed=8117753;
RA Hilbers M.P., Rossi A., Finazzi-Agro A., Veldink G.A.,
RA Vliegenthart J.F.G.;
RT "The primary structure of a lipoxigenase from the shoots of etiolated
RT lentil seedlings derived from its cDNA.";
RL Biochim. Biophys. Acta 1211:239-242(1994).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTAINING
CC A CIS, CIS-1,4-PENTADIENE STRUCTURE.
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron, one atom tightly bound per molecule.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC
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CC
CC EMBL; X71344; CAA50483.1; -
CC HSP; P08170; 2SBL.
CC InterPro; IPR000907; Lipoxigenase.
CC InterPro; IPR01024; Lipoxigenase_LH2.
CC InterPro; IPR008976; PLAT_LH2.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 06:32:08 ; Search time 78 Seconds

(without alignments)
3598.008 Million cell updates/sec

Title: US-10-059-909-16

Perfect score: 4723

Sequence: 1 MFHWGVADRLGKNKEAWSE.....VTGEKAEGLTAMGIPNSISI 887

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3703	78.4	877	10 Q8S6D6	Q8S6D6 oryza sativ
2	3369.5	71.3	876	10 Q42846	Q42846 hordeum vul
3	3052	64.6	864	10 Q8W0V2	Q8W0V2 zea mays (m
4	3049	64.6	864	10 Q9AXG8	Q9AXG8 zea mays (m
5	3023	64.0	866	10 Q8S6D9	Q8S6D9 oryza sativ
6	3018.5	63.9	863	10 Q8S6E8	Q8S6E8 oryza sativ
7	2960	62.7	870	10 Q7Y1F4	Q7Y1F4 oryza sativ
8	2958	62.6	873	10 Q9LKL4	Q9LKL4 zea mays (m
9	2860	60.6	864	10 Q42847	Q42847 hordeum vul
10	2768	58.6	862	10 Q3LEA9	Q3LEA9 prunus dulc
11	2754.5	58.3	873	10 Q93Y18	Q93Y18 corylus ave
12	2739	58.0	884	10 Q7X9G5	Q7X9G5 fragaria an
13	2730	57.8	862	10 Q8W4X6	Q8W4X6 prunus dulc
14	2724.5	57.7	862	10 Q43800	Q43800 nicotiana t
15	2714.5	57.5	865	10 Q93W22	Q93W22 gossypium h
16	2701.5	57.2	862	10 Q9FT17	Q9FT17 lycopersico

17	2595.5	57.1	862	10 Q43191	Q43191 solanum tub
18	2630.5	55.7	857	10 Q41238	Q41238 solanum tub
19	2626.5	55.6	860	10 Q43190	Q43190 solanum tub
20	2624.5	55.6	857	10 Q8GV02	Q8GV02 brassica na
21	2605	55.2	861	10 Q24379	Q24379 solanum tub
22	2604	55.1	861	10 Q9SC16	Q9SC16 solanum tub
23	2603	55.1	844	10 Q9SAP1	Q9SAP1 solanum tub
24	2603	55.1	861	10 Q43189	Q43189 solanum tub
25	2601	55.1	864	10 Q43150	Q43150 solanum tub
26	2599	55.0	861	10 Q22507	Q22507 solanum tub
27	2598.5	55.0	854	10 Q9FNX7	Q9FNX7 arabidopsis
28	2596.5	55.0	881	10 Q9M463	Q9M463 cucumis sat
29	2592	54.9	861	10 Q22508	Q22508 solanum tub
30	2578.5	54.6	882	10 Q9LUW0	Q9LUW0 arabidopsis
31	2552	54.0	858	10 Q9ZU05	Q9ZU05 persea aner
32	2511	53.2	859	10 Q42873	Q42873 lycopersico
33	2498.5	52.9	876	10 Q41430	Q41430 solanum tub
34	2478.5	52.5	866	10 Q99870	Q99870 glycine max
35	2433	51.5	877	10 Q42705	Q42705 cucumis sat
36	2426.5	51.4	878	10 Q42704	Q42704 cucumis sat
37	2423.5	51.3	878	10 Q42710	Q42710 cucumis sat
38	2420	51.2	865	10 Q24320	Q24320 phaseolus v
39	2394	50.7	853	10 Q43446	Q43446 glycine max
40	2393.5	50.7	856	10 Q42780	Q42780 glycine max
41	2393.5	50.7	868	10 Q24470	Q24470 pisum sativ
42	2389	50.6	859	10 Q43440	Q43440 glycine max
43	2385.5	50.5	858	10 Q04919	Q04919 vicia faba
44	2353.5	49.8	856	10 Q9M684	Q9M684 phaseolus v
45	2353	49.8	839	10 Q43438	Q43438 glycine max

ALIGNMENTS

RESULT 1

Q8S6D6	PRELIMINARY;	PRT;	877 AA.
ID	Q8S6D6		
AC	Q8S6D6		
DT	01-JUN-2002 (TREMREL. 21, Created)		
DT	01-JUN-2002 (TREMREL. 21, Last sequence update)		
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)		
DE	Putative lipoxigenase.		
GN	OSJNB0024B16.26		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,		
RA	Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,		
RA	Teitelin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pal G.,		
RA	VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,		
RA	Salzberg S.L., White O., Fraser C.M.;		
RT	"Oryza sativa chromosome 3 BAC OSJNB0024B16 genomic sequence.";		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC093017; AL83623.1; -		
DR	Gramene; Q8S6D6; -		
DR	GO; GO:0005506; F:iron ion binding; IEA.		
DR	GO; GO:0016165; F:lipoxigenase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR000907; Lipoxigenase.		
DR	InterPro; IPR001024; Lipoxigenase_LH2.		
DR	InterPro; IPR008976; PLAT_LH2.		
DR	Pfam; PF00305; lipoxigenase; 1.		
DR	Pfam; PF01477; PLAT; 1.		
DR	PRINTS; PR00087; LIPOXYGENASE.		
DR	SMART; SW00308; LH2; 1.		
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.		
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.		
DR	PROSITE; PS50095; PLAT; 1.		

RP SEQUENCE FROM N.A.
RA Wilson R.A., Gardner H.W., Keller N.P.;
RT "Cultivar-dependent expression of a maize lipoxigenase responsive to
seed-infecting fungi";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF329371; AAG61118.1; -
DR HSRF; P09186; ILNH.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS50095; PLAT; 1.
SQ SEQUENCE 864 AA; 96476 MW; 639156E1C6EB8D2B CRC64;
Query Match 64.6%; Score 3049; DB 10; Length 864;
Best Local Similarity 66.2%; Pred. No. 1.5e-225;
Matches 585; Conservative 100; Mismatches 175; Indels 24; Gaps 10;
QY 5 GVADRLTGKNEANSEKIRGTVELVKKEVLVDGDFENASLLDGVHRLGWDGVAFLVLS 64
Db 4 GIIDLTGANKHA-----RLKGTVMRKVNLDLNDFGATVVDISIFLG--KGVTCQLIS 57
QY 65 ATAADPNNGRGKGVKGAHLEAAVSLKSTADGETVYRVSEFWD--BSQIPGAVLVRLNQ 123
Db 58 STLVDANNNGRGRVGAELNQLTSLPSLTGESKEGVTEDVEVKLGVPGAUVKNNH 117
QY 124 HAEFFLKTLEGGVPGGTGVFVANSVWYVPHKLYSQERIFANDTVLPSPKMPAALVPYRQ 183
Db 118 AAEFFLKTILDDVPFGAVTFVANSVWYVYAGKRYNRVFFSNDTLPSPMPAALPKPYRD 177
QY 184 DELKILRGDNDPGYQEHDRYRYDYNDLGDPKGBEHARPLIGSGQEHFPRRCRTGR 243
Db 178 DELANLRGDDQGGYQEHDRYRYDYNDLGEPPDG--NRPILGGSADHPYPRRCRTGR 235
QY 244 HPTKDPNSRSLFLNLNIVYPRDERFGLKMSDFGLSKLTIIEAVLPTLGTFFVDDTP 303
Db 236 KPTKDPNSRSLVLE-QIYVPRDERFGLKMSDFGLSKLTIQIIPAVTYDDTP 294
QY 304 KEFDSFEDIILGLYELGPEAPNPLIAIRKIPSEFLRSILPNSGSDHPLKMLPNIKVS 363
Db 295 GEPDSFDIINLYEGGIKPKIQALEDMRKLFPQLVAKDLPPAG--DYLKLPPIQIE 353
QY 364 DVLKKAPEFKGWRITDEEPARETLAGNPNVILKRLTEFFPAKSTLDPRQGDHTSKITEAH 423
Db 354 D-----KNAWRTDEEPAREVLAVGNPNVITLTFEPKSTLDPSKYGDHTSTITAEH 405
QY 424 IRHNMGLSVQNALRNKRLFTLDHDFMFPYLDDEINELEGNFYASRTLLFLKDDGTLPK 483
Db 406 IEKNLEGTIVQALDGNRLYLDHDFMFPYLDVNNLEGNFYATRTLFFLRGDLAP 465
QY 484 LAIELSLPHDPDQQRGAVSKYTPAHTGVGHWQLAKAVACVNDGSAHQLSHWLNTA 543
Db 466 LAIELSEFYDGLDTVAKSKYTPPASSGVVEAWWQLAKAVAVNDGSHQLVSHWLNTEA 525
QY 544 VIEPFIATNRQLSVHPVHKLSPHYRDTLNLNALAROTLINAGGVFEERTVPPAKYALG 603
Db 526 VMEPFIATNRQLSVHPVHKLSHSHFDTMTNALAROTLINAGGVFEERTVPPAKYALG 585
QY 604 MSADVYKSNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKVYPVADGLVITWAIERWV 663
Db 586 MSSVYVYKSNFTEQGLPADLVKRGVAVADSPSPYKRLATIEDYPYASDGLAIWHATEQWV 645
QY 664 KEYLDIYYPNDGELQORDELQAWKKEVREEAHGDLDKRDWWRPMDTVQOLARACTIIVV 723
Db 646 GEYLAIIYYPDDGALRGDEELQAWKKEVREVGHGHDKAPWPKQAVSELASACTIIVV 705

QY 724 ASALHAANVFGQPYAGYLPNRPTASRRMPPEPSSHDKYKLGAGOEADVMVIRITTSQF 783
Db 706 ASALHAANVFGQPYAGYLPNRPTVSRMRPEPGSKEYEEL---ERDERGFIHTTSQI 762
QY 784 QTIIGISLIEILSKHSSDEVILGQDEDPRTWTSKALDAPKRGSRVLYQENRIKTWND 843
Db 763 QTIIGISLIEILSKHSSDEVILGQDRTPE-WTSARALAAAFKRFSDALVKIEGVVGENR 821
QY 844 SPDLKNRKGPEMPYMLLYPNTSDVTGKAKGLTAMGIPNISI 887
Db 822 DQLENRNGPAEFFYMLLYPNTSDHSG-AAAGLTAKGIPNISI 864
* RESULT 5
QSS6D9 PRELIMINARY; PRT; 866 AA.
AC QSS6D9; DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Putative lipoxigenase.
GN OSUNBB0024B16.16 OR OSUNBB0017F17.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Heiao J., Zismann V., Blunt S., Pai G.,
RA Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBB0024B16 genomic sequence";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.B., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosen D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBB0017F17 genomic sequence";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
DR EMBL; AC093017; AAL63618.1; -
DR EMBL; AC093017; AAL63618.1; -
DR Gramene; QSS6D9; -
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS50095; PLAT; 1.
SQ SEQUENCE 866 AA; 96251 MW; CFABP7A03604367D CRC64;
Query Match 64.0%; Score 3023; DB 10; Length 866;
Best Local Similarity 65.9%; Pred. No. 1.5e-223;
Matches 584; Conservative 103; Mismatches 173; Indels 26; Gaps 12;
QY 5 GVADRLTGKNEANSEKIRGTVELVKKEVLVDGDFENASLLDGVHRLGWDGVAFLVLS 64
Db 4 GIIDLTGANKHA-----RLKGTVMRKVNLDLNDFGATVVDISIFLG--KGVTCQLIS 57


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Db 465 LAIELSLPHITGNTSASKVHTPASGISWVWQAKAYAVANDSGHQLISHWLNTHA 524
QY 544 VIEPFIATNQLSVHPVHKLSPHYRDTNINALARQTLINAGGVFTVFPKAYALG 603
Db 525 VMEPFIATNQLSVHPVHKLSPHYRDTNINALARQTLINAGGVFTVFPKAYALG 584
QY 604 MSADYKSWNNEQALPADLVKRGVAVDPQSSPGVGVRLIKDPIYAVDGLVWIERWV 663
Db 585 MSSAVYKWNNEQALPADLVKRGVAVDPQSSPGVGVRLIKDPIYAVDGLVWIERWV 644
QY 664 KEYLDIYVNDGELQDVELQAWKKEVREBAHGLKDRDWMPRMDTVQOQLARACTIIV 723
Db 645 TEYCAIYVNDGELQDVELQAWKKEVREBAHGLKDRDWMPRMDTVQOQLARACTIIV 704
QY 724 ASALHAAVNFGQYAGVLPNRPASRRPMPPEPGSHDYKKGAGQKEADWVFTTTSQF 783
Db 705 ASALHAAVNFGQYAGVLPNRPASRRPMPPEPGSHDYKKGAGQKEADWVFTTTSQF 761
QY 784 QTLIGSLIELSKHSDDEVYLGQDPRDWTSDAKALDAKFRGSLVOIENRIKTMND 843
Db 762 QTLIGSLIELSKHSDDEVYLGQDPRDWTSDAKALDAKFRGSLVOIENRIKTMND 820
QY 844 SPDLKNRKGPVEMPMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 821 DPLKNRKGPVEMPMLLYPNTSDVTGKAEGLTAMGIPNSISI 863

RESULT 7
QY ID Q7Y1F4 PRELIMINARY; PRT; 870 AA.
AC Q7Y1F4;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase L-2; lipoxigenase.
GN OSNBA0057G07.15.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrash D.W., Tallon L.J., Koo H., Zismann V., Hailao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 3 BAC OSNBA0057G07 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117988; AAP44707.1; --
SQ SEQUENCE 870 AA; 97183 MW; 63344755867DA680 CRC64;

Query Match
Best Local Similarity 62.7%; Score 2960; DB 10; Length 870;
Matches 569; Conservative 112; Mismatches 178; Indels 32; Gaps 14;

QY 5 GVADELTKNKEANSEKIRGTIVLVKEVLDVGDVFNASLLDGVHRLGDDGVAFOLVS 64
Db 4 GIIGLGT-KNNA-----LRKSLVLMRKALDINDFGATVIDGISEFLG--RGVTCQLVS 56
QY 65 ATAADPSNGRGKGVKAHLSEAVVSLKSTADGETVTVRVSPED-ESQGIPIGAVLVNQLQ 123
Db 57 SSLVDPNNGRGRVTEASLEQWLTSLPSLTGTGSKGVTFEWEKMGIPGALIVKNH 116

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QY 124 HAEFFLKITLTLEGVPGKCTVVFVANSWVYVPHKLVSQERIPFANDTYLPSKMPAALVPRQ 183
Db 117 AAEFFLKITLTLDNVFPGHGVAVFVANSWVYVPHKLVSQERIPFANDTYLPSKMPAALVPRQ 176
QY 184 DELKILRGDNDPGVQOEHDHVRVYDYNLDGDPKGEHARPIILGSGSEHPYPRRCRGR 243
Db 177 DELNLRGDNDPGVQOEHDHVRVYDYNLDGDPKGEHARPIILGSGSEHPYPRRCRGR 234
QY 244 HPTKXDPNSESRLFILNINIVPRDERFGLHKNDFGLYSUKTIEAVLPTLGFVDDTP 303
Db 235 KPTKTDPTAESRLSLE-NIYVPRDERFGLHKNDFGLYSUKTIEAVLPTLGFVDDTP 293
QY 304 KEFDFEFIDILGILYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHPLKMP;PNVTKS 363
Db 294 GEFDFEFIDILGILYELGPEAPNPLIAETRKIPSEFLRSILPNSHSHPLKMP;PNVTKS 352
QY 364 DVLKXAPKFKGWRTEEFARETLAGVNPVILKLTTEPPAKSTLDPROYDHTSKITBAH 423
Db 353 D--KKA-----WMTDFEFARETLAGVNPVILKLTTEPPAKSTLDPROYDHTSKITBAH 404
QY 424 IRHNMGGISLVQNALNENKELFILDHHHHPMPYLDDEINELGNFIYASRTLLFLKDDGTLKP 483
Db 405 VERGLEGTVQQAIDGNLLVYVDDHHPMPYLDDEINELGNFIYASRTLLFLKDDGTLKP 464
QY 484 LAIELSLPH-PDGOORGAIVSKYITPAHTG-----VEGHVWQLAKAYACVNDSAWHQLIS 536
Db 465 LAIELSLPHLQDDGLITARTSTVTPAARGGTGAGAVENWVWQAKAYVNVNDYCHWQLIS 524
QY 537 HMLNTHAVIEPIVATNQLSVHPVHKLSPHYRDTNINALARQTLINAGGVFTVFP 596
Db 525 HMLNTHAVIEPIVATNQLSVHPVHKLSPHYRDTNINALARQTLINAGGVFTVFP 584
QY 597 PAKYALGMSADYKSWNNEQALPADLVKRGVAVDPQSSPGVGVRLIKDPIYAVDGLVW 656
Db 585 PRKHALMSSAFYKDWSPADQALPDLVKGAVVDPDPAAPYKVRLLIEDYVANDGLAVM 644
QY 657 WAIERWVKEYLDIYVNDGELQDVELQAWKKEVREBAHGLKDRDWMPRMDTVQOQLARA 716
Db 645 HAIEQWATEYLAIIYVNDGELQDVELQAWKKEVREBAHGLKDRDWMPRMDTVQOQLARA 704
QY 717 CTTIITWASALHAAVNFGQYAGVLPNRPASRRPMPPEPGSHDYKKGAGQKEADWVFI 776
Db 705 CATIITWASALHAAVNFGQYAGVLPNRPASRRPMPPEPGSHDYKKGAGQKEADWVFI 761
QY 777 RITTSQFQTLIGSLIELSKHSDDEVYLGQDPRDWTSDAKALDAKFRGSLVOIEN 836
Db 762 RITTSQFQTLIGSLIELSKHSDDEVYLGQDPRDWTSDAKALDAKFRGSLVOIEN 820
QY 837 RIKTWNDGSPDLKNRKGPVEMPMLLYPNTSDVTGKAEGLTAMGIPNSISI 887
Db 821 RVVANKDPRKNRKGPVEMPMLLYPNTSDVTGKAEGLTAMGIPNSISI 870

RESULT 8
QY ID Q9LKL4 PRELIMINARY; PRT; 873 AA.
AC Q9LKL4;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seedling;
RA Han O., Choi B., Kim Y., Kim E.;
RT "Methyl Jasmonate Induces Biphasic Accumulation of Lipoxigenase mRNA
in Maize Seedlings."

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RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR	ENBL; AP271894; AAF76207.1; -
DR	HSP; P08170; 2SBL
DR	GO; GO:000506; Firon ion binding; IEA.
DR	GO; GO:0016165; Filipoxygenase activity; IEA.
DR	GO; GO:0016491; Flixidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR000907; Lipoxigenase.
DR	InterPro; IPR001024; Lipoxigenase_LH2.
DR	InterPro; IPR008976; PLAT LH2
DR	Pfam; PF00305; lipoxigenase; 1.
DR	Pfam; PF01477; PLAT; 1.
DR	PRINTS; PRO0087; LIPOXYGENASE.
DR	SMART; SM00308; LH2; 1.
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR	PROSITE; PS00095; PLAT; 1.
KW	Oxidoreductase.
SQ	SEQUENCE 873 AA; 98163 MW; 1E70C3C1B98CA979 CRC64;

Query Match	62.6%; Score 2958; DB 10; Length 873;
Best Local Similarity	63.6%; Pred. No. 1.5e-218;
Matches 561; Conservative 115; Mismatches 180; Indels 26; Gaps 11;	

QY	10	LTKKKEAWSEKIGRTVRLVKVEV--LDVGDFNALSDDGVRIILGWDGGVAFLVSATA	67
DB	14	LTSKNKA---HLKGNVIVRKTVGLDVTSTAGSLDDGIGEFLG--RGVTCQLISSTV	67
QY	68	APDSNGRGKVGKAAHLEBAEVVLSKTADGETVYRVSFWD--ESQIGPAVLVRNLQAE	126
DB	68	VDPNNNGRKLGAELSQWLNPPLLSSENQPVFTFWEVEKQIGPAILIIVKXNHASE	127
QY	127	FELKTLTLEGVPKGTVVFVANSVYPHKLYSQERFFPANDTYLPSKMPAALVVPQDEL	186
DB	128	FELKITLNDVPGHTIVFVANSMIYQSKRYNRVFFSNDTYLPQMPPALKRPVDDDEL	187
QY	187	KILRGDDNFGPYQEHRDYRYDYNDLGDDPKGEHARPILGSQHYPFRRCRTGRHPT	246
DB	188	RNLRGDDQQGPYQEHRDYRYDVYNDLGLPSDG--NPRPVLGGTKELPYPRCRTRGXPT	245
QY	247	KDQPNSESRLFLLNLNIYVPRDERFCHLKMSDFLGYSLKTII EAVLPTLTGTVDTPKEF	306
DB	246	KSDPNSESRLTLVDGDVVYVPRDEPFCHI KKSDFGYAIKALVANVAIPALTITVDLSPEGF	305
QY	307	DSFEIDILGIYELGPAPNPIIAIRKKIIESEFLRSILPNGSHDHDKPLMPLNVTKSVL	366
DB	306	DSFKDIMKIYEGGILPKI PALEDLRQFPLELVKVGLVPGG-DYLLKLPMQLIKED--	362
QY	367	KXAPFEKGWRTDEBFARETLAGNPVI I KRLTFEPKASTLDPQVGDTHSKI TEAHIRH	426
DB	363	-----KTGMWTDEFGRILLAGYNPLMVRLTFEPPRSLSDFSKYGDHSTIREADLEN	416
QY	427	NMGGLSVQNALNKRLFLTLDHHDFMPYDLBINELEGNFIYASRTLFLFKDDGTLKPALAI	486
DB	417	KLEGLTVQCALHGRLYLILDHDFNMFLVRVNSLEGNFIYATRVLFLRGDGLVPAI	476
QY	487	EUSLPHPDGQRGASKVYTP-AHTGVGHVWOLAKAYACVNDSAMWHQLISHLMNHAVI	545
DB	477	EUSLPELSDGLTTAKSTVYTPKSTTGAEAWHWHLAKAYANVNDYCVHQLISHLWNTHVM	536
QY	546	EPFVLTANROLSSVHPVHKLLSPHYRDTLNALAQTLINAGGVPERTVFPKALCMS	605
DB	537	EPFVLTANROLSSVTHPVHKLLLPHYRDTMINSNARQMLVNAGGITVTFPRQAFEMS	596
QY	606	ADVYKSNWFNQALPADLVKRGVAVPDOSSPYGVRLIKIDPYAVDGLVIMWAIBRWYKE	665
DB	597	SVIYKDWNFTEQALPDDLITKGNMAVADPSSPYKRVRLVEDPYPASGLAIMHAIBQWYTE	656
QY	666	YLDIYYPNDELORDVELQAWKEVREAEAGDLKDQWMPMDTVOOLARACTTIIWAS	725
DB	657	YLAVYYPNDGVLRADVELQAWKEAREVGHADLKDAFWPKQTVAELVKACTTIINIATAS	716
QY	726	ALHAAVNTFGQYPIAGYLPNRFPTASRRPMPFGSHDYKCLGAGQEKADMVPIRTITSQFT	785

Db	717	ALHAAVNFQGYAGYGLPNRPVSVKKMPAPGSDYAEI	--ERKPEKVFPVRTITSQFOA	773		
Qy	786	ILGISLIEILSHSHSDEVYLGQRPDRWTSDAKALDAFKFQSR	LVQIENRIKTMNDSP	845		
Db	774	LVGISLLEILSHSHSDEVYLGQRTKE	WTSDAKAQAFKFGARL	TEIEKRVVTNNADP	832	
Qy	846	DLKRNKGPVEMPYMLLYNTSDVTGKARGITAMGIPNSIS	I	887		
Db	833	RLKRNRPAPFPYLLYNTSDTKGD	AAGITAKGIPNSIS	I	873	
RESULT	9					
Q42847	ID	Q42847	PRELIMINARY;	PRT;	864	AA.
AC	Q42847;					
DT	01-NOV-1996	(TRENBLrel. 01,	Created)			
DT	01-NOV-1996	(TRENBLrel. 01,	Last sequence update)			
DT	01-OCT-2003	(TRENBLrel. 25,	Last annotation update)			
DE	Lipoxigenase 2	(EC 1.13.11.12)				

RESULT 9

QD2847	
ID	Q42847 PRELIMINARY; PRT; 864 AA.
AC	Q42847;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Lipoxygenase 2 (EC 1.13.11.12).
GN	LOXC
OS	Hordeum vulgare (Barley).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
OC	Triticeae; Hordeum.
OX	NCBI_TaxID=4513;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=99308521; PubMed=10380814;
RA	van Mechelen J.R.; Schuurink R.C.; Smits M., Graner A., Douna A.C.,
RA	Sedee N.J., Schmitt N.F., Valk B.E.;
RT	"Molecular characterization of two lipoxygenases from barley.";
RL	Plant Mol. Biol. 39:1283-1298(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Van Mechelen J.R.;
RA	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; LJ37358; AAB70865.1; -.
DR	PIR; T05945; T05945.
DR	HSPG; P08170; 2SBL.
DR	GO; GO:0005506; F:iron ion binding; IEA.
DR	GO; GO:0016165; F:lipoxygenase activity; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0008110; F:electron transport; IEA.
DR	InterPro; IPR000907; Lipoxygenase.
DR	InterPro; IPR001024; Lipoxygenase_LH2.
DR	InterPro; IPR008976; PLAT LH2.
DR	Pfam; PF00305; lipoxygenase; 1.
DR	Pfam; PF01477; PLAT; 1.
DR	PRINTS; PR00087; LIPOXYGENASE..
DR	SMART; SM00308; LH2; 1.
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR	PROSITE; PS00095; PLAT; 1.
XO	Oxidoreductase.
SW	SEQUENCE 864 AA; 96748 MW; A15DA282FBF7F9973 CRC64;

Query Match	60.6%	Score 2860;	DB 10;	Length 864;
Best Local Similarity	62.2%;	Pred. No. 5.3e-211;		
Matches 551;	Conservative 117;	Mismatches 188;	Indels 30;	Gaps 11
QY	5	GVADRLTKNKEAWSEKIGRTGVRLLVKVELDVGDFNASLLDGVHRLIGDWDGVAFAQLVS	64	
Db	6	GIVSDLTGGIRGA---HLKGSVLMRKNALDFNDFGAFVMDGVTELLG--RGVTCQLIS	59	
QY	65	ATAADPSNGRGKVGKAAHLEAAV--SLKSTADGTVTYRVSPFWD--ESQSGPGVALVYRN	121	
Db	60	STVVDHNGGKGVGAANLEQWLLPTNLPFITTGKFAVTFDMSVDKLGVPFGAIIYKN	119	
QY	122	LQHAFFFKTUTLGGVPGKGTVPFVANSWYYPHKLVSQRIFPANDTYTPSKMDAALVPY	181	
Db	120	NHASEFFFKTITLDNVPGRTYTFVANSWYYPQAKTYRVRVFANDTYLPHQMPAALXPY	179	
QY	182	RODELKILRGDNDPGPYQEHDRVVRDYDYNLDGDPDKGEEHARPLGGSQEHFYPRRCRT	241	


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Db 93 GKIAYLEKWTATSLTAGDTAFASIDWDSMGVPCALMITNHHESQFYKLTITLDDVL 152
QY 139 GKGTVVAVSWVYVPHKLYQERIFFANDYLSKMPAALVYRQDELKILRGDDNPGPY 198
Db 153 GHGRVHVFCVSWVYPAHRYKYNLFFNKNAYLSQTEPLLRYREBELNLRIGS-GEL 211
QY 199 QEDRVYRYDYNDLGDGPDGEEHARPILGSGEHPYPRCGRPTKKDPSERLFL 258
Db 212 KENDRVYDYAYNDLGSFDPGEYERPVLGSGEYPPRGRGRTKTDHNSERLFL 271
QY 259 LNLNIVPRDERFGLHKLMSDFLGSYKLTITLAVPLTGTVDTPKFEFDEILGYEL 318
Db 272 LSLDIYVPRDERFGLHKLMSDFLGSYKLTITLAVPLTGTVDTPKFEFDEILGYEL 331
QY 319 GPEAPNPLAEIRKKIPSPFLRSILPNSGHDHPLKMPLNIVKSDVLKAPKFKGWT 378
Db 332 GIKLPNGPTLKKLRDRYPWELLKELL-RSDGERFLKFPMDVTKVD-----KSAWIT 382
QY 379 DEEPARETLAGVNPVITIKRTEPPAKSLTPROVGDHTSKITTAHTRHNMGLSVONALR 438
Db 383 DEEPARETLAGVNPVITIKRTEPPAKSLTPROVGDHTSKITTAHTRHNMGLSVONALR 442
QY 439 NKRLFIIDHDFHMPYLDENELGNFIYASRTLLFLKODGTLLKPLAIELSLPHDPQQR 498
Db 443 SNRFIIDHDFHMPYLDENELGNFIYASRTLLFLKODGTLLKPLAIELSLPHDPQQR 501
QY 499 GAVSKVTPAHTGVGHVWOLAKAYACVNDNSAMHQLISHWLNTHAVIEPFIATNRQLSV 558
Db 502 GAVSKVTPAHTGVGHVWOLAKAYACVNDNSAMHQLISHWLNTHAVIEPFIATNRQLSV 561
QY 559 VHPVHKLSPHYRDTLNALQTLNAGGVVETVPPAKYALGWSADVYKSWNECOA 618
Db 562 LHPIHKLQPHFRDTLNALQTLNAGGVVETVPPAKYALGWSADVYKSWNECOA 621
QY 619 LPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVWIAERWVKEIYDIYYPNDGELQ 678
Db 622 LPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVWIAERWVKEIYDIYYPNDGELQ 681
QY 679 RDVLOQWKEVREAHGDLKDRDWPMDTVQOLARACTIITWASALHAANFQOYPY 738
Db 682 SDTELOQWKEVREAHGDLKDRDWPMDTVQOLARACTIITWASALHAANFQOYPY 741
QY 739 AGYLPNPTASRRMPPEPGSHDYKLGAGQKADMFVIRITTSQFOTLIGSLIETLSKH 798
Db 742 AGYLPNPTASRRMPPEPGSHDYKLGAGQKADMFVIRITTSQFOTLIGSLIETLSKH 798
QY 799 SDEVLGQDEPDRWTSKALDAPKRGSLRVQIENRIKTWNSPDLKNRKGPVEMPY 858
Db 799 ATDEIYLQDRTPE-WTSDGEALAAFGFGEKLEIEKRIETRTDRERLKNRVPKMPY 857
QY 859 MLLVYNTSDVTGKAEGLTAMGIPNSISI 887
Db 858 TLLYFSTSDYSRE--GGLTGKGIPIINSISI 884

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RESULT 13

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Q8W4X6 PRELIMINARY; PRT; 862 AA.
AC Q8W4X6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lipoxigenase (EC 1.13.11.12).
GN LOX.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Scorza verde;

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RA Mita G., Gallo A., Pasano P., Zaslura C., Casey R., Santino A.;
RT "Molecular cloning of an almond lipoxigenase gene expressed during the
RL Submitted (NOV-2001) to the EMBL/GenBank/DBSJ databases.
EMBL; AJ418043; CAD10779.2; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxigenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPXYGENASE_1; 1.
DR PROSITE; PS00081; LIPXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 862 AA; 97751 MW; 3FAC9D205DCBCL31 CRC64;

Query Match          57.8%; Score 2730; DB 10; Length 862;
Best Local Similarity 59.0%; Pred. No. 5.5e-201;
Matches 523; Conservative 130; Mismatches 205; Indels 28; Gaps 11;

QY 4 HGVADRLLTGKKEAWSEKIRGTVRLVYKEVLDVGDNFASLLDGVHRLGDDGVAFQV 63
Db 3 HNLFDKITGQSQNGKNGKIKGTIVLMKNVLDNFNFASVLDVRVHLLG--QGVSLQ 60
QY 64 SATAADPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSPFWDSESGQIPGAVLVN 123
Db 61 SADHGDSENGFKGLGEPAVLEWDITITPLTVGDSAYNTVDFEIEIGVPGALLIKNNH 120
QY 124 HAEFFLTKLTLEGVPGKGTVVVAVNSWYYPHKLVSQERIIFPANDTYLPSKNPAALV 183
Db 121 HSEFFLTKVTLVEDVPRGRVHFCVNSWYPAKYTKDRVFNKTFLPSETPLRKYRE 180
QY 184 DELKILRGDDNPGYQEHDRVYVDYNDLGDGPDGEEHARPILGSGEHPYPRCGR 243
Db 181 BELVHLRG-DKGELQEDWRVDYAYNDLGNPKGSKYARPTLGGSGGYPYPRGRTGR 239
QY 244 HPTKDPNSESRL-FLNLNIVPRDERFGLHKLMSDFLGSYKLTITIEAVLFTLGTVD 302
Db 240 PATKDPNSESRIPLIMSLNIVVPRDERFGLHKLSDFLAYALKSIQVQFIRPEALPDKT 299
QY 303 PKGFDSFDIILGYELGPEADNPLIAIRKKIPSEFIRSL-ENGSHDPLKMPNVI 361
Db 300 PNEFDSFDVILKYIGGIPLPEG-LKDKIGNIPAEMLKEIFRTDGA--QLLRFPMPQVI 356
QY 362 KSDVLKKAPEFKGWRITDEEPARETLAGVNPVITIKRTEPPAKSLTPROVGDHTSKITE 421
Db 357 EED-----KSAWRTDEEPARETLAGVNPVITIKRTEPPAKSLTPROVGDHTSKITE 408
QY 422 AHIRNMGGLSVONALNRKLFILDHHDHMPYLDENELGNFIYASRTLLFLKODGTLL 481
Db 409 QDIGNKLDGLTVHEALKQNKLFILDHHDHMPYLDENELGNFIYASRTLLFLKODGTLL 467
QY 482 KPLAIELSLPHDPDQSGGAVSKVYTPAHTGVGHVWOLAKAYACVNDNSAMHQLISHW 541
Db 468 KPLVIELSLPHDPDQSGGAVSKVYTPAHTGVGHVWOLAKAYACVNDNSAMHQLISHW 527
QY 542 HAVIEPFIATNRQLSVVHPVHKLSPHYRDTLNALQTLNAGGVVETVPPAKY 601
Db 528 HAVCEPVVATNRQLSVVHPVHKLSPHYRDTLNALQTLNAGGVVETVPPAKY 587
QY 602 LGMSADVYKSWNECOALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVWIAER 661
Db 588 MELSSVTKDQWTFTEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPYAVDGLVWIAER 647
QY 662 VWKEYLDIYYPNDGELQDVELQAWKEVREAHGDLKDRDWPMDTVQOLARACTIIT 721
Db 648 WVEDYCSFYKTDITIEQEDTELQSWKVELVEEGHGDKKDEPWPWPKMOTREDLVETCTI 707

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QY 722 WVASALHAANFGQVYAGYLPNRPRTASRRPMPEFGSHDYKLGAGQKADWVFIRTTTS 781
 Db 708 WTASALHAANFGQVYAGYLPNRPRTLSKFWPEKGTPEYKEL-----ESSPDVFLKTITA 764
 QY 782 QFQTILGISLILSHSDEVLGQRPDWTSDAKALDAFKFSGSLRVLQIENRIKTM 841
 Db 765 QLOTVGLIALIELSRHSDEVLGQRTPE-WTADTEPLKAFDKFGKRLAKIEDRITMS 823
 QY 842 NPSDPLKRNKRGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSIS 887
 Db 824 NNDKLNKRGVPMKPYTLFFPTSG-----GLTGRGIPNSVSI 862

RESULT 14
 Q43800 PRELIMINARY; PRT; 862 AA.
 AC Q43800;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lipoxigenase (EC 1.13.11.12).
 GN LOX1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wisconsin 38;
 RA Veronesi C., Fournier J., Rickauer M., Marolda M.,
 RA Esquerre-Tugay M.T.;
 RT "Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA
 (PG895-009).";
 RL Plant Physiol. 108:1342-1342(1995).
 DR EMBL; X84040; CAA58859.1; -.
 DR PIR; S57964; S57964.
 DR HSP; P08170; 2SBL.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016165; F:lipoxigenase activity; IEA.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000907; Lipoxigenase.
 DR InterPro; IPR01024; Lipoxigenase_LH2.
 DR InterPro; IPR008976; PLAT_LH2.
 DR Pfam; PF00305; Lipoxigenase_1.
 DR Pfam; PF01477; PLAT_1.
 DR PRINTS; PR00087; LIPOXYGENASE.
 DR SMART; SM00308; LH2; 1.
 DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
 DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
 DR PROSITE; PS00095; PLAT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 862 AA; 97552 MW; D2E7B8D323D5CE34 CRC64;

Query Match 57.7%; Score 2724.5; DB 10; Length 862;
 Best Local Similarity 59.9%; Pred. No. 1.4e-200;
 Matches 533; Conservative 111; Mismatches 215; Indels 31; Gaps 11;
 QY 1 MFHGVADRLTGKNEANSEG-KIRGTVRLVKKEVLVDGDFNASILQGVHRLGWDGVA 59
 Db 1 MFELIVDAITGK-----DGKVKGTVLMKQNVLDFTDINASVLDGVLEFLG--RRVS 53
 QY 60 FQLVSATAADPSNGRGKVGKAAHLEAVSLKSTADGETVYRVSWFEDSQ-GIPGAVL 118
 Db 54 LELISSVNADPANGLOQKRKAALVLENLNTSTPIAAGESAFRTVFDWDBEEFGVPGAFI 113
 QY 119 VRNLQHAFFKLTLEGVPGKGTWVFVANSWVPHKLYSRIFFANDTLPKMAAL 178
 Db 114 IKNLHFSEFFKLSLTLEVPNHGKVFVNCNSWVPAKYSKSDRIFFANQAYLPSETPTL 173
 QY 179 VPYRQDELKILRGDDNPGFYQEHDRVYRYDYNLDGDPDKGEEHARPILOGSQSHHPYPR 238

Db 174 RKYRENLVTLRG-DGTGKLEWDRVYAYYNDLGDPKQDLSFVLGSGSEYYPYPR 232
 QY 239 CRTGRHPTKDPNSESL-FLNLNLVYPRDERFGLKMSDPLGYSLKTIIEAVLPTLGT 297
 Db 233 GRTGRKPTKDPNSESRIPLLMSLDIYVPRDERFGLKLSDFLTALKSIQVLLPEFKA 292
 QY 298 FVDTTPKPFOSFDIILGVELGPEANPNLIABIRKIPSEFLRSILPNSGHDHPLKML 357
 Db 293 LFDSTHNEFDSFEDVLKLYEGGKLPQGLLKAITDSIPLEILKELL-RSDGRLKYPT 351
 QY 358 PNKSDVLKKAPEFKFGWRTDEEFARETLAGVNPVIKELTEFFPAKSTLDDPROYGDHNS 417
 Db 352 PQVIQED-----KTAWRTDEEFREMLAGVNPVILSELQFPPKSLDKPIYGNQNS 403
 QY 418 KITEAHIRNMGGLSVQNALRNKRLFILDHHDHFMPLYDEINELEGNFYASTLLFLKD 477
 Db 404 TITREQIEDKLDGLTIDEAKTNRLFILNHDILMPLYLRINTSTDTKTYASTLLFLQD 463
 QY 478 DGTLPKPLATELSLPHDPGQGRGAVSKVYTPAHTGVGHVWOLAKAYACVNDSAWHOLISH 537
 Db 464 NGTLKPSALELSLPHDPGQGFQAVSKVYTPADQGVGSIWOLAKAYAAVNDSGVHOLISH 523
 QY 538 WLNTHAVIEPFIATNRQLSVVHPVHKLSLPHYRDTLNINALARQTLINAGGVFEFTVPP 597
 Db 524 WLNTHAIEPFIATNRQLSALHPHYKLLHPHRETMINALARQTLINGGLLELTVPF 583
 QY 598 AKYALGMSADVYKSWNFNEQALPADLVKGVAVPDQSSPGVRLLIKDYPAVDGLVIW 557
 Db 584 AKYSMEMSAVYKDWYFPEQALPTDLIKRGVAVEDSSPLGIRLLTQDYPYAVDGLKIWS 643
 QY 658 AIERWVKYLDIYYPNDGLQRLDELQAWKVEEHAHGDLDKRDWPMRMTVQQLARAC 717
 Db 644 AIKSWTEYCNYYKSDDAVQKDTLQAWKLEEGHGDKDEPWPWPMQVQLIDSC 703
 QY 718 TTIWVASALHAANFGQVYAGYLPNRPRTASRRPMPEFGSHDYKLGAGQKADWVFIR 777
 Db 704 TITWIASALHAANFGQVYAGYLPNRPRTLSRPFPEGSPEYBEL---KTNPKVFLK 760
 QY 778 TITSQFQTLIGSLILSHSDEVLGQRPDWTSDAKALDAFKFSGSLRVLQIENK 837
 Db 761 TITPQTLIGSLILSHSDEVLGQRPDWTSDAKALDAFKFSGSLRVLQIENK 819
 QY 838 IKTMNDSPDLKRNKRGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSIS 887
 Db 820 IMQMVNDKRNKRGVEMPYMLLYPNTSDVTGKAEGLTAMGIPNSIS 862

RESULT 15
 Q93WZ2 PRELIMINARY; PRT; 865 AA.
 AC Q93WZ2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Bacterial-induced lipoxigenase (EC 1.13.11.12).
 GN LOX1.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OC NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Reba B50; TISSUE=Cotyledon;
 RA Assigbetse K., Jalloul A., Delannoy E., Marmey P., Daniel J.-F.,
 RA Geiger J.-P., Nicole M.;
 RT "Gossypium hirsutum bacterial-induced lipoxigenase mRNA";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF361893; AAK50778.2; ...
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016165; F:lipoxigenase activity; IEA.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR000907; Lipoxxygenase.
DR InterPro: IPR010104; Lipoxxygenase_LH2.
DR InterPro: IPR008976; PLAT_LH2.
DR Pfam: PF00305; Lipoxxygenase; 1.
DR Pfam: PF01477; PLAT; 1.
DR PRINTS: PR00087; LIPOXYGENASE.
DR SMART: SM00308; LH2; 1.
DR PROSITE: PS00711; LIPOXYGENASE_1; 1.
DR PROSITE: PS00081; LIPOXYGENASE_2; 1.
DR PROSITE: PS00095; PLAT; 1.
KW Oxidoreductase.
SQ SEQUENCE 865 AA; 98685 MW; 695CAC4E4A3BCE37 CRC64;

Query Match 57.5%; Score 2714.5; DB 10; Length 865;

Best Local Similarity 60.7%; Pred. No. 8.6e-200;

Matches 537; Conservative 102; Mismatches 219; Indels 27; Gaps 11;

QY	4	HGVADRLTGKKEAWSEKIRGTVLVAKVEYLDVGDNFASLLDGVHRLGMDGVAFLV	63
DB	7	HAVAGDDNG-NKKWKPE-KIRGTVVVQKNVLDNFHAFDGFHLLG--KRVSFQLI	62
QY	64	SATAADPSNGRGKVGKAAHLEEAVALSKSTADGETVYRVSEFENDESQGI	123
DB	63	SSQHVADADNGLQGLKGLKAYLEDWNSTETSAVAGESKFDVDFEIEIGLPGAF	122
QY	124	HAERFLKTLLEGVPGKTVVVFVANSVYVPHKLYSQERIIFANDTYLPSKMPAAL	183
DB	123	HSEFYKTLTLHEVPGHGRFHVCSWVYDPKKYDNPVFTNKTYLPHDMPKPLQY	182
QY	184	DELKILRGDDNPGYQBEHDRVYRYDNDLGDPKBEHARPIIGSQEHYPRRCRT	243
DB	183	QELMTLRG-NGQGLQEWDRVYDVAIYNDLGNPKPEYARVLGGSVKYPPRRGT	241
QY	244	HPTKKDPSSESL-FLNLNIYVPRDERFGLKMSDFLGYSLKTII	302
DB	242	PPAKSDPKTESRIIFLLSLNIYVPRDERFGLKMSDFLAYALKSI	301
QY	303	PKFEDSFEDILGLYELAPEANNPLIAEIRKIPSEFRLSILPNSGSHDHLKMP	362
DB	302	HNEFDSLEDVLKLYGGVKLPSGFLDNIINNIPLMLKEIF-RTDEAQLKFPVQ	360
QY	363	SDVLKKAPEFEGHRTDEEPARETAGVNPVIRKLTPEPAKSTLDPQYGDHTSK	422
DB	361	-----DSKTARTDEEPAREMLAGVNPVIRLQEFSPASNLDPKVGYNQNSA	412
QY	423	HIRNMGSLSYONALRNKRLFILDHDFMPYLDINELEGNFYASRTLLFLKDDG	482
DB	413	HIENLEGLTVEEALRTNRLFILDHDSLMPLRINTTTK-TYASRTILLRNDG	471
QY	483	PLATELSLPHDPGQGRGAVSKVYTPAHTGVEGHVWQAKAYACVNDGSAWHL	542
DB	472	PLVIELSLPHENGLGAVNKVYTPAEHGVGEGSIWQAKAYAVVNDGSAHQLI	531
QY	543	AVIEPFVIATNRQLSVVHPVHKLSPHYRDTLINALAROTLINAGGVFERTVP	602
DB	532	AMEEFTVIATNRQLSVVHPVHKLSPHYRDTMINAFARILLNGGVLELTVP	591
QY	603	GMSADVYSKWNFNQALPADLVKGVAVPQSSPYGVRLLIKOYPYAVDGLVIW	662
DB	592	EMSSVIYKSMNLLDQALPRDLKKGAVVDDKSSPHGLRLIKDYPYAVDGLVI	651
QY	663	VKEYLDIYPNDGLQDELQAWKVEEAEAGDLKDRDMPRMDTVQOLARACTII	722
DB	652	VRDYCSFYTKTDENVQDPELQAWKELREEGHGDKEDEPNWPMQTRRELID	711
QY	723	VASALHAAVNFGQYFYAGYLPNRPTRASRRMPPEFGSHDYKKLGAGQKEA	782
DB	712	VASALHAAVNFGQYFYAGYLPNRPTRASRRMPPEFGSHDYKKLGAGQKEA	768
QY	783	FOTILGISLILSKHSDDEVILQORDEPDRWTSDAKALDAFYRFGSRLVQI	842
DB	769	LOTLLGISLILSKHSDDEVILQORASPE-WTSDETPLAAPDFGKRLTGIE	827

QY 843 DSPDLKRRKGPVEMPVMLLYPNNTSDVTGKAEGLTAMGIPNSISI 887
DB 828 NDEQLKRVGVPMVETLLYPTSEG-----GLTGKGIPIINSVSI 865

Search completed: March 23, 2004, 07:00:58
Job time : 83 secs